

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: July 29, 2004, 09:19:04 ; Search time 16 seconds
(without alignments)
96.192 Million cell updates/sec
Title: US-09-661-992B-105
Perfect score: 80
Sequence: 1 CXYGNSPKGFAYXC 16
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 253366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 2772
Minimum DB seq length: 0
Maximum DB seq length: 16
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database : PIR.78:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	31.2	15	2 A36279	chemoattractant pr
2	25	31.2	15	2 PH1443	T-cell receptor al
3	24	30.0	14	1 NPG14	hypothalamic tetra
4	24	30.0	15	2 S51735	T-cell receptor be
5	24	30.0	15	2 A53085	lipid transfer pro
6	24	30.0	15	2 PH1435	T-cell receptor al
7	23	28.7	9	2 A28495	conopressin G - co
8	23	28.7	9	2 G41946	T-cell receptor ga
9	23	28.7	9	2 S39040	lysine-conopressin
10	23	28.7	13	2 S47358	T-cell antigen rec
11	23	28.7	14	2 PH1608	Ig H chain V-D-J r
12	23	28.7	15	2 PN0144	serine proteinase
13	22	27.5	13	2 PH0796	T-cell receptor al
14	21	26.2	8	2 PQ0701	unidentified 6.5/3
15	21	26.2	12	2 PH1182	T-cell receptor al
16	21	26.2	12	2 PH1174	T-cell receptor al
17	21	26.2	12	2 B49033	T-cell receptor de
18	21	26.2	14	2 S57572	T-cell receptor V-
19	21	26.2	15	2 S26517	T-cell receptor al
20	21	26.2	15	2 S26518	T-cell receptor al
21	21	26.2	15	2 PA0036	glycine cleavage s
22	21	26.2	15	2 PH1441	T-cell receptor al
23	21	26.2	16	2 PH1317	Ig heavy chain DJ
24	20	25.0	9	2 B28495	conopressin S - co
25	20	25.0	9	2 A29477	diuretic neurotict
26	20	25.0	9	2 S06375	arginine vasotocin
27	20	25.0	9	2 B61364	vasotocin - common
28	20	25.0	9	2 PD0027	pev-tachykinin - p
29	20	25.0	10	2 A61131	hydrin 2 - bullfro

30 20 25.0 11 2 S19775 wound-induced prot
31 20 25.0 12 2 A33900 hydrin 1 - African
32 20 25.0 12 2 PH1171 T-cell receptor al
33 20 25.0 13 1 UNBO neurotensin - bovi
34 20 25.0 13 2 JQ1350 hypothetical prote
35 20 25.0 14 2 PH1586 Ig H chain V-D-J r
36 20 25.0 15 2 S26515 T-cell receptor al
37 20 25.0 15 2 PA0046 protein Qa100044 - r
38 20 25.0 15 2 PH1610 Ig H chain V-D-J r
39 20 25.0 15 2 PH0751 T-cell receptor be
40 20 25.0 16 2 A44897 ferredoxin-NADp re
41 19 23.8 8 2 PH0934 T-cell receptor be
42 19 23.8 9 2 A61363 bradykinin - commo
43 19 23.8 9 2 S65433 bradykinin - horn
44 19 23.8 9 2 A43065 hydroxyproline-3-b
45 19 23.8 10 2 S70721 heat shock protein

ALIGNMENTS

RESULT 1
A36279
chemoattractant protein - earthworm (Lumbricus terrestris) (fragment)
C;Species: Lumbricus terrestris (common earthworm)
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 30-Sep-1993
C;Accession: A36279
R;Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.
J. Biol. Chem. 265, 8736-8744, 1990
A;Title: Purification and characterization of a chemoattractant from electric shock-ind
snakes.
A;Reference number: A36279; MUID:90256800; PMID:2160465
A;Accession: A36279
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <JIA>
Query Match 31.2%; Score 25; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 PKGFAY 13
DB 5 PRGFTY 10

RESULT 2
PH1443
T-cell receptor alpha chain (clone A3/H2R2) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
C;Accession: PH1443
R;Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K
J. Exp. Med. 177, 811-820, 1993
A;Title: T cell receptor selection by and recognition of two class I major histocompatil
A;Reference number: PH1430; MUID:93171821; PMID:8436911
A;Accession: PH1443
A;Molecule type: mRNA
A;Residues: 1-15 <CAS>
A;Experimental source: cytolytic T-lymphocyte
C;Superfamily: immunoglobulin homology
C;Keywords: receptor; T-cell
Query Match 31.2%; Score 25; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PKGFA 12
DB 5 PRGFA 9

RESULT 3

NYPG14

hypothalamic tetradecapeptide - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 23-Aug-1996
 C:Accession: A01419
 R:Schlesinger, D.H.; Niall, H.D.; Linthicum, G.L.; Dupont, A.; Schally, A.V.
 submitted to the Atlas, November 1976
 A:Reference number: A01419
 A:Accession: A01419
 A:Molecule type: protein
 A:Residues: 1-14 <SCH>
 C:Superfamily: hypothalamic tetradecapeptide
 C:Keywords: amidated carboxyl end; hypothalamic
 F:14/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 30.0%; Score 24; DB 1; Length 14;
 Best Local Similarity 80.0%; Pred. No. 6.6e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNP 8
 |||||
 Db 3 YGKGP 7

RESULT 4

S51735
 T-cell receptor beta-chain joining region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
 C:Accession: S51735
 R:Durinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.
 submitted to the EMBL Data Library, November 1993
 A:Reference number: S51732
 A:Accession: S51735
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-15 <BUR>
 A:Cross-references: EMBL:Z28344; NID:g607122; PIDN:CAA82198.1; PID:g607123
 C:Keywords: T-cell receptor

Query Match 30.0%; Score 24; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 7e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GNSPKGF 11
 |||||
 Db 9 GNQPKHF 15

RESULT 5

A53085
 lipid transfer protein - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
 C:Accession: A53085
 R:Ko, K.W.; Oikawa, K.; Ohnishi, T.; Kay, C.M.; Yokoyama, S.
 Biochemistry 32, 6729-6736, 1993
 A:Title: Purification, characterization, and conformational analysis of rabbit plasma li
 A:Reference number: A53085; MUID:93320050; PMID:8329397
 A:Accession: A53085
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <KOL>
 A:Experimental source: plasma
 A>Note: sequence extracted from NCBI backbone (NCBIP:135263)

Query Match 30.0%; Score 24; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 7e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PKGFAY 13
 |||||
 Db 2 PKGASY 7

RESULT 6

PH1435
 T-cell receptor alpha chain (clone 223/27) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 C:Accession: PH1435
 R:Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Ko
 J. Exp. Med. 177, 811-820, 1993
 A:Title: T cell receptor selection by and recognition of two class I major histocompatib
 A:Reference number: PH1430; MUID:93171821; PMID:8436911
 A:Accession: PH1435
 A:Molecule type: mRNA
 A:Residues: 1-15 <CAS>
 A:Experimental source: cytolytic T-lymphocyte
 C:Superfamily: immunoglobulin homology
 C:Keywords: receptor; T-cell

Query Match 30.0%; Score 24; DB 2; Length 15;
 Best Local Similarity 83.3%; Pred. No. 7e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 SPKGFA 12
 |||||
 Db 4 SDKGFA 9

RESULT 7

A28495
 conopressin G - cone shell (Conus geographus)
 N:Alternate names: Lys-conopressin-G
 C:Species: Conus geographus (geography cone)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 25-Apr-1997
 C:Accession: A28495
 R:Cruz, L.J.; de Santos, V.; Zafaralla, G.C.; Ramilo, C.A.; Zeikus, R.; Gray, W.R.; Oliv
 J. Biol. Chem. 262, 15821-15824, 1987
 A:Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from C
 A:Reference number: A92617; MUID:88058932; PMID:3680228
 A:Accession: A28495
 A:Molecule type: protein
 A:Residues: 1-9 <CRU>
 C:Superfamily: oxytocin-neurophysin
 C:Keywords: amidated carboxyl end; venom
 F:1-6/Disulfide bonds: #status experimental
 F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 28.7%; Score 23; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSPKG 10
 |||||
 Db 5 NCPKG 9

RESULT 8

G41946
 T-cell receptor gamma chain (2t.23) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C:Accession: G41946
 R:Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
 Mol. Cell. Biol. 11, 5902-5909, 1991
 A:Title: Rearrangement and functional-site sequence analyses of T-cell receptor gamma ge
 A:Reference number: A41946; MUID:92049316; PMID:1658619
 A:Accession: G41946
 A>Status: preliminary; not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-9 <WHE>
 C:Keywords: T-cell receptor

Query Match 28.7%; Score 23; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNSPKGF 11
||: ||
Db 2 YGSYSSGF 9

RESULT 9
S39040
lysine-conopressin - Erpobdella octoculata
C:Species: Erpobdella octoculata
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C:Accession: S39040
R:Salzet, M.; Bulet, P.; van Dorsseleer, A.; Malecha, J.
Eur. J. Biochem. 217, 897-903, 1993
A:Title: Isolation, structural characterization and biological function of a lysine-conopressin from the leech Erpobdella octoculata
A:Reference number: S39040; MUID:94039146; PMID:8223646
A:Accession: S39040
A:Molecule type: protein
A:Residues: 1-9 <SAL>

Query Match 28.7%; Score 23; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSPKG 10
||: ||
Db 5 NCPKG 9

RESULT 10
S47358
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47358
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell epitopes
A:Reference number: S47355
A:Accession: S47358
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35682; NID:G527453; PIDN:CAA84751.1; PID:G527454
C:Keywords: T-cell receptor

Query Match 28.7%; Score 23; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.2e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNSPKGF 11
||: ||
Db 6 YRNQPOHF 13

RESULT 11
Ph1608
Ig H chain V-D-J region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: Ph1608; Ph1603
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A:Reference number: Ph1580; MUID:93301609; PMID:8315387
A:Accession: Ph1608
A:Molecule type: DNA
A:Residues: 1-14 <LEV>
A:Experimental source: bone marrow pre-B lymphocyte, wild-type clone 335
A:Accession: Ph1603
A:Molecule type: DNA

A:Residues: 1-14 <LEV2>
A:Experimental source: bone marrow pre-B lymphocyte, wild-type clone 324
C:Keywords: immunoglobulin

Query Match 28.7%; Score 23; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 9.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNYS 7
|: ||
Db 1 CARVGNYS 7

RESULT 12
PN0144
serine proteinase (EC 3.4.21.-) II - fungus (Acremonium chrysogenum) (fragment)
C:Species: Acremonium chrysogenum
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 27-Jan-1995
C:Accession: PN0144
R:Stepanov, V.M.; Rudenskaya, G.N.; Vasilyeva, L.I.; Krestyanova, I.N.; Khodova, O.M.; I
Biokhimiya 51, 1476-1483, 1986
A:Title: Serine proteinase II from Acremonium chrysogenum.
A:Reference number: PN0144
A:Accession: PN0144
A:Molecule type: protein
A:Residues: 1-15 <STF>
A:Note: article in Russian with English abstract
C:Keywords: hydrolase; serine proteinase

Query Match 28.7%; Score 23; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 NSPKGFA 12
|: ||
Db 7 NAPXGLA 13

RESULT 13
PH0796
T-cell receptor alpha chain (F15) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0796
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex alleles: allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0796
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Cross-references: EMBL:X60901
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 27.5%; Score 22; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXXYGNSPK 9
|: ||
Db 1 CAGTGNTGK 9

RESULT 14
PQ0701
unidentified 6.5/31X protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PQ0701
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993

A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension

A:Reference number: PQ0696

A:Accession: PQ0701

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-8 <KOM>

Query Match 26.2%; Score 21; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. NO. 2.8e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNSPKG 10

Db 1 YGNPVTG 7

RESULT 15

PH1182

T-cell receptor alpha chain V region (Cw3/4A3) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: PH1182

R:Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid

J. Exp. Med. 176, 439-447, 1992

A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A:Reference number: S26512; MUID:92364546; PMID:1380061

A:Accession: PH1182

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-12 <CAS>

Query Match 26.2%; Score 21; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. NO. 1.9e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 SPKGFA 12

Db 4 SDRGFA 9

Search completed: July 29, 2004, 09:22:31

Job time : 16 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 09:15:34 ; Search time 13 Seconds
(without alignments)
64.086 Million cell updates/sec

Title: US-09-661-992B-105
Perfect score: 80
Sequence: 1 CXYGNPKGFAYXXC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 880

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	30.0	7	1 UN06_PINPS	P81675 pinus pinas
2	24	30.0	14	1 HY14_PIG	P01155 sus scrofa
3	23	28.7	9	1 CONO_CONGE	P05486 conus geogr
4	21	26.2	15	1 UC19_MAIZE	P80625 zea mays (m
5	20	25.0	9	1 CONO_CONST	P05487 conus stria
6	20	25.0	9	1 DNFI_LOCHI	P16339 locusta mig
7	20	25.0	9	1 OXYT_CYPCA	P23879 cyprinus ca
8	20	25.0	9	1 TRP4_LEUNA	P81736 leucophaea
9	20	25.0	15	1 CYSK_CLOPA	P81340 clostridium
10	20	25.0	16	1 FENR_STRGR	P24134 streptomyce
11	19	23.8	9	1 OXYF_SCYCA	P42997 scyllorhinu
12	19	23.8	9	1 OXYT_RAJCL	P42994 raja clavav
13	19	23.8	9	1 TKLI_LOCHI	P16223 locusta mig
14	19	23.8	12	1 PSP3_PHYPA	P80662 physcomitri
15	19	23.8	13	1 BRK_FARID	P42717 parapolybia
16	19	23.8	15	1 ACT_FINPS	P81085 pinus pinas
17	18	22.5	9	1 KNL3_BOMVA	P83058 bombina var
18	18	22.5	10	1 PKCK_FASHE	P80525 fasciola he
19	18	22.5	11	1 BRK_MEGEL	P12797 megascolia
20	18	22.5	15	1 UPOI_METAN	P83440 metathidium
21	17.5	21.9	14	1 TKNI_SCHGR	P82470 schistocerc
22	17	21.2	8	1 RS7_MYCIT	P33564 mycobacteri
23	17	21.2	8	1 UF06_MOUSE	P38644 mus musculu
24	17	21.2	9	1 ALI0_CARWA	P81813 carcinus ma
25	17	21.2	9	1 OXYT_EISPO	P42998 eisenia foe
26	17	21.2	10	1 GONI_ALLMI	P37041 alligator m
27	17	21.2	10	1 QBOB_COMTE	P80465 comanchnas t
28	17	21.2	15	1 TERM_BPM2	P19897 bacterioph
29	17	21.2	15	1 UC30_MAIZE	P80636 zea mays (m
30	16	20.0	4	1 ACHI_ACHFU	P35904 achatina fu
31	16	20.0	9	1 OXYA_SCYCA	P42996 scyllorhinu
32	16	20.0	9	1 OXYA_SQUAC	P42999 squalus aca
33	16	20.0	9	1 OXYT_OCTVU	P80027 octopus vul

34	16	20.0	9	1 OXYT_RABIT	P32878 oryctolagus
35	16	20.0	9	1 OXYV_SQUAC	P43000 squalus aca
36	16	20.0	10	1 GONI_CLUPA	P81749 clupea pall
37	16	20.0	11	1 TKN2_UPERU	P08616 uperoleia r
38	16	20.0	12	1 V14K_WSSV	P82606 white spot
39	16	20.0	13	1 PROX_ORYSA	P83647 oryza sativ
40	16	20.0	13	1 PSBP_FINPS	P81668 pinus pinas
41	16	20.0	14	1 TAT_HVI28	P12509 human immun
42	16	20.0	14	1 TAT_HVI28	P12511 human immun
43	16	20.0	15	1 CBPB_PROAT	P19628 protopertus
44	16	20.0	15	1 GUAN_DIDMA	P55936 didelphis m
45	16	20.0	15	1 UC14_MAIZE	P80620 zea mays (m

ALIGNMENTS

RESULT 1					
ID	UN06_PINPS	STANDARD;	PRT;	7 AA.	
AC	P81675;				
DT	15-JUL-1999 (Rel. 38, Created)				
DT	15-JUL-1999 (Rel. 38, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Unknown protein from 2D-page of needles (N141) (Fragment).				
OS	Pinus pinaster (Maritime pine)				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.				
OX	NCBI_TaxID=71647;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Needle;				
EX	MEDLINE=99274088; PubMed=10344291;				
RA	Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,				
RA	Frigerio J.-M., Plomion C.;				
RT	"Separation and characterization of needle and xylem maritime pine				
RT	proteins.";				
RL	Electrophoresis 20:1098-1108(1999).				
CC	-I- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown				
CC	protein is: 6.6, its MW is: 25 kDa.				
FT	NON_TER 1				
FT	NON_TER 7				
SQ	SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;				
Query Match 30.0%; Score 24; DB 1; Length 7;					
Best Local Similarity 80.0%; Pred. No. 1.4e+05;					
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
QY	4 YGNSP 8				
Db	2 YGNLP 6				
RESULT 2					
ID	HY14_PIG	STANDARD;	PRT;	14 AA.	
AC	P01155;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				
DT	21-JUL-1986 (Rel. 01, Last annotation update)				
DE	Hypoallamic tetradecapeptide.				
OS	Sus scrofa (Pig).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9823;				
RN	[1]				
RP	SEQUENCE.				
RA	Schlesinger D.H., Niall H.D., Linthicum G.L., Dupont A.,				
RA	Schally A.V.;				
RA	Submitted (NOV-1976) to the PIR data bank.				
DR	PIR; A01419; NYPG14.				
KW	Amidation.				
FT	MOD_RES 14 14				
FT	AMIDATION.				

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SQ SEQUENCE 14 AA; 1648 MW; 3DDF87E2419D3E47 CRC64;
Query Match 30.0%; Score 24; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 2.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNP 8
DB 3 YGKSP 7

RESULT 3
CONO CONGE STANDARD; PRT; 9 AA.
ID CONO CONGE STANDARD; PRT; 9 AA.
AC P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone)
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; A28495; A28495; Neurhyp_horm.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF0220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1037 MW; D4FC2768B4540059 CRC64;

Query Match 28.7%; Score 23; DB 1; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSPKG 10
DB 5 NCPKG 9

RESULT 4
UC19 MAIZE STANDARD; PRT; 15 AA.
AC P80625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of etiolated coleoptile (Spot 406)
DE (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.6, its MW is: 18.4 kDa.
DR Maize-2DPAGE; P80625; COLEOPTILE.
DR MaizeDB; 123951; -.
FT NON_TER 1 1
FT NON_TER 15 15
FT SEQUENCE 15 AA; 1672 MW; 1CF69D4DA8737F9D CRC64;

Query Match 26.2%; Score 21; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 8.4e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNP 8
DB 8 YGCS 12

RESULT 5
CONO CONST STANDARD; PRT; 9 AA.
ID CONO CONST STANDARD; PRT; 9 AA.
AC P05487;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arg-conopressin S.
OS Conus striatus (Striated cone)
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6493;
RN [1]
RP SEQUENCE.
RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";
RL J. Biol. Chem. 262:15821-15824(1987).
RN [2]
RP REVIEW.
RX MEDLINE=89024586; PubMed=3052286;
RA Gray W.R., Olivera B.M., Cruz L.J.;
RT "Peptide toxins from venomous Conus snails.";
RL Annu. Rev. Biochem. 57:665-700(1988).
CC -!- FUNCTION: Targets vasopressin-oxytocin related receptors.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; B28495; B28495.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF0220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9
FT SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 25.0%; Score 20; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSPKG 10
DB 5 NCPKG 9
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RESULT 6
DNFL LOCOMI STANDARD; PRT; 9 AA.
AC P16339;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locupressin (Diuretic neuropeptide Fl/F2).
OS Locusta migratoria (Migratory locust).
OC Eukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Suboesophageal ganglion, and Thoracic ganglion;
RX MEDLINE=88077077; PubMed=3689410;
RA Proux J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,
RA Delaage M., Schooley D.A.;
RT "Identification of an arginine vasopressin-like diuretic hormone from
RT Locusta migratoria."
RL Biochem. Biophys. Res. Commun. 149:180-186(1987).
CC -!- FUNCTION: DIURETIC HORMONE.
CC -!- SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; A29477; A29477.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Neuropeptide; Amidation.
FT DISULFID 1 6 IN FL.
FT DISULFID 1 1 INTERCHAIN (WITH C-6) (IN F2).
FT DISULFID 6 6 INTERCHAIN (WITH C-1) (IN F2).
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 976 MW; 56EB176EB3451A057 CRC64;

Query Match 25.0%; Score 20; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSPKG 10
DB 5 NCPRG 9

RESULT 7
OXYT CYPCA STANDARD; PRT; 9 AA.
AC P23879;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Vasotocin.
OS Cyprinus carpio (Common carp), and
OS Petromyzon marinus (Sea lamprey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962, 7757;
RN [1]
RP SEQUENCE.
RC SPECIES=C. carpio; TISSUE=Pituitary;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Characterization of neurohypophyseal hormones from a fresh water bony
RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea
RT water bony fishs."
RL Comp. Biochem. Physiol. 14:245-254(1965).
RN [2]
RP SEQUENCE.
RC SPECIES=P. marinus; TISSUE=Pituitary;
RX MEDLINE=86225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawachi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey

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RT (Petromyzon marinus): isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; B61364; B61364.
DR PIR; S06375; S06375.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;

Query Match 25.0%; Score 20; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSPKG 10
DB 5 NCPRG 9

RESULT 8
TRP4 LEUMA STANDARD; PRT; 9 AA.
AC P81736;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 4 (LemRP 4).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RC TISSUE=Midgut;
RX MEDLINE=97053012; PubMed=8897641;
RA Muren J.E., Naessel D.R.;
RT "Isolation of five tachykinin-related peptides from the midgut of
RT the cockroach Leucophaea maderae: existence of N-terminally extended
RT isoforms."
RL Regul. Pept. 65:185-196(1996).
CC -!- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
CC of spontaneous contractions and tonus of hindgut muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Midgut.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 953 MW; 2403987699C865A7 CRC64;

Query Match 25.0%; Score 20; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 SPKGF 11
DB 1 APSGF 5

RESULT 9
CYSK_CLOPA STANDARD; PRT; 15 AA.
AC P81340;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cysteine synthase (EC 2.5.1.47) (O-acetylserine sulphydrylase) (O-
DE acetylserine (thiol)-lyase) (Csease) (Cse) (CP 27) (Fragment).
GN CYSK.

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OS Clostridium pasteurianum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1501;
RN [1]
RP SEQUENCE.
RC STRAIN=W5;
RX MEDLINE=98291870; PubMed=9629918;
RT Flengstrand R., Skjeldal L.;
RT "Two-dimensional gel electrophoresis separation and N-terminal
RT sequence analysis of proteins from Clostridium pasteurianum WS.";
RL Electrophoresis 19:802-806(1998).
CC -!- CATALYTIC ACTIVITY: O(3)-acetyl-L-serine + H(2)S = L-cysteine +
CC acetate.
CC -!- COPACTOR: Pyridoxal phosphate (By similarity).
CC -!- PATHWAY: Cysteine biosynthesis.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the cysteine synthase/cystathionine beta-
CC synthase family.
DR InterPro; IPR001216; Cys synthase BS.
DR PROSITE; PS00301; CYS SYNTHASE; PARTIAL.
KW Transferase; Cysteine biosynthesis; Pyridoxal phosphate.
FT NON_TER 15
FT SEQUENCE 15 AA; 1625 MW; 0196582B9671A352 CRC64;

Query Match 25.0%; Score 20; DB 1; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GNSP 8
DB 7 GNTP 10

RESULT 10
FENR_STRGR : STANDARD; PRT; 16 AA.
ID_FENR_STRGR : STANDARD; PRT; 16 AA.
AC P24134;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Ferredoxin-NAD(+) reductase (EC 1.18.1.3) (Fragment).
OS Streptomyces griseus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1911;
RN [1]
RP SEQUENCE.
RX MEDLINE=92041607; PubMed=1938912;
RA Ramachandra M., Seetharam R., Emptage M.H., Sariafani F.S.;
RT "Purification and characterization of a soybean flour-inducible
RT ferredoxin reductase of Streptomyces griseus.";
RL J. Bacteriol. 173:7106-7112(1991).
CC -!- FUNCTION: COUPLE ELECTRON TRANSFER FROM NADH TO CYTOCHROME
CC P450(SOY) IN THE PRESENCE OF FERREDOXIN.
CC -!- CATALYTIC ACTIVITY: Reduced ferredoxin + NAD(+) = oxidized
CC ferredoxin + NADH.
CC -!- COPACTOR: FAD; requires magnesium.
DR PIR; A44897; A44897.
KW Oxidoreductase; Flavoprotein; NAD; FAD; Magnesium.
FT NON_TER 16
FT SEQUENCE 16 AA; 1485 MW; 27D11A7C37AC0510 CRC64;

Query Match 25.0%; Score 20; DB 1; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 GNSPKGF 11
DB 7 GGGPGGY 13

RESULT 11

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OXVF_SCYCA
ID_OXVF_SCYCA STANDARD; PRT; 9 AA.
AC P42937;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Phasvatocin.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauveau C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
RT fishes: asvatocin and phasvatocin, two oxytocin-like peptides
RT isolated from the spotted dogfish (Scyllorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -!- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1
FT MOD_RES 9
FT SEQUENCE 9 AA; 1016 MW; 17EDD76EB44449DB CRC64;

Query Match 23.8%; Score 19; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNSPKG 10
DB 3 FNNCPVG 9

RESULT 12
OXVT_RAJCL STANDARD; PRT; 9 AA.
AC P42934;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glumitocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hymnosqualea; Pristiogoralea; Batoidea;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE=66123415; PubMed=5880565;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurohypophysal peptides: isolation of a new hormone,
RT glumitocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,
RT the ray (Raja clavata).";
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -!- FUNCTION: ANTIDIURETIC HORMONE.
CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1
FT MOD_RES 9
FT SEQUENCE 9 AA; 984 MW; 17B9C76EB455B04B CRC64;

Query Match 23.8%; Score 19; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;

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Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 NSPKG 10

Db 5 NCPQG 9

RESULT 13

TKL1 LOCMI
ID TKL1 LOCMI STANDARD; PRT; 9 AA.
AC P1623;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locustatachycinin I (TK-I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachycinin I and II, two novel insect neuropeptides with
RL homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990).
CC -!- FUNCTION: Myoactive peptide. Stimulates the contraction of the
CC oviduct and foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
DR PIR; S08285; ECLQIM.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 9 9
SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match 23.8%; Score 19; DB 1; Length 9;

Best Local Similarity 75.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 PKGF 11

Db 2 PSGF 5

RESULT 14

PSP3 PHVPA
ID PSP3 PHVPA STANDARD; PRT; 12 AA.
AC P80662;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Oxygen-evolving enhancer protein 2 (OEE2) (24 kDa subunit of oxygen
DE evolving system of photosystem II) (Fragment).
OS Physcomitrella patens (Moss).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Funariidae; Funariales; Funariaceae; Physcomitrella.
OX NCBI_TaxID=3218;
RN [1]
RP SEQUENCE.
RC TISSUE=Protonema;
RX MEDLINE=97275459; PubMed=9129336;
RA Kasten B., Buck F., Nuske J., Reski R.;
RT "Cytokinin affects nuclear- and plastome-encoded energy-converting
RT plastid enzymes";
RL Planta 201:261-272(1997).
CC -!- FUNCTION: May be involved in the regulation of photosystem II.
CC -!- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex.
CC -!- INDUCTION: By light.
CC -!- SIMILARITY: Belongs to the psbP family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;

KW Multigene family.

FT NON_TER 12

SQ SEQUENCE 12 AA; 1182 MW; 8D2B0D54D7C4DC5 CRC64;

Query Match 23.8%;

Best Local Similarity 50.0%; Score 19; DB 1; Length 12;

Matches 4; Conservative 0; Mismatches 0; Gaps 0;

QY 4 YGNSPKGF 11

Db 2 YGESANVF 9

RESULT 15

BRK PARID
ID BRK PARID STANDARD; PRT; 13 AA.
AC P42717;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Waspkinin.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Mecoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Parapolybia.
OX NCBI_TaxID=31921;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Toki T., Yasuhara T., Nakajima T.;
RT "Isolation and sequential analysis of peptides on the venom sac of
RL Bisei Dobutsu 39:105-111(1988).
CC -!- FUNCTION: Induces smooth muscle contraction.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- SIMILARITY: Belongs to the bradykinin family.
KW Bradykinin; Vasodilator; Pyrrolidone carboxylic acid.
FT MOD RES 1 1
SQ SEQUENCE 13 AA; 1573 MW; 2673CB3D83ECC867 CRC64;

Query Match 23.8%;

Best Local Similarity 60.0%; Score 19; DB 1; Length 13;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PKGFA 12

Db 5 PPGFS 9

Search completed: July 29, 2004, 09:21:19

Job time : 13 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 09:18:34 ; Search time 34 Seconds
(without alignments)
148.479 Million cell updates/sec

Title: US-09-661-992B-105

Perfect score: 80

Sequence: 1 CXYGNPKGFAYXXC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 4499

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SPTEMBL 25:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	30.0	15	4 Q8IZG4	Q8IZG4 homo sapien
2	24	30.0	15	4 Q8IZG3	Q8IZG3 homo sapien
3	24	30.0	15	6 QTRF5	QTRF5 oryctolagus
4	24	30.0	16	10 Q9S8A0	Q9S8A0 pinus monti
5	23	28.7	14	3 Q8J1G0	Q8J1G0 ashbya goss
6	23	28.7	16	2 Q9RP22	Q9RP22 citrobacter
7	23	28.7	16	4 Q3UC99	Q3UC99 homo sapien
8	23	28.7	16	15 Q75710	Q75710 human immun
9	22	27.5	9	15 Q7ZPK1	Q7ZPK1 human immun
10	22	27.5	9	15 Q7ZPU7	Q7ZPU7 human immun
11	22	27.5	12	4 Q9UMQ9	Q9UMQ9 homo sapien
12	22	27.5	12	15 Q9Q0D1	Q9Q0D1 human immun
13	22	27.5	12	15 Q7ZPJ9	Q7ZPJ9 human immun
14	22	27.5	14	10 Q945P2	Q945P2 cicier ariet
15	22	27.5	16	4 Q8J026	Q8J026 homo sapien
16	21.5	26.9	11	11 Q9QXM6	Q9QXM6 mus musculus

17	21	26.2	10	2 Q48469	Q48469 klebsiella
18	21	26.2	10	6 Q8MJ78	Q8MJ78 bos mutus g
19	21	26.2	10	11 Q9QVJ7	Q9QVJ7 mus sp. mep
20	21	26.2	11	7 Q19718	Q19718 homo sapien
21	21	26.2	13	10 Q43174	Q43174 solanum tub
22	21	26.2	16	2 Q99374	Q99374 staphylococ
23	21	26.2	16	10 Q8RVF4	Q8RVF4 zea mays (m
24	21	26.2	16	10 Q40656	Q40656 oryza sativ
25	20	25.0	11	4 Q75811	Q75811 homo sapien
26	20	25.0	11	10 Q41131	Q41131 lycopersico
27	20	25.0	11	13 Q9PS22	Q9PS22 xenopus lae
28	20	25.0	13	6 Q8WNS4	Q8WNS4 bos taurus
29	20	25.0	13	11 Q8QWZ0	Q8QWZ0 rattus sp.
30	20	25.0	15	3 Q14379	Q14379 schizosacch
31	20	25.0	15	4 Q9UCH0	Q9UCH0 homo sapien
32	20	25.0	15	10 Q9S8V7	Q9S8V7 triticum ae
33	20	25.0	15	12 Q69353	Q69353 herpes simp
34	20	25.0	16	10 Q84RM4	Q84RM4 boea crassi
35	19	23.8	10	2 Q44693	Q44693 bacillus am
36	19	23.8	10	13 Q90Y93	Q90Y93 gallus gall
37	19	23.8	11	2 Q47345	Q47345 escherichia
38	19	23.8	11	12 Q89616	Q89616 avian infec
39	19	23.8	12	4 Q9UMZ8	Q9UMZ8 homo sapien
40	19	23.8	12	5 Q17140	Q17140 crassostrea
41	19	23.8	12	6 Q8MJQ0	Q8MJQ0 saguinus fu
42	19	23.8	12	6 Q8MJP8	Q8MJP8 callinico g
43	19	23.8	12	6 Q8MCP7	Q8MCP7 callithrix
44	19	23.8	12	6 Q8MCP9	Q8MCP9 leontopithe
45	19	23.8	12	6 Q8MJE3	Q8MJE3 saimiri sci

ALIGNMENTS

RESULT 1

Q8IZG4 PRELIMINARY; PRT; 15 AA.
ID Q8IZG4;
AC Q8IZG4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SSX2/SS18 fusion protein (Fragment).
GN SSX2/SS18 FUSION.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wei Y., Sun M., Wang J., Zhu X., Larsson C., Dwight T., Xie Y.,
RA Nilsson G., Larsson O.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY138494; AN39536.1; -;
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1590 MW; D969CBED245AFEB2 CRC64;

Query Match 30.0%; Score 24; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 15e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GNSPKG 10
|||
Db 10 GNLPEG 15

RESULT 2

Q8IZG3 PRELIMINARY; PRT; 15 AA.
ID Q8IZG3;
AC Q8IZG3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

```

DE SSX2/SS18 fusion protein (Fragment).
GN Homo sapiens (Human).
OS SSX2/SS18 FUSION.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_TaxID=9606;
RP SEQUENCE FROM N.A.
RA Wei Y., Sun M., Wang J., Zhu X., Larsson C., Dwight T., Xie Y.,
RA Nilsson G., Larsson O.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV138495; AAN39537.1; -.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1590 MW; D969CBED245AFEB2 CRC64;

Query Match 30.0%; Score 24; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GNSPKG 10
DB 10 GNLPEG 15

RESULT 3
QSTRFS PRELIMINARY; PRT; 15 AA.
ID Q9TRFS
AC Q9TRFS
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Lipid transfer protein (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]_TaxID=9986;
RP SEQUENCE.
RX MEDLINE=93320050; PubMed=8329397;
RA KO K.W., Oikawa K., Ohnishi T., Kay C.M., Yokoyama S.;
RT "Purification, characterization, and conformational analysis of rabbit
RT plasma lipid transfer protein."
RL Biochemistry 32:6729-6736(1993).
DR PIR; A53085; A53085.
SQ SEQUENCE 15 AA; 1581 MW; 6F7F95A003BA22E3-CRC64;

Query Match 30.0%; Score 24; DB 6; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PKGPAY 13
DB 2 PKGASY 7

RESULT 4
Q9S8A0 PRELIMINARY; PRT; 16 AA.
ID Q9S8A0
AC Q9S8A0
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Ribulose BIPHOSPHATE carboxylase small subunit (Fragment).
OS Pinus monticola (Western white pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3345;
RN [1]_TaxID=3345;
RP SEQUENCE.
RX MEDLINE=96213005; PubMed=8665095;
RA Ekramoddoullah A.K., Taylor D.W.;
RT "Seasonal variation of western white pine (Pinus monticola D. Don)

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RT foliage proteins."
RL Plant Cell Physiol. 37:189-199(1996).
SQ SEQUENCE 16 AA; 1803 MW; 27D4934C881717DE CRC64;

Query Match 30.0%; Score 24; DB 10; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNSPK 9
DB 7 YGNAAK 12

RESULT 5
Q8JIG0 PRELIMINARY; PRT; 14 AA.
ID Q8JIG0
AC Q8JIG0
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE YPL154 (Fragment).
GN YPL154.
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Ashbya.
OX NCBI_TaxID=33169;
RN [1]_TaxID=33169;
RP SEQUENCE FROM N.A.
RA Alberti-Segui C., Dietrich F., Philippsen P.;
RT "Identification of kinesin-related proteins in the filamentous fungus
RT Ashbya gossypii."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF378570; AAN87141.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 14 AA; 1412 MW; DB6760605D321PCD CRC64;

Query Match 28.7%; Score 23; DB 3; Length 14;
Best Local Similarity 44.4%; Pred. No. 2.2e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNSPKGPA 12
DB 3 FGNAVGLA 11

RESULT 6
Q9RP22 PRELIMINARY; PRT; 16 AA.
ID Q9RP22
AC Q9RP22
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE IntI (Fragment).
GN INTI.
OS Citrobacter freundii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Citrobacter.
OX NCBI_TaxID=546;
RN [1]_TaxID=546;
RP SEQUENCE FROM N.A.
RC STRAIN=CCUG42386; TRANSPOSON=class I integron;
RA Nørskov-Lauritsen N., Sandvang D., Hedegaard J., Fussing V.,
RA Nørskov K.K., Sperling-Petersen H.O., Frimodt-Møller N.,
RA Schønheyder H.C.;
RT "Clonal origin of aminoglycoside-resistant Citrobacter freundii in a
RT Danish county."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF175203; AAD55062.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 16 AA; 1830 MW; 389BB7D833A6115C CRC64;

Query Match 28.7%; Score 23; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;

```

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXXYGNSP 8

Db 9 CYAAGQSP 16

RESULT 7

ID Q9UC99 PRELIMINARY; PRT; 16 AA.

AC Q9UC99;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE EOC-P-1-EOSINOPHIL-chemotactic cytokine (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE

RX MEDLINE=95028770; PubMed=7524281;

RA Schroder J.M., Kameyoshi Y., Christophers E.;

RT "Platelets secrete an eosinophil-chemotactic cytokine which is a

member of the C-C-chemokine family.";

RL Adv. Exp. Med. Biol. 351:119-128(1993).

DR GO; GO:0008009; F:chemokine activity; NAS.

DR GO; GO:0006935; P:chemotaxis; NAS.

FT NON_TER 1

FT NON_TER 16

SQ SEQUENCE 16 AA; 1786 MW; 8B041B46AEACC2A1 CRC64;

Query Match 28.7%; Score 23; DB 4; Length 16;

Best Local Similarity 57.1%; Pred. No. 2.5e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 SPKGFAY 13

Db 8 TPXXFAY 14

RESULT 8

ID Q75710 PRELIMINARY; PRT; 16 AA.

AC Q75710;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Envelope glycoprotein (Fragment).

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ID4-77;

RX MEDLINE=97000995; PubMed=8444025;

RA Wang W.K., Mayer K.H., Essex M., Lee T.H.;

RT "Sequential change of cysteine residues in hypervariable region 1 of

glycoprotein 120 in primary HIV type 1 isolates of subtype B.";

RL AIDS Res. Hum. Retroviruses 12:1195-1197(1996).

DR EMBL; U60160; AAC55027.1; -.

FT NON_TER 1

FT NON_TER 16

SQ SEQUENCE 16 AA; 1750 MW; 9D961C780BFBAB88 CRC64;

Query Match

Best Local Similarity 42.9%; Score 23; DB 15; Length 16;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXXYGNS 7

Db 8 CTDWGN 14

RESULT 9

ID Q7ZPK1

AC Q7ZPK1; PRELIMINARY; PRT; 9 AA.

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Gag protein (Fragment).

GN GAG.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3-022877;

RA Agwale S.M., Zeh C., Paxinos E., Odama L., Pienazek D., Wambele C.,

RA Kalish M.L., Ziermann R.;

RT "Genotypic and Phenotypic Analyses of Human Immunodeficiency Virus

Type-1 in Antiretroviral Drug-Naive Nigerian Patients.";

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY181068; AAC16649.1; -.

FT NON_TER 1

FT NON_TER 9

SQ SEQUENCE 9 AA; 990 MW; 5E16A44879C735B3 CRC64;

Query Match

Best Local Similarity 27.5%; Score 22; DB 15; Length 9;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNSP 8

Db 5 FGNDP 9

RESULT 10

ID Q7ZPJ7

AC Q7ZPJ7; PRELIMINARY; PRT; 9 AA.

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Gag protein (Fragment).

GN GAG.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3-022879;

RA Agwale S.M., Zeh C., Paxinos E., Odama L., Pienazek D., Wambele C.,

RA Kalish M.L., Ziermann R.;

RT "Genotypic and Phenotypic Analyses of Human Immunodeficiency Virus

Type-1 in Antiretroviral Drug-Naive Nigerian Patients.";

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY181070; AAC16653.1; -.

FT NON_TER 1

FT NON_TER 9

SQ SEQUENCE 9 AA; 990 MW; 5E16A44879C735B3 CRC64;

Query Match

Best Local Similarity 27.5%; Score 22; DB 15; Length 9;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNSP 8

Db 5 FGNDP 9

RESULT 11

ID Q9UMQ9

AC Q9UMQ9; PRELIMINARY; PRT; 12 AA.

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

FT NON TER 16 16
SQ SEQUENCE 16 AA; 1733 MW; FF7D79CB38B88EF6 CRC64;
Query Match 27.5%; Score 22; DB 4; Length 16;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 5 GNSPKG 10
|:|:
Db 7 GSQPRG 12

Search completed: July 29, 2004, 09:22:06
Job time : 36 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 09:15:09 ; Search time 51 Seconds
(without alignments)
88.642 Million cell updates/sec

Title: US-09-661-992B-105
Perfect score: 80
Sequence: 1 CXXYGNPKGFAYXXC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 459173

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 29Jan04:*

1: geneseq1980s:*	1	72	90.0	16	4	AAB20444
2: geneseq1990s:*	2	58	72.5	10	4	AAB20388
3: geneseq2000s:*	3	37	46.2	12	2	AAR15366
4: geneseq2001s:*	4	35	43.8	12	3	AAV66808
5: geneseq2002s:*	5	35	43.8	13	7	ABR61868
6: geneseq2003as:*	6	34	42.5	9	3	ABE79021
7: geneseq2003bs:*	7	34	42.5	9	4	AAU07681
8: geneseq2004s:*	8	34	42.5	9	6	ABU61712

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	72	90.0	16	4	AAB20444	Aab20444 Anti-FIX/
2	58	72.5	10	4	AAB20388	Aab20388 Anti-FIX/
3	37	46.2	12	2	AAR15366	Aar15366 Ig idicty
4	35	43.8	12	3	AAV66808	AAV66808 T cell an
5	35	43.8	13	7	ABR61868	ABR61868 Mouse Mab
6	34	42.5	9	3	ABE79021	ABE79021 Lanthioni
7	34	42.5	9	4	AAU07681	AAU07681 Synthetic
8	34	42.5	9	6	ABU61712	ABU61712 Lanthioni
9	32	40.0	16	2	AAR28794	Aar28794 High endo
10	32	40.0	16	2	AAW37605	AAW37605 Synergist
11	32	40.0	16	2	AAW79866	AAW79866 Peptide s
12	31	38.8	9	3	ABE79022	ABE79022 Lanthioni
13	31	38.8	9	4	AAU07682	AAU07682 Synthetic
14	31	38.8	9	6	ABU61713	ABU61713 Lanthioni
15	31	38.8	15	5	AAU07647	Aau07647 Mouse lig
16	31	38.8	16	2	AAR28796	Aar28796 High endo
17	31	38.8	16	2	AAW37607	AAW37607 Synergist
18	31	38.8	16	2	AAW79868	AAW79868 Peptide s
19	30	37.5	9	3	ABE79023	ABE79023 Lanthioni
20	30	37.5	9	4	AAU07683	Aau07683 Synthetic
21	30	37.5	9	6	ABU61714	ABU61714 Lanthioni
22	30	37.5	9	7	ABR84746	ABR84746 Bovine po
23	30	37.5	10	5	ABP62399	ABP62399 Human imm
24	30	37.5	10	6	AAE38105	AAE38105 Human COU
25	30	37.5	11	5	ABP62415	ABP62415 Human imm

26	30	37.5	11	7	ABR63928	ABr63928 Murine C5
27	30	37.5	14	7	ADD23823	Add23823 Breast ca
28	30	37.5	15	2	AAR57170	Aar57170 Peptide "
29	30	37.5	16	2	AAR32784	Aar32784 GVIA omeg
30	29	36.2	9	2	AAW70576	Aaw70576 Vasopress
31	29	36.2	9	5	ABP62425	Abp62425 Human imm
32	29	36.2	10	2	AAW12564	Aaw12564 SH2 bindi
33	29	36.2	10	2	AAW12575	Aaw12575 SH2 bindi
34	29	36.2	10	3	AAW94219	Aaw94219 Murine 16
35	29	36.2	13	4	AAW71019	Aaw71019 Cellulose
36	29	36.2	13	4	AAW71020	Aaw71020 Cellulose
37	29	36.2	16	1	AAW81818	Aaw81818 Sequence
38	29	36.2	16	1	AAW81819	Aaw81819 Sequence
39	29	36.2	16	1	AAW81817	Aaw81817 Sequence
40	29	36.2	16	2	AAR28797	Aar28797 High endo
41	29	36.2	16	2	AAW07990	Aaw07990 gp120 pep
42	29	36.2	16	2	AAW37604	Aaw37604 Synergist
43	29	36.2	16	2	AAW37608	Aaw37608 Synergist
44	29	36.2	16	2	AAW79865	Aaw79865 Peptide s
45	29	36.2	16	2	AAW79869	Aaw79869 Peptide s

ALIGNMENTS

RESULT 1
AAB20444
ID AAB20444 standard; peptide; 16 AA.
XX
XX AAB20444;
AC XX
DT 21-JUN-2001 (first entry)
XX
DE Anti-FIX/FIXa antibody CDR3.
XX
KW Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW complementarity determining region; CDR.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /notes "any amino acid"
FT Misc-difference 3 /notes "any amino acid"
FT Misc-difference 14 /notes "any amino acid"
FT Misc-difference 15 /notes "any amino acid"
FT Misc-difference 15 /notes "any amino acid"
W0200119992-A2.
XX
PD W0200119992-A2.
XX
XX 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-EP008936.
XX
XX 14-SEP-1999; 99AT-00001576.
XX
XX (BAXT) BAXTER AG.
XX
XX Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX WPI; 2001-290358/30.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Claim 7; Page 74; 138pp; English.
XX
XX The present sequence is that of complementarity determining region 3

CC (CDR3) of an antibody having anti-Factor IX (FIX) or anti-activated
 CC Factor IX (FIXa) activity. Such antibodies and their derivatives
 CC (including those that comprise the present CDR3 peptide) have Factor
 CC VIIa (FVIIa) cofactor activity or FIXa activating activity.
 CC Administration of the antibodies or their derivatives leads to an
 CC increase in the procoagulant activity of FIXa, even in the presence of
 CC FVIIa inhibitors. This allows for rapid blood coagulation even in the
 CC absence of FVIII or FVIIa, and in the case of FVIII inhibitor patients.
 CC The antibodies or their derivatives are used in a claimed pharmaceutical
 CC composition for treating patients with blood coagulation disorders,
 CC especially haemophilia A and haemorrhagic diathesis
 XX
 SQ Sequence 16 AA;

Query Match 90.0%; Score 72; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAYXXC 16
 |||||
 Db 1 CXXYGNSPKGFAYXXC 16

RESULT 2
 AAB20388
 ID AAB20388 standard; peptide; 10 AA.
 XX
 AC AAB20388;
 XX
 DT 21-JUN-2001 (first entry)
 XX
 DE Anti-FIX/FIXa antibody 193/AD3 CDR3.

Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;
 Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
 complementarity determining region; CDR.

Mus musculus;

WO200119992-A2.

22-MAR-2001.

13-SEP-2000; 2000WO-EP008936.

14-SEP-1999; 99AT-00001576.

(BAXT) BAXTER AG.

Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
 WPI; 2001-290358/30.

New factor IX/factor IXa antibodies and their derivatives useful for
 increasing amidolytic activity of factor IXa, and for treating blood
 coagulation disorders such as hemophilia A and hemorrhagic diathesis.

Claim 7; Page 74; 138pp; English.

The present sequence is that of complementarity determining region 3
 (CDR3) of the heavy chain of an antibody expressed by mouse hybridoma
 193/AD3. This antibody has anti-Factor IX (FIX) or anti-activated Factor
 IX (FIXa) activity. It is an example of anti-FIX/FIXa antibodies of the
 invention. Such antibodies and their derivatives (including those that
 comprise the present CDR3 peptide) have Factor VIIa (FVIIa) cofactor
 activity or FIXa activating activity. Administration of the antibodies or
 their derivatives leads to an increase in the procoagulant activity of
 FIXa, even in the presence of FVIIa inhibitors. This allows for rapid
 blood coagulation even in the absence of FVIII or FVIIa, and in the case
 of FVIII inhibitor patients. The antibodies or their derivatives are used
 in a claimed pharmaceutical composition for treating patients with blood
 coagulation disorders, especially haemophilia A and haemorrhagic

CC diathesis
 XX
 SQ Sequence 10 AA;
 Query Match 72.5%; Score 58; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 YGNSPKGFAY 13
 |||||
 Db 1 YGNSPKGFAY 10

RESULT 3
 AAR15366
 ID AAR15366 standard; protein; 12 AA.

XX
 AC AAR15366;

XX 25-MAR-2003 (revised)

DT 05-MAR-1992 (first entry)

XX
 DE Ig idiotypic determinant PSL3.

XX Rheumatoid factor; RF; Sie; antigen; light chain; CDR; IGM.

XX Synthetic.

XX
 FH Key

FT Region

FT 1

XX /note= "residue belonging to adjacent framework region"

PN US068177-A.

XX 26-NOV-1991.

PD 05-AUG-1985; 85US-00762698.

XX 05-AUG-1985; 85US-00762698.

XX (SRI) SCRIPPS CLINIC & RES FOUND.

XX Carson DA, Fong S, Chen PP;

XX WPI; 1991-368612/50.

XX Synthetic polypeptide(s) for inducing anti-idiotypic antibodies - useful
 PT for treating auto immune-, endocrine- and rheumatic-diseases and
 PT myasthenia gravis.

XX Claim 23; Page 43; 44pp; English.

XX The sequence is as reported by Capra et al. [(Proc. Natl. Acad. Sci. USA,
 CC 71:4032 (1974); and Proc. Natl. Acad. Sci. USA, 78: 3699 (1981)]. PSL3
 CC means as follows: 'p' designates that the code named material is a
 CC synthetic peptide; the second letter designates the corresp. parent
 CC protein (Sie 88-99); the third letter designates the light (L) chain; the
 CC numeral designates the CDR, the idiotypic antigenic determinant of the
 CC IGM-rheumatoid factor. See also AAR15365-74 and AAR15375. (Updated on 25-
 CC MAR-2003 to correct PA field.)

XX Sequence 12 AA;

Query Match 46.2%; Score 37; DB 2; Length 12;

Best Local Similarity 54.5%; Pred. No. 21;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGF 11

Db 1 CQYGNSPQTF 11

RESULT 4


```

AAV66808
ID AAV66808 standard; peptide; 12 AA.
XX
AC AAV66808;
XX
DT 11-APR-2000 (first entry)
XX
DE T cell antigen receptor Vbeta 12 chain peptide.
XX
KW Rheumatoid arthritis; arthrosis deformans; T-cell antigen receptor;
KW Vbeta chain; autoantigen; immunological tolerance.
XX
OS Homo sapiens.
XX
FN WO9963084-A1.
XX
PD 09-DEC-1999.
XX
PF 28-MAY-1999; 99WO-JP002814.
XX
PR 29-MAY-1998; 98JP-00149855.
PR 14-OCT-1998; 98JP-00328761.
XX
PA (TORI ) TORII PHARM CO LTD.
XX
FI Nishioka K, Yoshino S;
XX
DR WPI; 2000-086978/07.
DR N-PSDB; AAZ96538.
XX
PT T-cell antigen receptor V-beta chain CDR3 region sequences accumulated in
PT synovial membranes of rheumatoid arthritis patients.
XX
PS Example 3; Page 41; 136pp; Japanese.
XX
CC The invention relates to peptide sequences present in the synovial fluid
CC and membranes of rheumatoid arthritis patients, arising from the CDR
CC region of oligoclonal pathogenic T-cell antigen receptor Vbeta chains.
CC Compositions which contain autoantigenic peptides binding specifically to
CC T-cells expressing receptors containing the peptide sequences, which
CC include antigen-specific immunological tolerance to rheumatoid arthritis
CC can be used for the treatment and prevention of rheumatoid arthritis. The
CC invention can be used for the diagnosis, treatment and prevention of
CC rheumatoid arthritis. Sequences AAV66771-958 represent peptides from the
CC various Vbeta chains of T cell antigen receptor
XX
SQ Sequence 12 AA;
Query Match 43.8%; Score 35; DB 3; Length 12;
Best Local Similarity 45.5%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXYGNSPKGF 11
Dd 2 CATWGNQPHF 12
: : : : :
: : : : :

RESULT 5
ABR61868
ID ABR61868 standard; peptide; 13 AA.
XX
AC ABR61868;
XX
DT 12-SEP-2003 (first entry)
XX
DE Mouse MAb 1A1 heavy chain variable region CDR3 fragment.
XX
KW Antibody; beta-chemokine; monocyte chemotactic protein; MCP-1; MCP-2;
KW MCP-3; antiinflammatory; nephrotrophic; dermatological; hepatotrophic;
KW neuroprotective; antiatherosclerotic; antirheumatic; antiarthritis;
KW cytostatic; anticonvulsant; antidiabetic; ophthalmological; vasotropic;
KW immunomodulator; cerebroprotective; antitumor; antiparkinsonian; MAb;
KW monoclonal antibody; 1A1; complementarity determining region; CDR.

Mus musculus.
WO2003048083-A2.
12-JUN-2003.
27-NOV-2002; 2002WO-US038229.
30-NOV-2001; 2001US-0343391P.
24-MAY-2002; 2002US-0383277P.
01-AUG-2002; 2002US-0400469P.
(BIOJ ) BIOGEN INC.
De Fougerolles AR, Kotelianski VE, Garber E, Reid C;
WPI; 2003-532819/50.
Novel antibody or its antigen binding fragment that specifically binds to
monocyte chemotactic protein-2 and other beta-chemokine, useful for
detecting presence of beta-chemokine in sample, and blocking chemotaxis.
Example 9; Page 67; 100pp; English.
The invention relates to an antibody or its antigen binding fragment (AF)
that specifically binds to a plurality of beta-chemokines, particularly
monocyte chemotactic proteins MCP-1, MCP-2 and MCP-3. The antibodies are
useful in an immunoassay method for detecting the presence of a beta-
chemokine in a sample, and for blocking chemotaxis. The antibodies or
their AFs are useful for treating a subject suffering from a disorder
chosen from glomerulonephritis, scleroderma, multiple sclerosis, lupus
nephritis, cirrhosis, atherosclerosis, inflammatory bowel disease or
rheumatoid arthritis. The antibodies are also useful for treating
oncogenic disease or cancer, Crohn's disease, diabetic nephropathy,
cachexia, stroke, ulcerative colitis, coronary restenosis, Huntington's
disease and Parkinson's disease. Sequences ABR61868-68 represent murine
monoclonal antibody (MAb) 1A1 heavy chain variable region CDR1-3
(CC complementarity determining region) fragments
XX
SQ Sequence 13 AA;
Query Match 43.8%; Score 35; DB 7; Length 13;
Best Local Similarity 70.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 13
Dd 4 YGTSYGGFAY 13
: : : : :
: : : : :

RESULT 6
ABR79021
ID ABR79021 standard; peptide; 9 AA.
XX
AC ABR79021;
XX
DT 01-AUG-2002 (first entry)
XX
DE Lanthionine peptide SEQ ID NO:12.
XX
KW Lanthionine; lanthionine bridge.
XX
OS Synthetic.
XX
FN Key Location/Qualifiers
FT Misc-difference 1..6 /note= "forms a lanthionine bridge"
FT US6028168-A.
PD 22-FEB-2000.
XX

```


Query Match 42.5%; Score 34; DB 6; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGNSPKG 10
 :|||||
 Db 3 FGNSPRG 9

RESULT 9
 AAR28794
 ID AAR28794 standard; peptide; 16 AA.
 XX
 AC AAR28794;
 XX
 DT 25-MAR-2003 (revised)
 DT 23-MAR-1993 (first entry)
 XX
 DE High endotoxin affinity polypeptide.
 XX
 KW Lipopolysaccharide affinity; tachyplesin-like; polyphemusin-like;
 KW antitaxal activity; HIV; human immunodeficiency virus.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT Modified-site 16 /note= "Arg-NH2"
 FT
 XX EP513613-A1.

XX
 PD 19-NOV-1992.
 XX
 PF 04-MAY-1992; 92EP-00107509.
 XX
 PR 02-MAY-1991; 91JP-00130410.
 XX
 PA (SEKG) SEIKAGAKU KOGYO CO LTD.
 XX
 PI Fujii N, Yanamoto N, Matsumoto A, Waki M;
 XX
 DR WPI; 1992-383533/47.
 XX
 PT New tachyplesin- and polyphemusin-like polypeptide(s) - have endotoxin-
 PT binding activity, antibacterial activity and antiviral activity, partic.
 PT anti-HIV activity.

XX Disclosure; Page 5; 17pp; English.

XX The polypeptide has an ability to bind endotoxins, an antibacterial
 CC activity and an activity to haemolyse endotoxin-sensitised haemocytes. It
 CC also has antiviral activity, specifically anti-HIV activity. It exhibits
 CC higher anti-HIV activity than known related high endotoxin affinity
 CC polypeptides, e.g. tachyplesins I, II or III or Polyphemusins I or II. It
 CC may be prep'd. by solid phase synthesis or recombinant DNA techniques.
 CC Opt. the Cys residues at positions 2 and 15 are linked through a
 CC disulphide linkage as are the Cys residues at positions 6 and 11. See
 CC also AAR28775-R28799 and AAR28804. (Updated on 25-MAR-2003 to correct PN
 CC field.)

XX Sequence 16 AA;

Query Match 40.0%; Score 32; DB 2; Length 16;
 Best Local Similarity 46.2%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 YGNSPKGAYXXC 16
 :|||||
 Db 3 YRKCYKGFYRKC 15

RESULT 10

AAW37605
 ID AAW37605 standard; peptide; 16 AA.
 XX
 AC AAW37605;
 XX
 DT 10-MAR-1998 (first entry)
 XX
 DE Synergistic HIV enzyme inhibitor enhancing peptide (50).
 XX
 KW Human immunodeficiency virus; HIV; reverse transcriptase; protease;
 KW inhibitor; antiviral; synergistic enhancer.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT Disulfide-bond 2..15 /note= "optional"
 FT Modified-site 16 /note= "amidated"
 FT

XX JP09025240-A.
 PN

XX 28-JAN-1997.
 PD

XX 11-JUL-1995; 95JP-00197129.
 PF

XX 11-JUL-1995; 95JP-00197129.
 PR

XX (SEKG) SEIKAGAKU KOGYO CO LTD.
 PA

XX WPI; 1997-149771/14.
 DR

XX Antiviral compen. against human immunodeficiency virus - contg. specified
 PT polypeptide and HIV reverse transcriptase inhibitor or HIV protease
 PT inhibitor.

XX Example; Page 7; 13pp; Japanese.

XX A novel medicinal composition, comprising the present peptide and a human
 CC immunodeficiency virus (HIV) reverse transcriptase or protease inhibitor,
 CC can be used as an antiviral drug. The composition is highly active
 CC against HIV, and can be administered over a long period. The dose of the
 CC HIV enzyme inhibitor can be reduced, because combined use with the
 CC present peptide synergistically enhances its antiviral activity

XX Sequence 16 AA;

Query Match 40.0%; Score 32; DB 2; Length 16;
 Best Local Similarity 46.2%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 4 YGNSPKGAYXXC 16
 :|||||
 Db 3 YRKCYKGFYRKC 15

RESULT 11

AAW79866

ID AAW79866 standard; peptide; 16 AA.

XX AAW79866;

XX 08-DEC-1998 (first entry)

XX Peptide sequence of the specification.

XX Reverse-transcriptase inhibitor; HIV protease inhibitor;

XX HIV surface protein gp120; cell surface protein CD4; treatment; AIDS;

XX AIDS-associated syndrome.

XX Synthetic.

XX OS
 XX WO9843995-A1.
 PN

XX PD 08-OCT-1998.
 XX PF 26-MAR-1998; 98WO-JP001366.
 XX PR 28-MAR-1997; 97JP-00092801.
 XX PA (SEK) SEIKAGAKU CORP.
 XX PI Fujii N;
 XX DR WPI; 1998-542630/46.
 XX PT New therapeutic compositions comprise anti-HIV complexes - useful for
 PT homing drug substance to target cells to enhance anti-HIV activity, for
 PT treatment of AIDS.
 PS Disclosure; Page 11; 44pp; Japanese.
 XX CC AAW79817-85 appear in the specification. The specification describes
 CC complexes which comprise at least one reverse-transcriptase inhibitor
 CC and/or HIV protease inhibitor chemically bonded to polypeptides with an
 CC affinity for HIV surface protein gp120 and/or HIV host target cell
 CC surface protein CD4. The complexes can be used to prepare therapeutics
 CC for treatment of AIDS and AIDS-associated syndromes
 XX SQ Sequence 16 AA;
 Query Match 40.0%; Score 32; DB 2; Length 16;
 Best Local Similarity 46.2%; Pred. No. 1.9e+02;
 Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 4 YGNSPKGFAYXXC 16
 DB 3 YRKCYKGFYRKC 15
 RESULT 12
 ABB79022
 ID ABB79022 standard; peptide; 9 AA.
 XX AC ABB79022;
 XX DT 01-AUG-2002 (first entry)
 XX DE Lanthionine peptide SEQ ID NO.13.
 XX KW Lanthionine; lanthionine bridge.
 XX OS Synthetic.
 XX PH Key Location/Qualifiers
 PH Misc-difference 1..6
 FT /note= "forms a lanthionine bridge"
 XX US6028169-A.
 XX PD 22-FEB-2000.
 XX PF 06-JUN-1995; 95US-00467472.
 XX PR 09-AUG-1991; 91US-00742908.
 XX PR 28-JAN-1993; 93US-00021606.
 XX PA (KOLB/) KOLBECK W.
 XX PI Osapay G, Goodman M;
 XX DR WPI; 2000-348922/30.
 XX PT New lanthionine bridged peptide compounds derived from naturally linear
 FT peptide e.g. virus related peptides.
 XX

PS Example; Col 59; 50pp; English.
 XX CC The present invention describes lanthionine bridged peptide compounds
 CC (I). (I) Have improved biological activity compared to the corresponding
 CC linear peptide. The present sequence represents a peptide given in the
 CC exemplification of the present invention
 XX SQ Sequence 9 AA;
 Query Match 38.8%; Score 31; DB 3; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GNSPKG 10
 DB 4 GNSPRG 9
 RESULT 13
 AAU07682
 ID AAU07682 standard; peptide; 9 AA.
 XX AC AAU07682;
 XX DT 04-DEC-2001 (first entry)
 XX DE Synthetic lanthionine-oxytocin bridged peptide #1.
 XX KW Lanthionine bridged peptide; thioether bond; monosulphide bridge;
 XX hormone; neurotoxin; plant regulating agent; lanthionine-oxytocin.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1..6
 FT /label= OTHER
 FT /note= "OTHER= lanthionine bridge"
 XX US6268339-B1.
 XX PD 31-JUL-2001.
 XX PF 26-AUG-1999; 99US-00384061.
 XX PR 09-AUG-1991; 91US-00742908.
 XX PR 28-JAN-1993; 93US-00021606.
 XX PR 06-JUN-1995; 95US-00467472.
 XX PA (KOLB/) KOLBECK W.
 XX PI Goodman M, Osapay G;
 XX DR WPI; 2001-549070/51.
 XX PT New peptides comprising monosulfide bridges, are useful as
 PT pharmacologically active agents such as hormones.
 XX PS Disclosure; Col 57; 49pp; English.
 XX CC The sequences represent synthetic lanthionine bridged peptides. The
 CC peptides of the invention all comprise a lanthionine bridge, a thioether
 CC bond also called a monosulphide bridge. The peptides can be used as
 CC pharmacologically active agents, for example, as hormones, as neurotoxins
 CC and as plant regulating agents. The sequences have a higher biological
 CC activity than their corresponding naturally occurring peptides. This
 CC sequence represents a lanthionine-oxytocin peptide
 XX SQ Sequence 9 AA;
 Query Match 38.8%; Score 31; DB 4; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY      5 GNSPKG 10
DB      4 GNSPRG 9

RESULT 14
ABU61713
ID      ABU61713 standard; peptide; 9 AA.
XX      AC      ABU61713;
XX      DT      13-AUG-2003 (first entry)
XX      DE      Lanthionine bridged peptide #13.
XX      KW      Lanthionine bridged peptide; monosulphide bridge; thioether bond;
XX      KW      improved biological activity; vasopressin; somatostatin; enkephalin;
XX      KW      endothelin; pharmaceutically active compound.
XX      OS      Synthetic.
XX      FH      Key      Location/Qualifiers
XX      FT      Modified-site      1..6
XX      FT      /note= "Residues 1 and 6 linked by a lanthionine bridge"
XX      FN      US2002165132-A1.
XX      PD      07-NOV-2002.
XX      PE      10-MAY-2001; 2001US-00852870.
XX      PR      09-AUG-1991; 91US-00742908.
XX      PR      28-JAN-1993; 93US-00021606.
XX      PR      06-JUN-1995; 95US-00467472.
XX      PR      26-AUG-1999; 99US-00384061.
XX      PA      (GOOD/) GOODVAN M.
XX      PA      (OSAP/) OSAPAY G.
XX      PI      Goodman M, Osapay G;
XX      DR      WPI; 2003-391607/37.
XX      PT      Novel lanthionine-bridged biologically active peptides e.g. vasopressin,
XX      PT      somatostatin or enkephalin, useful as pharmaceutically active compounds.
XX      PS      Disclosure; Page 15; 24pp; English.
XX      CC      The present invention relates to lanthionine bridged peptides which are
XX      CC      analogues of peptide compounds comprising a disulphide bridge. The
XX      CC      disulphide bridge is replaced by monosulphide bridge or thioether bond,
XX      CC      designated a lanthionine bridge. Such analogues or lanthionine bridged
XX      CC      peptides have improved biological activity compared to the original
XX      CC      peptide compounds e.g. vasopressin, somatostatin, enkephalin, and
XX      CC      endothelin. The lanthionine-bridged peptides are useful as
XX      CC      pharmaceutically active compounds. ABU61701-ABU61724 represent
XX      CC      lanthionine bridged peptides
XX      SQ      Sequence 9 AA;
XX      Query Match      38.8%; Score 31; DB 6; Length 9;
XX      Best Local Similarity      83.3%; Pred. No. 1.4e+06;
XX      Matches      5; Conservative      1; Mismatches      0; Indels      0; Gaps      0;

QY      5 GNSPKG 10
DB      4 GNSPRG 9

RESULT 15
AAU70447
ID      AAU70447 standard; peptide; 15 AA.
XX

```

```

AAU70447;
XX
XX      14-FEB-2002 (first entry)
XX
XX      Mouse light chain immunoglobulin framework region 2 #4.
XX
XX      Immunoglobulin; antibody; light chain; heavy chain; CDR; FR;
XX      KW      complementarity determining region; framework region; IGBP;
XX      KW      transgenic plant; immunoglobulin binding protein array; IgM; IgG; IgA;
XX      KW      IgD; IgE; IgY; IgM; kappa; lambda; CHBP.
XX
XX      Mus musculus.
XX
XX      WO200183806-A1.
XX
XX      08-NOV-2001.
XX
XX      02-MAY-2001; 2001WO-US014349.
XX
XX      02-MAY-2000; 2000US-00563222.
XX
XX      (EPIC-) EPICYTE PHARM INC.
XX
XX      Hiatt AC, Hein MB;
XX
XX      WPI; 2002-055482/07.
XX
XX      Preparing immunoglobulin binding protein array in plant cells by
XX      PT      transforming the cells with different polynucleotides encoding binding
XX      PT      protein polypeptides specific to ligand, selecting plant cells for
XX      PT      preparing array.
XX
XX      Disclosure; Fig 1A; 129pp; English.
XX
XX      The invention relates to transforming a population of cells (e.g. plant
XX      CC      cells), comprising using a library of two different polynucleotides
XX      CC      encoding different immunoglobulin binding protein (IGBP) polypeptides
XX      CC      that specifically bind to a ligand or form one or more disulphide bonds
XX      CC      with polypeptides in transfected cells, to generate an IGBP that binds to
XX      CC      a ligand, and transformed plant cells are selected, and preparing an IGBP
XX      CC      array in plant cells. At least one peptide sequence has at least 75%
XX      CC      sequence identity to a framework region (FR) of a native IgM, IgG, IgA,
XX      CC      IgD, IgE, IgY, kappa or lambda immunoglobulin molecule. The method is
XX      CC      useful for preparing an immunoglobulin binding protein array, preferably
XX      CC      heavy chain binding protein (CHBP) array in eukaryotic cells especially
XX      CC      plant cells (e.g. Agrobacterium tumefaciens or maize) or other eukaryotic
XX      CC      cells (e.g. insect cells or mammalian cells). The CHBP is useful for
XX      CC      discovery of e.g. screening assays of IGBPs having desired
XX      CC      characteristics. The present sequence is a mammalian immunoglobulin
XX      CC      derived peptide that may be incorporated into an IGBP of the invention
XX      SQ      Sequence 15 AA;
XX      Query Match      38.8%; Score 31; DB 5; Length 15;
XX      Best Local Similarity      66.7%; Pred. No. 2.6e+02;
XX      Matches      6; Conservative      1; Mismatches      2; Indels      0; Gaps      0;

QY      5 GNSPKG 13
DB      7 GNSPKLW15
XX
XX      Search completed: July 29, 2004, 09:20:56
XX      Job time : 52 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 09:22:10 ; Search time 41 Seconds
(without alignments)
122.413 Million cell updates/sec

Title: US-09-661-992B-105
Perfect score: 80
Sequence: 1 CXYGNSPKGFAYXXC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues 221736

Total number of hits satisfying chosen parameters: 221736

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	42.5	9	9	US-09-852-870A-12	Sequence 12, Appl
2	31	38.8	9	9	US-09-852-870A-13	Sequence 13, Appl
3	31	38.8	15	10	US-09-563-222-127	Sequence 127, App
4	30	37.5	9	9	US-09-852-870A-14	Sequence 14, Appl
5	29.5	36.9	14	11	US-09-791-551-97	Sequence 97, Appl
6	29	36.2	10	13	US-10-140-555-7	Sequence 7, Appli
7	29	36.2	12	15	US-10-428-408A-3	Sequence 3, Appli
8	29	36.2	12	16	US-10-428-894-3	Sequence 3, Appli
9	29	36.2	15	11	US-09-791-551-101	Sequence 101, App
10	28	35.0	15	9	US-09-949-559-90	Sequence 90, Appl
11	28	35.0	15	10	US-09-875-221A-90	Sequence 90, Appl
12	28	35.0	16	14	US-10-062-710-40	Sequence 40, Appl
13	28	35.0	16	14	US-10-322-142-10	Sequence 10, Appl
14	27	33.8	9	9	US-09-828-708-52	Sequence 52, Appl
15	27	33.8	9	9	US-09-828-708-56	Sequence 56, Appl

16	27	33.8	9	9	US-09-852-870A-15	Sequence 15, Appl
17	27	33.8	9	16	US-10-663-244-32	Sequence 32, Appl
18	27	33.8	11	15	US-10-360-101-73	Sequence 73, Appl
19	27	33.8	12	10	US-09-747-802-29	Sequence 29, Appl
20	27	33.8	12	10	US-09-868-294-21	Sequence 21, Appl
21	27	33.8	12	16	US-10-789-619-29	Sequence 29, Appl
22	27	33.8	14	12	US-09-747-287-102	Sequence 102, App
23	27	33.8	14	12	US-09-874-350A-69	Sequence 69, Appl
24	27	33.8	15	10	US-09-563-222-135	Sequence 135, App
25	27	33.8	16	12	US-09-747-287-81	Sequence 81, Appl
26	27	33.8	16	12	US-09-747-287-82	Sequence 82, Appl
27	27	33.8	16	12	US-09-874-350A-47	Sequence 47, Appl
28	27	33.8	16	12	US-09-874-350A-48	Sequence 48, Appl
29	27	33.8	16	14	US-10-031-874A-160	Sequence 160, App
30	26	32.5	8	12	US-10-418-819-13	Sequence 13, Appl
31	26	32.5	9	10	US-09-977-797A-68	Sequence 68, Appl
32	26	32.5	10	8	US-08-996-140-15	Sequence 15, Appl
33	26	32.5	11	12	US-10-398-104-241	Sequence 241, App
34	26	32.5	11	14	US-10-059-261-90	Sequence 90, Appl
35	26	32.5	11	14	US-10-059-261-198	Sequence 198, App
36	26	32.5	13	14	US-10-244-367-59	Sequence 59, Appl
37	26	32.5	14	12	US-10-651-563-89	Sequence 89, Appl
38	26	32.5	15	9	US-09-952-768-16	Sequence 16, Appl
39	26	32.5	15	9	US-09-861-294-23	Sequence 23, Appl
40	26	32.5	15	9	US-09-954-697-65	Sequence 65, Appl
41	26	32.5	15	10	US-09-749-873-125	Sequence 125, App
42	26	32.5	15	12	US-10-462-062-127	Sequence 127, App
43	26	32.5	15	12	US-10-668-955-16	Sequence 16, Appl
44	26	32.5	15	12	US-09-746-731-27	Sequence 27, Appl
45	26	32.5	15	13	US-10-059-749-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1

US-09-852-870A-12
; Sequence 12, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9123-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 12
; TYPE: PRT
; LENGTH: 9
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-12

Query Match 42.5%; Score 34; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGNSPKG 10

Db 3 FGNSPRG 9

RESULT 2

US-09-852-870A-13
; Sequence 13, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray

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; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
; US-09-852-870A-13

Query Match      38.8%; Score 31; DB 9; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      5 GNSPKG 10
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Db      4 GNSPRG 9

RESULT 3
US-09-563-222-127
; Sequence 127, Application US/09563222
; Publication No. US20030079253A1
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT APPLICATION NUMBER: US/09/563,222
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-563-222-127

Query Match      38.8%; Score 31; DB 10; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 GNSPKGFAY 13
        |||||
Db      7 GNSPKLWY 15

RESULT 4
US-09-852-870A-14
; Sequence 14, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT

; APPLICANT: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
; US-09-852-870A-14

Query Match      37.5%; Score 30; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 YGNSPKG 10
        :|||||
Db      3 FGNSPLG 9

RESULT 5
US-09-791-551-97
; Sequence 97, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/027869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus sp.
; US-09-791-551-97

Query Match      36.9%; Score 29.5; DB 11; Length 14;
Best Local Similarity 70.0%; Pred. No. 3e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY      4 YGNSPKGFAY 13
        |||||
Db      6 YGSSP-WFAY 14

RESULT 6
US-10-140-555-7
; Sequence 7, Application US/10140555
; Publication No. US20020127227A1
; GENERAL INFORMATION:
; APPLICANT: Julie A. Abrahamson
; APPLICANT: Stephen D. Holmes
; APPLICANT: Jeffrey R. Jackson
; TITLE OF INVENTION: RHAMM Antagonist Antibodies
; FILE REFERENCE: P50857
; CURRENT APPLICATION NUMBER: US/10/140,555
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/443,790
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/109,041
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(10)
; OTHER INFORMATION: heavy chain CDR 3
; US-10-140-555-7

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Query Match      36.2%; Score 29; DB 13; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GNSPKGFAY 13
Db 2 GSSLLGFAY 10

RESULT 7
US-10-428-408A-3
; Sequence 3, Application US/10428408A
; Publication No. US20030233869A1
; GENERAL INFORMATION:
; APPLICANT: Celltech R&D limited
; TITLE OF INVENTION: BIOLOGICAL PRODUCTS
; FILE REFERENCE: CARP0004-100
; CURRENT APPLICATION NUMBER: US/10/428,408A
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: mouse
; NAME/KEY: DOMAIN
; OTHER INFORMATION: mouse monoclonal 5/44 CDR-H3
US-10-428-408A-3

Query Match      36.2%; Score 29; DB 15; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 13
Db 3 YGNYGAWFAY 12

RESULT 8
US-10-428-894-3
; Sequence 3, Application US/10428894
; Publication No. US20040082764A1
; GENERAL INFORMATION:
; APPLICANT: WYETH HOLDINGS CORPORATION.; KINZ, ARTHUR ET AL.
; TITLE OF INVENTION: CALICHEAMICIN DERIVATIVE-CARRIER CONJUGATES
; FILE REFERENCE: AX100788
; CURRENT APPLICATION NUMBER: US/10/428,894
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: mouse
; NAME/KEY:
; OTHER INFORMATION: mouse monoclonal 5/44 CDR-H3
US-10-428-894-3

Query Match      36.2%; Score 29; DB 16; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 13
Db 3 YGNYGAWFAY 12

RESULT 9
US-09-791-551-101
; Sequence 101, Application US/09791551
; Publication No. US20030235584A1
; GENERAL INFORMATION:
; APPLICANT: KLOETZER, WILLIAM S.
; APPLICANT: HANNA, NABIL
; TITLE OF INVENTION: METHOD FOR PREPARING ANTI-MIF ANTIBODIES
; FILE REFERENCE: 037003/0277869
; CURRENT APPLICATION NUMBER: US/09/791,551
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/185,390
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 60/233,625
; PRIOR FILING DATE: 2000-09-18
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-791-551-101

Query Match      36.2%; Score 29; DB 11; Length 15;
Best Local Similarity 60.0%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 13
Db 6 YGSSYDPFAY 15

RESULT 10
US-09-949-559-90
; Sequence 90, Application US/09949559
; Patent No. US20020151682A1
; GENERAL INFORMATION:
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0095
; CURRENT APPLICATION NUMBER: US/09/949,559
; CURRENT FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 0013810.7GB
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: 09/875,221
; PRIOR FILING DATE: 2001-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 90
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: hTNF40 framework L2
US-09-949-559-90

Query Match      35.0%; Score 28; DB 9; Length 15;
Best Local Similarity 55.6%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GNSPKGFAY 13
Db 7 GQSPKALY 15

RESULT 11
US-09-875-221A-90
; Sequence 90, Application US/09875221A
; Publication No. US20030026805A1
; GENERAL INFORMATION:

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; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Brown, Derek Thomas
; APPLICANT: Weir, Andrew Neil Charles
; APPLICANT: Popplewell, Andrew George
; APPLICANT: Chapman, Andrew Paul
; APPLICANT: King, David John
; TITLE OF INVENTION: Biological Products
; FILE REFERENCE: Carp-0089
; CURRENT APPLICATION NUMBER: US/09/875,221A
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: GB0013810.7
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 90
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HTNF40 framework L2
US-09-875-221A-90

Query Match 35.0%; Score 28; DB 10; Length 15;
Best Local Similarity 55.6%; Pred. No. 5.8e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GNSPKGFAY 13
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Db 7 GQSPKALIV 15

RESULT 12
US-10-062-710-40
; Sequence 40, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Liang

; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of
; TITLE OF INVENTION: MHC-Recognized Epitopes
; TITLE OF INVENTION: Via Peptide Vaccines
; FILE REFERENCE: 3781-001-27
; CURRENT APPLICATION NUMBER: US/10/062,710
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/310,498
; PRIOR FILING DATE: 2001-08-08
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV Helper-T Cell Epitopes

US-10-062-710-40
Query Match 35.0%; Score 28; DB 14; Length 16;
Best Local Similarity 55.6%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PKGFAYXXC 16
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Db 2 PAGFAILXC 10

RESULT 13
US-10-322-142-10
; Sequence 10, Application US/10322142
; Publication No. US20030113322A1
; GENERAL INFORMATION:
; APPLICANT: BES, CEDRIC
; APPLICANT: BRIANT-LONGUET, LAURENCE

; APPLICANT: CERUTTI, MARTINE
; APPLICANT: CHARGES, THIERRY
; APPLICANT: DEVAUCHELLE, GERARD
; APPLICANT: DEVAUX, CHRISTIAN
; APPLICANT: GRANIER, CLAUDE
; APPLICANT: MAMAS, CLAUDE
; APPLICANT: OLIVE, DANIEL
; APPLICANT: PAU, BERNARD
; TITLE OF INVENTION: CDR-HI-DERIVED PETIDE CB11, PHARMACEUTICAL COMPOSITIONS
; TITLE OF INVENTION: MADE THEREFROM AND METHODS OF TREATING DISORDERS IN
; TITLE OF INVENTION: MAMMALS
; FILE REFERENCE: 1129-R-02
; CURRENT APPLICATION NUMBER: US/10/322,142
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 60/341,349
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/374,754
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 10
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-322-142-10

Query Match 35.0%; Score 28; DB 14; Length 16;
Best Local Similarity 55.6%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PKGFAYXXC 16
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Db 1 PAGFAILKC 9

RESULT 14
US-09-828-708-52
; Sequence 52, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to Glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005U51
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-52

Query Match 33.8%; Score 27; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGNSPK 9
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Db 3 YGSSPR 8

RESULT 15
US-09-828-708-56
; Sequence 56, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:

; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-56

Query Match 33.8%; Score 27; DB 9; Length 9;
Best Local Similarity 66.7%; Pred.No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YGNSPK 9
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Db 3 YGSSPR 8

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OM protein - protein search, using sw model

Run on: July 29, 2004, 09:21:00 ; Search time 165 Seconds
(without alignments)
94.648 Million cell updates/sec

Title: US-09-661-992B-105

Perfect score: 80

Sequence: 1 CXXVGNPKGFAYXXC 16

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Gapop 10.0 , Gapext 0.5

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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3	58	72.5	10	20	US-09-661-992-5	Sequence 5, Appli
4	58	72.5	10	20	US-09-661-992B-5	Sequence 5, Appli
5	36.5	45.6	13	1	PCT-US03-32945-68	Sequence 68, Appl
6	36.5	45.6	13	1	US-10-687-035-68	Sequence 68, Appl
7	35	43.8	13	1	PCT-US02-38229-15	Sequence 15, Appl
8	35	43.8	13	1	PCT-US03-37834-15	Sequence 15, Appl
9	34	42.5	15	17	US-08-021-606C-12	Sequence 12, Appl
10	32	40.0	15	17	US-09-381-955A-50	Sequence 50, Appl
11	31	38.8	9	4	US-08-021-606C-13	Sequence 13, Appl
12	31	38.8	15	19	PCT-US01-14349-127	Sequence 127, App
13	31	38.8	15	19	US-09-563-222-127	Sequence 127, App
14	31	38.8	15	19	US-09-563-222C-120	Sequence 120, App
15	31	38.8	16	17	US-09-381-955A-52	Sequence 52, Appl
16	30	37.5	6	1	PCT-US03-34693-365	Sequence 365, App
17	30	37.5	6	1	PCT-US03-34747-365	Sequence 365, App
18	30	37.5	6	1	PCT-US03-34821-365	Sequence 365, App
19	30	37.5	6	31	US-10-699-088-365	Sequence 365, App
20	30	37.5	6	31	US-10-699-113-365	Sequence 365, App
21	30	37.5	6	31	US-10-699-114-365	Sequence 365, App
22	30	37.5	9	1	PCT-US03-01623-6	Sequence 6, Appli
23	30	37.5	9	4	US-08-021-606C-14	Sequence 14, Appl
24	30	37.5	10	1	PCT-US02-02303-246	Sequence 246, App
25	30	37.5	10	1	PCT-US03-00297-24	Sequence 24, Appl
26	30	37.5	11	1	PCT-US02-02303-262	Sequence 262, App
27	30	37.5	15	20	US-09-641-528A-47942	Sequence 47942, A
28	30	37.5	15	20	US-09-641-528A-50788	Sequence 50788, A
29	30	37.5	15	20	US-09-641-528B-47942	Sequence 47942, A
30	30	37.5	15	20	US-09-641-528B-50788	Sequence 50788, A
31	29.5	36.9	14	22	US-09-791-551-97	Sequence 97, Appl
32	29	36.2	9	1	PCT-US02-02303-272	Sequence 272, App
33	29	36.2	9	1	PCT-US03-31303-110	Sequence 110, App
34	29	36.2	10	1	PCT-US09-27565-7	Sequence 7, Appli
35	29	36.2	10	18	US-09-443-790-7	Sequence 7, Appli
36	29	36.2	10	27	US-10-140-555-7	Sequence 7, Appli
37	29	36.2	12	1	PCT-US03-13910-3	Sequence 3, Appli
38	29	36.2	12	30	US-10-428-408A-3	Sequence 3, Appli
39	29	36.2	12	30	US-10-428-894-3	Sequence 3, Appli
40	29	36.2	12	31	US-10-699-874-3	Sequence 3, Appli
41	29	36.2	12	31	US-10-699-874-3	Sequence 3, Appli
42	29	36.2	15	22	US-09-791-551-101	Sequence 101, App
43	29	36.2	15	25	US-09-950-083-3331	Sequence 3331, Ap
44	29	36.2	15	25	US-09-950-083B-3331	Sequence 3331, Ap
45	29	36.2	15	27	US-10-105-299-4335	Sequence 4335, Ap

ALIGNMENTS

RESULT 1

US-09-661-992-105
; Sequence 105, Application US/09661992
; GENERAL INFORMATION:
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Kerschbaumer, Rudolf
; APPLICANT: Falkner, Falko-Gunter
; APPLICANT: Dörner, Friedrich
; TITLE OF INVENTION: Factor IX/Activating Antibodies and Antibody Derivativ
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/661,992
; CURRENT FILING DATE: 2000-09-14
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 105
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence:CDR3 region
US-09-661-992-105

Query Match 90.0%; Score 72; DB 20; Length 16;

Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXYGNPKGFAYXXC 16
Db 1 CXXYGNPKGFAYXXC 16

RESULT 2

US-09-661-992B-105
; Sequence 105, Application US/09661992B
; GENERAL INFORMATION:
; APPLICANT: Scheifflinger, Friedrich
; APPLICANT: Kerschbaumer, Randolf
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Dörner, Friedrich
; APPLICANT: Baxter Aktiengesellschaft
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody
; TITLE OF INVENTION: Derivatives
; FILE REFERENCE: 20695C-005900US
; CURRENT APPLICATION NUMBER: US/09/661.992B
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: AT A157600
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:CDR3 peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(16)
; OTHER INFORMATION: Xaa = any amino acid
US-09-661-992B-105

Query Match 90.0%; Score 72; DB 20; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXYGNPKGFAYXXC 16
Db 1 CXXYGNPKGFAYXXC 16

RESULT 3

US-09-661-992-5
; Sequence 5, Application US/09661992
; GENERAL INFORMATION:
; APPLICANT: Scheifflinger, Friedrich
; APPLICANT: Kerschbaumer, Randolf
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Dörner, Friedrich
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody Derivative
; TITLE OF INVENTION: Derivatives
; FILE REFERENCE: 20695C-005900US
; CURRENT APPLICATION NUMBER: US/09/661.992
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: AT A157600
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of the artificial sequence:CDR3 region
US-09-661-992-5

Query Match 72.5%; Score 58; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 13
Db 1 YGNSPKGFAY 10

RESULT 4

US-09-661-992B-5
; Sequence 5, Application US/09661992B
; GENERAL INFORMATION:
; APPLICANT: Scheifflinger, Friedrich
; APPLICANT: Kerschbaumer, Randolf
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Dörner, Friedrich
; APPLICANT: Baxter Aktiengesellschaft
; TITLE OF INVENTION: Factor IX/Factor IXa Activating Antibodies and Antibody
; TITLE OF INVENTION: Derivatives
; FILE REFERENCE: 20695C-005900US
; CURRENT APPLICATION NUMBER: US/09/661.992B
; CURRENT FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: AT A157600
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:hybridoma cell
; OTHER INFORMATION: line 193/AD3 heavy chain CDR3 region
US-09-661-992B-5

Query Match 72.5%; Score 58; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 13
Db 1 YGNSPKGFAY 10

RESULT 5

PCT-US03-32945-68
; Sequence 68, Application PC/TUS0332945
; GENERAL INFORMATION:
; APPLICANT: Euro-Celtique S.A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-228
; CURRENT APPLICATION NUMBER: PCT/US03/32945
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 16H9 VH3 CDR
PCT-US03-32945-68

Query Match 45.6%; Score 36.5; DB 1; Length 13;
Best Local Similarity 80.0%; Pred. No. 86;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 4 YGNSPKGFAY 13
Db 5 YGN-PPGFAY 13

RESULT 6

US-10-687-035-68
 ; Sequence 68, Application US/10687035
 ; GENERAL INFORMATION:
 ; APPLICANT: Albone, Earl F.
 ; APPLICANT: Soltis, Daniel A.
 ; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
 ; FILE REFERENCE: CA 125/0772P AND METHODS OF USE THEREOF
 ; CURRENT APPLICATION NUMBER: US/10/687,035
 ; PRIOR FILING DATE: 2003-10-15
 ; PRIOR FILING DATE: 2003-07-10
 ; PRIOR FILING DATE: 2003-07-10
 ; PRIOR FILING DATE: 2003-10-12
 ; NUMBER OF SEQ ID NOS: 71
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 68
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: 16H9 VH3 CDR
 US-10-687-035-68

Query Match 45.6%; Score 36.5; DB 31; Length 13;
 Best Local Similarity 80.0%; Pred. No. 86;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 4 YGNSPKGFAY 13

Db 5 YGN-PGGFAY 13

RESULT 7

PCT-US02-38229-15
 ; Sequence 15, Application PC/TUS0238229
 ; GENERAL INFORMATION:
 ; APPLICANT: Biogen, Inc. et al.
 ; TITLE OF INVENTION: ANTIBODIES AGAINST MONOCYTE CHEMOTACTIC PROTEINS
 ; FILE REFERENCE: BGN-006PC
 ; CURRENT APPLICATION NUMBER: PCT/US02/38229
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: US 60/343391
 ; PRIOR FILING DATE: 2001-11-30
 ; PRIOR APPLICATION NUMBER: US 60/383277
 ; PRIOR FILING DATE: 2002-05-24
 ; PRIOR APPLICATION NUMBER: US 60/400469
 ; PRIOR FILING DATE: 2002-08-01
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 PCT-US02-38229-15

Query Match 43.8%; Score 35; DB 1; Length 13;
 Best Local Similarity 70.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 YGNSPKGFAY 13

Db 4 YGTSYGGFAY 13

RESULT 8

PCT-US03-37834-15
 ; Sequence 15, Application PC/TUS0337834
 ; GENERAL INFORMATION:
 ; APPLICANT: Biogen Idec MA Inc.
 ; APPLICANT: DE FOUGEROLLES, Antonin R.

; APPLICANT: KOTELIANSKI, Victor E.
 ; APPLICANT: GARBER, Ellen
 ; APPLICANT: REID, Carl
 ; APPLICANT: SALDANHA, Jose
 ; APPLICANT: VAN VLIJMEN, Herman
 ; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST MONOCYTE
 ; FILE REFERENCE: BGN-010PC
 ; CURRENT APPLICATION NUMBER: PCT/US03/37834
 ; CURRENT FILING DATE: 2003-11-25
 ; PRIOR APPLICATION NUMBER: 60/430007
 ; PRIOR FILING DATE: 2002-11-27
 ; NUMBER OF SEQ ID NOS: 69
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 15
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 PCT-US03-37834-15

Query Match 43.8%; Score 35; DB 1; Length 13;
 Best Local Similarity 70.0%; Pred. No. 1.6e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 YGNSPKGFAY 13

Db 4 YGTSYGGFAY 13

RESULT 9

US-08-021-606C-12
 ; Sequence 12, Application US/08021606C
 ; GENERAL INFORMATION:
 ; APPLICANT: GOODMAN, MURRAY
 ; APPLICANT: OSAPAY, GEORGE
 ; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
 ; STREET: 99 PARK AVENUE
 ; CITY: NEW YORK
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 10016
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 5.25" FLOPPY DISC
 ; COMPUTER: AT&T - IBM COMPATIBLE
 ; OPERATING SYSTEM: MS-DOS Version 3.10
 ; SOFTWARE: ASCII
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/021,606C
 ; FILING DATE: 28-JANUARY-1993
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/742,908
 ; FILING DATE: 9-AUGUST-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: ROBINSON, WILLIAM R.
 ; REGISTRATION NUMBER: 27,224
 ; REFERENCE/DOCKET NUMBER: LKR-9122A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 697-3355
 ; TELEFAX: (212) 557-5635
 ; TELEX: NONE
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 9
 ; TYPE: AMINO ACID
 ; TOPOLOGY: LINEAR
 ; MOLECULE TYPE:
 ; DESCRIPTION: PEPTIDE
 ; HYPOTHETICAL: N/A
 ; ANTI-SENSE: N/A

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; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: COMMERCIALY AVAILABLE FROM BECHAN BIOSCIENCE, INC.,
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: N/A
; LOCATION: N/A
; IDENTIFICATION METHOD: N/A
; OTHER INFORMATION: water is removed and thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; TITLE: DEHYDROAMINO ACIDS: THEIR PREPROPEPTIDES AND
; TITLE: POSSIBILITIES FOR BIOENGINEERING
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: LANTHIONINE BRIDGE
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; AUTHORS: WAKAMIYA, TATEAKI
; AUTHORS: FUKASE, KOICHI
; AUTHORS: SANO, AKIHIKO
; AUTHORS: SHIMBO, KUNIYAKI
; AUTHORS: UEKI, YASUYUKI
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: LANTHIONINE BRIDGE
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; AUTHORS: CARR, STEVEN A.
; AUTHORS: ESCHER, EMANUEL
; AUTHORS: NEUGEBAUER, W.
; AUTHORS: SAMANEN, JAMES
; TITLE: IDENTIFICATION OF A THIOETHER BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE BY
; TITLE: TANDEM MASS SPECTROMETRY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
; RELEVANT RESIDUES IN SEQ ID NO: LANTHIONINE BRIDGE AND GENERAL PEPTIDE STRUCTURE
US-08-021-606C-12
Query Match 42.5%; Score 34; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 5.5e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 YGNSPKG 10

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Db 3 FCNSPRG 9
; RESULT 10
; US-09-381-955A-50
; Sequence 50, Application US/09381955A
; GENERAL INFORMATION:
; APPLICANT: FUJII, Nobutaka
; TITLE OF INVENTION: NOVEL ANTI-HIV COMPLEXES AND MEDICINAL COMPOSITIONS
; FILE REFERENCE: 9378-0006-OPCT
; CURRENT APPLICATION NUMBER: US/09/381,955A
; CURRENT FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: PCT/JP98/01366
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: JP HEI-9-092801
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: peptide
US-09-381-955A-50
Query Match 40.0%; Score 32; DB 17; Length 15;
Best Local Similarity 46.2%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 4 YGNSPKGPRAYXXC 16
Db 3 YRKYKGFYRKC 15
; RESULT 11
; US-08-021-606C-13
; Sequence 13, Application US/08021606C
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; APPLICANT: OSAPAY, GEORGE
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BROOKS HAJDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25" FLOPPY DISC
; COMPUTER: AT&T - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 3.10
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,606C
; FILING DATE: 28-JANUARY-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 13:

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SEQUENCE CHARACTERISTICS:

LENGTH: 9
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
DESCRIPTION: N/A
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: COMMERCIALY AVAILABLE FROM BECHAN BIOSCIENCE, INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
TITLE: DEHYDROAMINO ACIDS: THEIR PREPEPTIDES AND
TITLE: POSSIBILITIES FOR BIOENGINEERING
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: LANTHIONINE BRIDGE
PUBLICATION INFORMATION:
AUTHORS: SHIRA, TETSUO
AUTHORS: WAKAMIYA, TATEAKI
AUTHORS: FUKASE, KOICHI
AUTHORS: SANO, AKIHIKO
AUTHORS: SHIMBO, KUNIYUKI
AUTHORS: Ueki, YASUYUKI
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: LANTHIONINE BRIDGE
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK P.
AUTHORS: CARR, STEVEN A.
AUTHORS: ESCHER, EMANUEL
AUTHORS: NEUGEBAUER, W.
AUTHORS: SAVANEN, JAMES
TITLE: IDENTIFICATION OF A THIOETHER BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN PEPTIDE
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: LANTHIONINE BRIDGE

US-08-021-606C-13

Query Match 38.8%; Score 31; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 5.5e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GNSPKG 10
| | | | |
Db 4 GNSPRG 9

RESULT 12

PCT-US01-14349-127
; Sequence 127, Application PC/TUS0114349
; GENERAL INFORMATION:
; APPLICANT: Epicyte Pharmaceuticals, Inc.
; APPLICANT: Hiatt, Andrew C.
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406PC
; CURRENT FILING DATE: 2001-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US01-14349-127

Query Match 38.8%; Score 31; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 8.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GNSPKG 13
| | | | |
Db 7 GNSPKLW 15

RESULT 13

US-09-563-222-127
; Sequence 127, Application US/09563222
; GENERAL INFORMATION:
; APPLICANT: Hiatt, Andrew
; APPLICANT: Hein, Mich B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN
; FILE REFERENCE: 310098.406
; CURRENT FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222-127

Query Match 38.8%; Score 31; DB 19; Length 15;
Best Local Similarity 66.7%; Pred. No. 8.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GNSPKG 13
| | | | |
Db 7 GNSPKLW 15

RESULT 14

US-09-563-222C-120
; Sequence 120, Application US/09563222C
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.

; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICHAEL
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/09/563,222C
; CURRENT FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-563-222C-120

Query Match 38.8%; Score 31; DB 19; Length 15;
Best Local Similarity 66.7%; Pred. No. 8.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 GNSPKGFAY 13
||||| : |
DB 7 GNSPKLWY 15

RESULT 15
US-09-381-955A-52
; Sequence 52, Application US/09381955A
; GENERAL INFORMATION:
; APPLICANT: FUJII, Nobutaka
; TITLE OF INVENTION: NOVEL ANTI-HIV COMPLEXES AND MEDICINAL COMPOSITIONS
; FILE REFERENCE: 9378-0006-0PCT
; CURRENT APPLICATION NUMBER: US/09/381,955A
; CURRENT FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: PCT/JP98/01366
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: JP HEI-9,092801
; PRIOR FILING DATE: 1997-03-28
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic
; OTHER INFORMATION: Peptide
US-09-381-955A-52

Query Match 38.8%; Score 31; DB 17; Length 16;
Best Local Similarity 62.5%; Pred. No. 9.5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 KGFAYYXC 16
||||| : |
DB 8 KGFCYKRC 15

Search completed: July 29, 2004, 09:25:57
Job time : 166 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 09:21:25 ; Search time 24 Seconds
(without alignments)
68.873 Million cell updates/sec

Title: US-09-661-992B-105

Perfect score: 80

Sequence: 1 CXXYGNPKGFAYXC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 594630 seqs, 103309165 residues

Total number of hits satisfying chosen parameters: 124060

Minimum DB seq length: 0

Maximum DB seq length: 16

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	35	43.8	13	6 US-10-855-013-15	Sequence 15, Appl
2	32	40.0	15	6 US-10-327-598-280	Sequence 280, App
3	32	40.0	15	6 US-10-327-598-355	Sequence 355, App
4	32	40.0	15	6 US-10-327-598A-280	Sequence 280, App
5	32	40.0	15	6 US-10-327-598A-355	Sequence 355, App
6	31	38.8	15	6 US-10-783-950-120	Sequence 120, App
7	30	37.5	6	6 US-10-806-924-328	Sequence 328, App
8	30	37.5	9	6 US-10-497-838-6	Sequence 6, Appl
9	30	37.5	10	6 US-10-883-020-24	Sequence 24, Appl
10	30	37.5	15	6 US-10-327-598-347	Sequence 347, App
11	30	37.5	15	6 US-10-327-598-348	Sequence 348, App
12	30	37.5	15	6 US-10-327-598-353	Sequence 353, App
13	30	37.5	15	6 US-10-327-598-358	Sequence 358, App
14	30	37.5	15	6 US-10-327-598-359	Sequence 359, App
15	30	37.5	15	6 US-10-327-598-365	Sequence 365, App
16	30	37.5	15	6 US-10-327-598A-347	Sequence 347, App
17	30	37.5	15	6 US-10-327-598A-348	Sequence 348, App
18	30	37.5	15	6 US-10-327-598A-353	Sequence 353, App
19	30	37.5	15	6 US-10-327-598A-358	Sequence 358, App
20	30	37.5	15	6 US-10-327-598A-359	Sequence 359, App
21	30	37.5	15	6 US-10-327-598A-365	Sequence 365, App
22	29	36.2	15	6 US-10-868-184A-3331	Sequence 3331, App
23	29	36.2	15	6 US-10-868-184-3331	Sequence 3331, App
24	28	35.0	15	1 PCT-US03-36499A-86	Sequence 86, Appl
25	27	33.8	8	6 US-10-111-983-1176	Sequence 1176, App
26	27	33.8	8	6 US-10-111-983-11743	Sequence 11743, A

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27 27 33.8 8 6 US-10-111-983-15420 Sequence 15420, A
28 27 33.8 8 6 US-10-111-983-27432 Sequence 27432, A
29 27 33.8 9 1 PCT-US03-29318-32 Sequence 32, Appl
30 27 33.8 9 1 PCT-IL04-00275-49 Sequence 49, Appl
31 27 33.8 9 6 US-10-663-244-32 Sequence 32, Appl
32 27 33.8 9 6 US-10-630-009-52 Sequence 52, Appl
33 27 33.8 9 6 US-10-630-009-56 Sequence 56, Appl
34 27 33.8 11 6 US-10-360-101A-73 Sequence 73, Appl
35 27 33.8 12 6 US-10-789-619-29 Sequence 29, Appl
36 27 33.8 12 6 US-10-861-614-21 Sequence 21, Appl
37 27 33.8 14 5 US-09-394-019B-55 Sequence 55, Appl
38 27 33.8 14 5 US-09-394-019B-300 Sequence 300, App
39 27 33.8 14 5 US-09-394-019C-55 Sequence 55, Appl
40 27 33.8 14 5 US-09-394-019C-300 Sequence 300, App
41 27 33.8 14 5 US-09-394-019C-300 Sequence 300, App
42 27 33.8 15 6 US-10-327-598-356 Sequence 356, App
43 27 33.8 15 6 US-10-327-598A-356 Sequence 356, App
44 27 33.8 15 6 US-10-783-950-127 Sequence 127, App
45 27 33.8 16 5 US-09-394-019B-46 Sequence 46, Appl

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ALIGNMENTS

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RESULT 1
US-10-855-013-15
; Sequence 15, Application US/10855013
; GENERAL INFORMATION:
; APPLICANT: Biogen, Inc. et al.
; TITLE OF INVENTION: ANTIBODIES AGAINST MONOCYTE CHEMOTACTIC PROTEINS
; FILE REFERENCE: BGN-006PC
; CURRENT APPLICATION NUMBER: US/10/855,013
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: US 60/343391
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/383277
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/400469
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-855-013-15

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Query Match 43.8%; Score 35; DB 6; Length 13;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

QY 4 YGNPKGFAY 13
Db 4 YGTSYGGFAY 13

```

RESULT 2

```

US-10-327-598-280
; Sequence 280, Application US/10327598
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, an
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0

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; SEQ ID NO 280
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; LENGTH: 15
;
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-280

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Query Match 40.0%; Score 32; DB 6; Length 15;
Best Local Similarity 66.7%;
Pred. No. 49;
Matches 6; Conservative 0; Mismatches 3; Indels

Qy 5 GNSPKGFAY 13
| | | | |
Db 7 GKSPKTFIY 15

RESULT 3

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US-10-327-598-355
; Sequence 355, Application US/10327598
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Hongliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 355
; LENGTH: 15
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-355

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Qy 5 GNSPKGFAY 13
|:|:|
Db 7 GHSPRGLEY 15

RESULT 4

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US-10-327-598A-280
; Sequence 280, Application US/10327598A
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598A
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 15
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598A-280

```

Qy	5	GNSPKGFAY	13
Db	7	GKSPKTFIY	15

RESULTS

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US-10-327-598A-355
; Sequence 355, Application US/10327598A
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598A
; CURRENT FILING DATE: 2003-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 355
; LENGTH: 15
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598A-355

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Qy 5 GNSPKGFAY 13
|:|:|
db 7 GHSRGLLY 15

RESULT 6

```

US-10-783-950-120
; Sequence 120, Application US/10783950
; GENERAL INFORMATION:
; APPLICANT: EPICYTE PHARMACEUTICALS, INC.
; APPLICANT: HIATT, ANDREW C.
; APPLICANT: HEIN, MICH B.
; TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEIN ARRAYS IN PLANT CELLS
; FILE REFERENCE: 068904-0501
; CURRENT APPLICATION NUMBER: US/10-783,950
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US/09/563,222
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: PCT/US01/14349
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: 09/563,222
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 120
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-783-950-120

```

Qy 5 GNSPKGFAY 13
||| : |
db 7 GNSPKLWY 15

RESULT. T 7

```
US-10-806-924-328
; Sequence 328, Application US/10806924
; GENERAL INFORMATION:
; APPLICANT: Geyssen, H. Mario
; APPLICANT: Ault-Riche, Dana
; TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
; FILE REFERENCE: 25885-1760
; CURRENT APPLICATION NUMBER: US/10/806,924
; CURRENT FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 911
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 328
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-806-924-328

Query Match      37.5%; Score 30; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 5.3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 NSPKGF 11
Db      1 NSPEGF 6

RESULT 8
US-10-497-838-6
; Sequence 6, Application US/10497838
; GENERAL INFORMATION:
; APPLICANT: Trustees of Dartmouth College
; APPLICANT: Rigby, William F.C.
; TITLE OF INVENTION: Compositions and Methods for Regulating RNA Stability by Using
; TITLE OF INVENTION: Polypyrimidine Tract Proteins
; FILE REFERENCE: DC-0217
; CURRENT APPLICATION NUMBER: US/10/497,838
; CURRENT FILING DATE: 2004-06-07
; PRIOR APPLICATION NUMBER: US 60/437,779
; PRIOR FILING DATE: 2003-01-02
; PRIOR APPLICATION NUMBER: US 60/349,869
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Bos taurus
US-10-497-838-6

Query Match      37.5%; Score 30; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YGNSP 8
Db      2 YGNSP 6

RESULT 9
US-10-883-020-24
; Sequence 24, Application US/10883020
; GENERAL INFORMATION:
; APPLICANT: Ditzel, Henrik
; APPLICANT: Jensenius, Jens
; TITLE OF INVENTION: The Scripps Research Institute
; FILE REFERENCE: 1361.017051
; CURRENT APPLICATION NUMBER: US/10/883,020
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: PCT/US03/00297
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US-10-806-924-328
; PRIOR FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 60/345,208
; PRIOR FILING DATE: 2002-01-03
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-883-020-24

Query Match      37.5%; Score 30; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 YGNSP 8
Db      3 YGNSP 7

RESULT 10
US-10-327-598-347
; Sequence 347, Application US/10327598
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, an
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 347
; LENGTH: 15
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-347

Query Match      37.5%; Score 30; DB 6; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 GNSPKGFAY 13
Db      7 GOSPEGLIY 15

RESULT 11
US-10-327-598-348
; Sequence 348, Application US/10327598
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, an
; TITLE OF INVENTION: for Making and Using Them
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 348
; LENGTH: 15
; TYPE: PRT
; ORGANISM: canis familiaris;
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US-10-327-598-348

Query Match 37.5%; Score 30; DB 6; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0;

QY 5 GNSPKGFAY 13
| | | | |
Db 7 GQSPGGLIY 15

RESULT 12

US-10-327-598-353
; Sequence 353, Application US/10327598
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 353
; LENGTH: 15
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-353

Query Match 37.5%; Score 30; DB 6; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0;

QY 5 GNSPKGFAY 13
| | | | |
Db 7 GQSPGGLIY 15

RESULT 13

US-10-327-598-358
; Sequence 358, Application US/10327598
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 358
; LENGTH: 15
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-358

Query Match 37.5%; Score 30; DB 6; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0;

QY 5 GNSPKGFAY 13
| | | | |
Db 7 GQSPGGLIY 15

RESULT 14

US-10-327-598-359
; Sequence 359, Application US/10327598
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 359
; LENGTH: 15
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-359

Query Match 37.5%; Score 30; DB 6; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0;

QY 5 GNSPKGFAY 13
| | | | |
Db 7 GQSPGGLIY 15

RESULT 15

US-10-327-598-365
; Sequence 365, Application US/10327598
; GENERAL INFORMATION:
; APPLICANT: Krah, Eugene
; APPLICANT: Guo, Honliang
; APPLICANT: Aiyappa, Ashok
; APPLICANT: Lawton, Robert
; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
; FILE REFERENCE: 01-799-A
; CURRENT APPLICATION NUMBER: US/10/327,598
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 60/344,874
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 1139
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 365
; LENGTH: 15
; TYPE: PRT
; ORGANISM: canis familiaris;
US-10-327-598-365

Query Match 37.5%; Score 30; DB 6; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0;

QY 5 GNSPKGFAY 13
| | | | |
Db 7 GQSPGGLIY 15

Search completed: July 29, 2004, 09:26:32
Job time : 25 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 09:20:00 ; Search time 18 Seconds
(without alignments)
45.890 Million cell updates/sec

Title: US-09-661-992B-105

Perfect score: 80
Sequence: 1 CXYGNSPKGFAYXC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 152138

Minimum DB seq length: 0
Maximum DB seq length: 16

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	34	42.5	9	3	US-09-384-061-12
3	34	42.5	9	4	US-09-852-870A-12
4	32	40.0	16	1	US-07-876-883-34
5	32	40.0	16	1	US-08-426-550-34
6	31	38.8	9	3	US-08-467-472C-13
7	31	38.8	9	3	US-09-384-061-13
8	31	38.8	9	4	US-09-852-870A-13
9	31	38.8	16	1	US-07-876-883-36
10	31	38.8	16	1	US-08-426-550-36
11	30	37.5	9	3	US-08-467-472C-14
12	30	37.5	9	3	US-09-384-061-14
13	30	37.5	9	4	US-09-852-870A-14
14	30	37.5	16	6	5189020-8
15	30	37.5	16	6	5424218-8
16	29	36.2	9	2	US-08-811-492-111
17	29	36.2	16	1	US-07-876-883-33
18	29	36.2	16	1	US-07-876-883-37
19	29	36.2	16	1	US-08-218-025A-136
20	29	36.2	16	1	US-08-306-116A-9
21	29	36.2	16	1	US-08-426-550-33
22	29	36.2	16	1	US-08-426-550-37
23	29	36.2	16	4	US-09-787-351B-13
24	28	35.0	11	3	US-08-226-376-7
25	28	35.0	12	2	US-08-475-081-6
26	28	35.0	13	2	US-08-894-922A-3
27	28	35.0	16	1	US-07-876-883-35

Sequence 35, Appl
Sequence 651, App
Sequence 652, App
Sequence 15, Appl
Sequence 15, Appl
Sequence 34, Appl
Sequence 15, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 37, Appl
Sequence 13, Appl
Sequence 70, Appl
Sequence 5, Appl
Sequence 64, Appl
Sequence 65, Appl
Sequence 653, App
Sequence 15, Appl
Sequence 14, Appl

16 1 US-08-426-550-35
28 35.0
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30 33.8
31 33.8
32 33.8
33 33.8
34 33.8
35 33.8
36 33.8
37 33.8
38 33.8
39 33.8
40 33.8
41 33.8
42 33.8
43 32.5
44 32.5
45 32.5

16 3 US-08-444-818-651
8 3 US-08-444-818-652
9 3 US-08-467-472C-15
9 3 US-09-384-061-15
9 4 US-09-852-870A-15
10 1 US-08-193-977-34
11 2 US-08-618-696-21
11 3 US-09-033-753-21
12 2 US-08-986-234-37
12 3 US-09-100-409A-13
14 3 US-08-802-981-70
15 1 US-07-907-190-5
16 3 US-08-802-981-64
16 3 US-08-802-981-65
8 3 US-08-444-818-653
10 4 US-09-649-063-15
11 4 US-09-431-705-14

ALIGNMENTS

RESULT 1
US-08-467-472C-12
; Sequence 12, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BROOKS HAIDT HAPFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104

IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAPFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LAR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
DESCRIPTION: N/A
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986

Query Match 42.5%; Score 34; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 0;
QY 4 YGNSPKG 10
DB 3 FGNSPRG 9

RESULT 2
US-09-384-061-12
Sequence 12, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24

DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK P.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-384-061-12

Query Match 42.5%; Score 34; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05; Indels 0;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

Qy 4 YGNSPKG 10
Db 3 FGNSPRG 9

RESULT 3

US-09-852-870A-12
Sequence 12, Application US/09852870A
Patent No. 6673769
GENERAL INFORMATION:
APPLICANT: Goodman, Murray
APPLICANT: Osapay, George
TITLE OF INVENTION: Lanthionin Bridged Proteins
FILE REFERENCE: LKR 9122-D
CURRENT APPLICATION NUMBER: US/09/852,870A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/384,601
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 12
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-12

Query Match 42.5%; Score 34; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05; Indels 0;
Matches 5; Conservative 2; Mismatches 0; Gaps 0;

Qy 4 YGNSPKG 10
Db 3 FGNSPRG 9

RESULT 4

US-07-876-883-34
Sequence 34, Application US/07876883
Patent No. 5449752
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5449752utaka
APPLICANT: Yamamoto, Naoki

APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
Lipopolysaccharides And Their Uses
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/876,883
FILING DATE: 19920429
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 863-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-876-883-34

Query Match 40.0%; Score 32; DB 1; Length 16;
Best Local Similarity 46.2%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 4 YGNSPKGFPAYXXC 16
Db 3 YRKYKGFYCYRKC 15

RESULT 5

US-09-426-550-34
Sequence 34, Application US/08426550
Patent No. 5710128
GENERAL INFORMATION:
APPLICANT: Fujii, No. 5710128utaka
APPLICANT: Yamamoto, Naoki
APPLICANT: Matsumoto, Akiyoshi
APPLICANT: Waki, Michinori
TITLE OF INVENTION: Pharmaceutical Compositions of
Lipopolysaccharide-Binding Polypeptides
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,550

FILING DATE: 21-APR-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Charles E.
REGISTRATION NUMBER: 24,576
REFERENCE/DOCKET NUMBER: 7568-006
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-426-550-34

Query Match 40.0%; Score 32; DB 1; Length 16;
Best Local Similarity 46.2%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Oy 4 YGNSPKGFAYXXC 16
| | | | |
Db 3 YRKYKGFYRKC 15

RESULT 6
US-08-467-472C-13
; Sequence 13, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LAR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A

; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: N/A
; LOCATION: N/A
; IDENTIFICATION METHOD: N/A
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; TITLE: BY
; TITLE: TANDEN MASS SPECTROMETRY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
; US-08-467-472C-13

Query Match 38.8%; Score 31; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 5 GNSPKG 10
| | | | |
Db 4 GNSPRG 9

RESULT 7
US-09-384-061-13
; Sequence 13, Application US/09384061
; Patent No. 6268339

GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAPFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS

VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
US-09-384-061-13
Query Match 38.8%; Score 31; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 GNSPKG 10
DB 4 GNSPRG 9
RESULT 8
US-09-852-870A-13
Sequence 13, Application US/09852870A
Patent No. 6673769
GENERAL INFORMATION:
APPLICANT: Goodman, Murray
TITLE OF INVENTION: Lanthionin Bridged Proteins
FILE REFERENCE: LKR 9122-D
CURRENT APPLICATION NUMBER: US/09/852,870A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/384,601
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-13
Query Match 38.8%; Score 31; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 5 GNSPKG 10
DB 4 GNSPRG 9
RESULT 9
US-07-876-883-36
Sequence 36, Application US/07876883
Patent No. 5449752

```

; GENERAL INFORMATION:
; APPLICANT: Fujii, No. 5449752utaka
; APPLICANT: Yamamoto, Naoki
; APPLICANT: Matsumoto, Akiyoshi
; APPLICANT: Waki, Michinori
; TITLE OF INVENTION: No. 5449752el Polypeptides With Affinity To
; TITLE OF INVENTION: Lipopolysaccharides And Their Uses
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/876,883
; FILING DATE: 19920429
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Charles E.
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 7568-003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-07-876-883-36

Query Match 38.8%; Score 31; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 KGfAYXXC 16
Db 8 KGfCYRKC 15

RESULT 10
US-08-426-550-36
; Sequence 36, Application US/08426550
; Patent No. 5710128
; GENERAL INFORMATION:
; APPLICANT: Fujii, No. 5710128utaka
; APPLICANT: Yamamoto, Naoki
; APPLICANT: Matsumoto, Akiyoshi
; APPLICANT: Waki, Michinori
; TITLE OF INVENTION: Pharmaceutical Compositions of
; TITLE OF INVENTION: No. 5710128el Lipopolysaccharide-Binding Polypeptides
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/426,550
; FILING DATE: 21-APR-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Miller, Charles E.
; REGISTRATION NUMBER: 24,576
; REFERENCE/DOCKET NUMBER: 7568-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-426-550-36

Query Match 38.8%; Score 31; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 66;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 KGfAYXXC 16
Db 8 KGfCYRKC 15

RESULT 11
US-08-467-472C-14
; Sequence 14, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR

```

MOLECULE TYPE: PEPTIDE
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC., MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE: 865 - 869
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: BY
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
JOURNAL: TANDEN MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
US-08-467-472C-14
Query Match 37.5%; Score 30; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 4 YGNSPKG 10
:|||||
Db 3 FGNSPLG 9

RESULT 12

US-09-384-061-14
Sequence 14, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5835
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC., MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE: 865 - 869
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
PUBLICATION INFORMATION:

;; AUTHORS: SHIBA, TETSUO
;; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
;; JOURNAL: BIOPOLYMERS
;; VOLUME: JOHN WILEY AND SONS, INC.
;; ISSUE: SUPPLEMENTARY
;; PAGES: 511 - 519
;; DATE: 1986
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
;; PUBLICATION INFORMATION:
;; AUTHORS: BEAN, MARK F.
;; TITLE: IDENTIFICATION OF A THIOETHER
;; TITLE: BY-PRODUCT
;; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
;; TITLE: BY
;; TITLE: TANDEN MASS SPECTROMETRY
;; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
;; JOURNAL: PEPTIDE
;; JOURNAL: SYMPOSIUM
;; VOLUME: ESCOM (LEIDEN 1990)
;; ISSUE: 443 - 445
;; DATE: 1990
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
US-09-384-061-14

Query Match 37.5%; Score 30; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YGNSPKG 10
Db 3 FGNSPLG 9

RESULT 13

US-09-852-870A-14
;; Sequence 14, Application US/09852870A
;; Patent No. 6673769
;; GENERAL INFORMATION:
;; APPLICANT: Goodman, Murray
;; TITLE OF INVENTION: Lanthionin Bridged Proteins
;; FILE REFERENCE: LKR 9122-D
;; CURRENT APPLICATION NUMBER: US/09/852,870A
;; CURRENT FILING DATE: 2001-05-10
;; PRIOR APPLICATION NUMBER: US 09/384,601
;; PRIOR FILING DATE: 1999-08-26
;; NUMBER OF SEQ ID NOS: 24
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 14
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-14

Query Match 37.5%; Score 30; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 YGNSPKG 10
Db 3 FGNSPLG 9

RESULT 14

5189020-8
;; Patent No. 5189020
;; APPLICANT: Miljanich, George P.; Bitner, Robert S.; Bowersox,
;; Stephen S.; Fox, James A.; Valentino, Karen L.; Yamashiro, Donald
;; H.; Tsubokawa, Makoto
;; TITLE OF INVENTION: METHOD OF REDUCING NEURONAL DAMAGE USING
;; OMEGA CONOTOXIN PEPTIDES
;; NUMBER OF SEQUENCES: 29
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/561,766
;; FILING DATE: 02-AUG-1990
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 440,094
;; FILING DATE: 22-NOV-1989
;; SEQ ID NO: 8:
;; LENGTH: 16
5189020-8

Query Match 37.5%; Score 30; DB 6; Length 16;
Best Local Similarity 31.2%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CXXYGNSPKGFAYXXC 16
Db 1 CKSXGSSASXTSYNAC 16

RESULT 15

5424218-8
;; Patent No. 5424218
;; APPLICANT: MILJANICH, GEORGE P.; BITNER, ROBERT S.; BOWERSOX,
;; STEPHEN S.; FOX, JAMES A.; VALENTINO, KAREN L.; YAMASHIRO, DONALD H.
;; TITLE OF INVENTION: SCREENING METHOD FOR NEUROPROTECTIVE COMPOUNDS
;; NUMBER OF SEQUENCES: 21
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/147,714
;; FILING DATE: 04-NOV-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 855,269
;; FILING DATE: 23-MAR-1992
;; APPLICATION NUMBER: 561,766
;; FILING DATE: 02-AUG-1990
;; APPLICATION NUMBER: 440,094
;; FILING DATE: 22-NOV-1989
;; SEQ ID NO: 8:
;; LENGTH: 16
5424218-8

Query Match 37.5%; Score 30; DB 6; Length 16;
Best Local Similarity 31.2%; Pred. No. 96;
Matches 5; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

Qy 1 CXXYGNSPKGFAYXXC 16
Db 1 CKSXGSSASXTSYNAC 16

Search completed: July 29, 2004, 09:23:00
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:27 ; Search time 0.979112 Seconds
(without alignments)
982.436 Million cell updates/sec

Title: US-09-661-992B-5
Perfect score: 58
Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42	72.4	626	2	B70749	probable Acyl-CoA
2	41	70.7	389	2	H90083	polyadenylate-bind
3	41	70.7	453	2	S75579	hypothetical prote
4	41	70.7	2515	2	A41519	posterior-group pr
5	39	67.2	401	2	H82175	multidrug resistan
6	39	67.2	568	1	A55377	CPE-binding protei
7	38	65.5	402	2	D90034	hypothetical prote
8	38	65.5	488	2	AD0735	conserved hypothe
9	38	65.5	488	2	AG0621	probable bacteriop
10	38	65.5	488	2	B96521	protein F21B18.20
11	38	65.5	583	2	B87204	probable acyl-CoA
12	38	65.5	585	2	JC7206	phosphoprotein pho
13	37	63.8	205	2	T19356	hypothetical prote
14	37	63.8	223	2	B70372	flagellar protein
15	37	63.8	306	1	S59863	polyA binding prot
16	37	63.8	331	2	D86413	cysteine proteinas
17	37	63.8	346	2	C86413	probable 4-hydroxy
18	37	63.8	390	2	G96028	4-hydroxybenzoate
19	37	63.8	390	1	AD3115	4-hydroxybenzoate
20	37	63.8	394	1	WHPSBF	4-hydroxybenzoate
21	37	63.8	394	1	WHPSBA	4-hydroxybenzoate
22	37	63.8	422	2	A98172	hypothetical prote
23	37	63.8	712	2	F97012	CD33 antigen homol
24	36	62.1	17	2	I67526	conserved hypothet
25	36	62.1	117	2	C83576	probable RNA-bindi
26	36	62.1	181	2	A96762	hypothetical prote
27	36	62.1	195	2	A95890	eggshell protein -
28	36	62.1	199	2	S38867	DNA repair protein
29	36	62.1	381	2	C90395	

30 36 62.1 452 2 S64211 probable transcript
31 36 62.1 611 2 S60914 lysine transport p
32 36 62.1 670 2 T02019 callus-associated
33 36 62.1 910 2 S38167 hypothetical prote
34 36 62.1 1414 1 S23809 collagen alpha 2(I
35 36 62.1 1928 2 JS0610 beta-galactosidase
36 35 60.3 109 2 F30607 Ig kappa chain V-I
37 35 60.3 112 2 JU0151 bipheryl-2,3-diol
38 35 60.3 113 2 F84671 hypothetical prote
39 35 60.3 157 2 S76232 hypothetical prote
40 35 60.3 166 2 T39586 rna binding protei
41 35 60.3 204 2 T29489 hypothetical prote
42 35 60.3 217 2 TS0004 RNA binding protei
43 35 60.3 258 2 S25624 coat protein - cas
44 35 60.3 270 2 AE1497 phosphoglycerate m
45 35 60.3 285 2 B82459 hypothetical prote

ALIGNMENTS

RESULT 1
B70749
probable Acyl-CoA Synthetase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: B70749
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Soares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:9825987; PMID:9634230
A;Accession: B70749
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-626 <COL>
A;Cross-references: GB:Z74697; GB:AL123456; NID:93261602; PIDN:CAA98985.1; PID:gl405966
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: fadD26
C;Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
F;103-610/Domain: acetate-CoA ligase homology <ACL>

Query Match 72.4%; Score 42; DB 2; Length 626;
Best Local Similarity 77.8%; Pred. No. 8.6;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFA 9
Db 73 YGSDPKGFA 81
||:|||||
||:|||||

RESULT 2
H90083
polyadenylate-binding protein [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: H90083
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Ren Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A95082; MUID:11323671; PMID:11323671
A;Accession: H90083
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <DOU>
A;Cross-references: GB:AF165818; NID:g13794428; PIDN:AAK39803.1; GSPDB:GN00150
C;Genetics:
A;Gene: pabl
A;Map position: 1

A:Genome: nucleomorph
C:Keywords: nucleomorph

Query Match 70.7%; Score 41; DB 2; Length 389;
Best Local Similarity 70.0%; Pred. No. 7.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
| : |||||
Db 222 YNSIPKGFAY 231

RESULT 3

S75579
hypotheical protein sll0804 - *Synechocystis* sp. (strain PCC 6803)

C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 02-Feb-2001
C:Accession: S75579
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 103-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S75579

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-453 <KAN>

A:Cross-references: EMBL:D90911; GB:AB001339; NID:gl653083; PIDN:BAA18140.1; PID:gl65322
A:Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: hypothetical protein sll0804; translation elongation factor Tu homology

C:Keywords: GTP binding; nucleotide binding; P-loop

F:62-176/Domain: translation elongation factor Tu homology <ETU>

F:68-75/Region: nucleotide-binding motif A (P-loop)

F:173-176/Region: GTP-binding NKXD motif

F:367-369/Region: GTP-binding SAX/L motif

Query Match 70.7%; Score 41; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPKG 7
| : |||||

Db 224 YGNSPKG 230

RESULT 4

A41519

posterior-group protein tudor - fruit fly (*Drosophila melanogaster*)

C:Species: *Drosophila melanogaster*

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999

C:Accession: A41519; S19019

R:Golubetski, G.S.; Bardsley, A.; Tax, F.; Boswell, R.E.

Genes Dev. 5, 2060-2070, 1991

A:Title: tudor, a posterior-group gene of *Drosophila melanogaster*, encodes a novel prote

A:Reference number: A41519; MUID:92038995; PMID:1936993

A:Accession: A41519

A:Molecule type: mRNA

A:Residues: 1-2515 <GOL>

A:Cross-references: GB:X62420; NID:g8753; PIDN:CAA44286.1; PID:g8754

C:Genetics:

A:Gene: tud

A:Cross-references: FlyBase:FBgn0003891

C:Superfamily: posterior-group protein tudor

Query Match 70.7%; Score 41; DB 2; Length 2515;
Best Local Similarity 87.5%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8
| : |||||

Db 2171 YGNSPKGF 2178

RESULT 5

H82175

multidrug resistance protein VC1634 [imported] - *Vibrio cholerae* (strain N16961 serogrou
C:Species: *Vibrio cholerae*
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: H82175

R:Reidberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: H82175

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-401 <HEI>

A:Cross-references: GB:AE003852; NID:G9656142; PIDN:AAF94785.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC1634

A:Map position: 1

C:Superfamily: bicyclomycin resistance protein

Query Match 67.2%; Score 39; DB 2; Length 401;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
| : |||||

Db 251 YGVSPDGFY 260

RESULT 6

A53377

CPE-binding protein - African clawed frog

N:Alternate names: cytoplasmic polyadenylation element-binding protein

C:Species: *Xenopus laevis* (African clawed frog)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: A53377

R:Hake, L.E.; Richter, J.D.

Cell 79, 617-627, 1994

A:Title: CPEB is a specificity factor that mediates cytoplasmic polyadenylation during X

A:Reference number: A53377; MUID:95042759; PMID:7954828

A:Accession: A53377

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-368 <HAK>

A:Cross-references: GB:U14169; NID:g987224; PIDN:AAA80483.1; PID:g624634

C:Superfamily: African clawed frog CPE-binding protein; ribonucleoprotein repeat homolog
F:314-388/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match 67.2%; Score 39; DB 1; Length 568;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10
| : |||||

Db 357 GNMPPKGYV 365

RESULT 7

D90034

hypothetical protein SA2135 [imported] - *Staphylococcus aureus* (strain N315)

C:Species: *Staphylococcus aureus*

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: D90034

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.

A;Reference number: AB9758; MUID:21311952; PMID:11418146
 A;Accession: D90034
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-402 <KUR>
 A;Cross-references: GB:BA000018; PID:g13702296; PIDN:BA843437.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: SA2135
 C;Superfamily: sodium-glutamate symport carrier protein

Query Match 65.5%; Score 38; DB 2; Length 402;
 Best Local Similarity 75.0%; Pred. No. 30;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8
 :|||:|:
 Db 368 YGNSPKAY 375

RESULT 8
 AD0735
 conserved hypothetical protein STY2039 [imported] - Salmonella enterica subsp. enterica
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AD0735
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AD0735
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-488 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD05592.1; PID:g16503079; GSPDB:GN00176
 C;Genetics:
 A;Gene: STY2039
 C;Superfamily: Haemophilus influenzae hypothetical protein HI1409

Query Match 65.5%; Score 38; DB 2; Length 488;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFA 9
 :|||:|:
 Db 323 FGQSPKGF 331

RESULT 9
 AG0621
 probable bacteriophage protein STY1048 [imported] - Salmonella enterica subsp. enterica
 C;Species: Salmonella enterica subsp. enterica serovar Typhi
 A;Note: this species has also been called Salmonella typhi
 C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C;Accession: AG0621
 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001
 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
 A;Reference number: AB0502; MUID:21534947; PMID:11677608
 A;Accession: AG0621
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-488 <PAR>
 A;Cross-references: GB:AL513382; PIDN:CAD05441.1; PID:g16502202; GSPDB:GN00176
 C;Genetics:
 A;Gene: STY1048

C;Superfamily: Haemophilus influenzae hypothetical protein HI1409

Query Match 65.5%; Score 38; DB 2; Length 488;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFA 9
 :|||:|:
 Db 323 FGQSPKGF 331

RESULT 10
 B9521
 protein F21D18.20 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C;Accession: B9521
 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86141; MUID:21016719; PMID:11130712
 A;Accession: B9521
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-488 <STO>
 A;Cross-references: GB:AE005173; NID:g8778515; PIDN:AAF79523.1; GSPDB:GN00141
 C;Genetics:
 A;Gene: F21D18.20
 A;Map position: 1

Query Match 65.5%; Score 38; DB 2; Length 488;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10
 :|||:|:
 Db 232 GSSPRGFKY 240

RESULT 11
 B87204
 probable acyl-CoA synthase [imported] - Mycobacterium leprae
 C;Species: Mycobacterium leprae
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 24-Aug-2001
 C;Accession: B87204
 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; H
 eam, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; S
 A;Title: Massive gene decay in the leprosy bacillus.
 A;Reference number: A86909; MUID:21128732; PMID:11234002
 A;Accession: B87204
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-583 <STO>
 A;Cross-references: GB:AL450380; NID:g13093967; PIDN:CAC31874.1; GSPDB:GN00147
 C;Genetics:
 A;Gene: fadD26
 C;Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase; acetate-CoA ligase homol

Query Match 65.5%; Score 38; DB 2; Length 583;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8

Db 30 YGSDPKGF 37
||: ||||

RESULT 12

JC7206
phosphoprotein phosphatase (EC 3.1.3.16) [validated] - shiitake mushroom
C:Species: Lentinula edodes (shiitake mushroom)
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 20-Apr-2001
C:Accession: JC7206
R: Ishizaki, T.; Yokoyama, H.; Kajiwara, S.; Shishido, K.
Biosci. Biotechnol. Biochem. 64, 438-442, 2000
A:Title: Basidiomycete fungal gene encoding a regulatory subunit A homologue of protein
A:Reference number: JC7206; MUID:20199469; PMID:10737208
A:Accession: JC7206
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-588 <ISH>
A:Cross-references: DDBJ:AB027711; GB:AB027711; NID:g7416049; PID:g7416050
C:Genetics:
A:Gene: paal
C:Superfamily: phosphoprotein phosphatase 65K regulatory chain
C:Keywords: phosphoric monoester hydrolase

Query Match 65.5%; Score 38; DB 2; Length 588;
Best Local Similarity 60.0%; Pred. No. 44;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
||: ||||
Db 544 YGNTPEGEAF 553

RESULT 13

T19356
hypothetical protein C17E4.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19356
R: Percy, C.
submitted to the EMBL Data Library, October 1996
A:Reference number: Z19113
A:Accession: T19356
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-205 <WIL>
A:Cross-references: EMBL:Z81037; PIDN:CA802750.1; GSPDB:GN00019; CESP:C17E4.5
A:Experimental source: clone C17E4
C:Genetics:
A:Gene: CESP:C17E4.5
A:Map position: 1
A:Introns: 22/3; 120/2

Query Match 63.8%; Score 37; DB 2; Length 205;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
||: ||||
Db 114 FSGHPKGFAY 123

RESULT 14

B70372
flagellar protein FlgA - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: B70372
R: Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: B70372
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-223 <AQF>
A:Cross-references: GB:AE000709; NID:g2983373; PIDN:AAC06962.1; PID:g2983376; GB:AE000065
A:Experimental source: strain VF5
A:Gene: flgA

Query Match 63.8%; Score 37; DB 2; Length 223;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
||: ||||
Db 75 YKNSPRGFLH 84

RESULT 15

S59863
PolyA binding protein II - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999
C:Accession: S59863
R: Nemeth, A.; Krause, S.; Blank, D.; Jenny, A.; Jenoe, P.; Lustig, A.; Wahle, E.
Nucleic Acids Res. 23, 4034-4041, 1995
A:Title: Isolation of genomic and cDNA clones encoding bovine poly(A) binding protein II
A:Reference number: S59863; MUID:96071160; PMID:7479061
A:Accession: S59863
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-306 <NEM>
A:Cross-references: EMBL:X89969; NID:g1065677; PIDN:CAA62006.1; PID:g1051125
A:Note: the nucleotide sequence was submitted to the EMBL Data Library July 1995
C:Superfamily: bovine polyA binding protein II; ribonucleoprotein repeat homology
F:173-239/Domain: ribonucleoprotein repeat homology <RRW2>

Query Match 63.8%; Score 37; DB 1; Length 306;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
||: ||||
Db 208 FSGHPKGFAY 217

Search completed: July 29, 2004, 08:51.46
JOB time : 2.97911 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 0.665796 Seconds
(without alignments)
782.073 Million cell updates/sec

Title: US-09-661-992B-5
Perfect score: 58
Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	72.4	332	1 NDP2_VIBVY	P60056 vibrio vuln
2	42	72.4	583	1 FD26_MYCTU	Q10976 mycobacteri
3	41	70.7	2515	1 TUD_DROME	P25823 drosophila
4	37	63.8	223	1 FLGA_AQUAE	O67005 aquifex ae
5	37	63.8	394	1 PHVY_PSEAE	P20596 pseudomonas
6	37	63.8	394	1 PHVY_PSEFL	P00438 pseudomonas
7	37	63.8	1180	1 RNT1_DROME	Q9V953 drosophila
8	36	62.1	452	1 HOS2_YEAST	P53096 saccharomyc
9	36	62.1	611	1 LYPI_YEAST	P32487 saccharomyc
10	36	62.1	910	1 YK69_YEAST	P36165 saccharomyc
11	36	62.1	1928	1 LPH_FAT	Q02401 rattus norv
12	35	60.3	290	1 TODE_PSEPU	P13453 pseudomonas
13	35	60.3	291	1 BHCL_RHOGO	P47231 rhodococcus
14	35	60.3	332	1 CLC3_CAVPO	Q9QZY6 cavia porce
15	35	60.3	349	1 RNFD_PASMU	Q9CNP3 pasteurella
16	35	60.3	373	1 NLPD_SALTI	Q56131 salmonella
17	35	60.3	377	1 NLPD_SALDU	P39700 salmonella
18	35	60.3	377	1 NLPD_SALTY	P40827 salmonella
19	35	60.3	379	1 NLPD_ECOLI	P33648 escherichia
20	35	60.3	396	1 PARC_ECOLI	P17283 escherichia
21	35	60.3	464	1 FMC2_PSEAE	Q91587 pseudomonas
22	35	60.3	464	1 FUMC_PSESM	Q885V0 pseudomonas
23	35	60.3	490	1 JIPI_DROME	Q9W0K0 drosophila
24	35	60.3	503	1 ATEL_YEAST	P16639 saccharomyc
25	35	60.3	674	1 AGUA_THEMEA	P56105 thermotoga
26	35	60.3	1230	1 UGS4_SOLTU	Q43846 solanum tub
27	34	58.6	83	1 YODI_BACSU	Q34654 bacillus su
28	34	58.6	220	1 HB7B_XENLA	P04476 xenopus lae
29	34	58.6	246	1 Y625_MYCTU	P36915 mycobacteri
30	34	58.6	260	1 COAT_TYLCV	P27256 tomato yell
31	34	58.6	289	1 HXD8_MOUSE	P23463 mus musculu
32	34	58.6	290	1 HXD8_HUMAN	P13378 homo sapien
33	34	58.6	350	1 YL85_PYRAE	Q8ZVP4 pyrobaculum

34 34 58.6 427 1 RUI7_ARATH
35 34 58.6 429 1 THD1_MYCTU
36 34 1058 1 U202_ARATH
37 34 58.6 1866 1 VGNB_CPMV
38 34 58.6 2329 1 YLJ6_CABEL
39 33 56.9 109 1 KV3G_HUMAN
40 33 56.9 226 1 YB62_THEMEA
41 33 56.9 258 1 COAT_CLVK
42 33 56.9 258 1 COAT_CLVN
43 33 56.9 292 1 CDD_HAEIN
44 33 56.9 298 1 MIAA_AGRTS
45 33 56.9 317 1 TFB3_HALNI

Q42404 arabidopsis
Q10766 mycobacteri
Q9XIK4 arabidopsis
P03600 cowpea mosa
P34369 casnothabdi
P04206 homo sapien
Q9XOP5 thermotoga
P03561 cassava lat
P14966 cassava lat
P44325 haemophilus
P34436 agrobacteri
Q9HHK5 halobacteri

ALIGNMENTS

RESULT 1
NDP2_VIBVY
ID NDP2_VIBVY STANDARD; PRT; 332 AA.
AC P60056;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Nucleoid-associated protein ndpA 2.
GN NDPA2 OR VVA0877.
OS Vibrio vulnificus (strain VJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen C.Y., Wu K.M., Chang Y.C., Chang C.H., Tsai H.C., Liao T.L.,
RA Liu Y.M., Chen H.J., Shen A.B., Li J.C., Su T.L., Shao C.P., Lee C.T.,
RA Hor L.I., Tsai S.F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Seems to be associated with the nucleoid (By
CC similarity).
CC -!- SIMILARITY: Belongs to the ndpA family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP005347; BAC96903.1; -;
DR HAMAP; MF_00730; -; 1.
KW Complete proteome.
SQ SEQUENCE 332 AA; 38241 MW; 9272959A747674B0 CRC64;

Query Match 72.4%; Score 42; DB 1; Length 332;
Best Local Similarity 77.8%; Pred. No. 2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 9
||:|||||
Db 48 YGDKPKGFA 56

RESULT 2
FD26_MYCTU
ID FD26_MYCTU STANDARD; PRT; 583 AA.
AC Q10976;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Putative fatty-acid--CoA ligase fadd26 (EC 6.2.1.-) (Acyl-CoA
DE synthetase).


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RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjaj M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC CC -1- FUNCTION: INVOLVED IN THE ASSEMBLY PROCESS OF THE P-RING
CC FORMATION. IT MAY ASSOCIATE WITH FLGP ON THE ROD CONSTITUTING A
CC STRUCTURE ESSENTIAL FOR THE P-RING ASSEMBLY OR MAY ACT AS A
CC MODULATOR PROTEIN FOR THE P-RING ASSEMBLY (BY SIMILARITY).
CC CC -1- SUBCELLULAR LOCATION: Periplasmic (Probable).
CC CC -1- SIMILARITY: Belongs to the flgA family.
CC CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AE000709; AAC06962.1; -.
DR F1R: B70372; B70372.
DR InterPro: IPR004924; FlgA.
DR Pfam: PF03240; FlgA; 1.
KW Flagellum; Periplasmic; Signal; Complete proteome.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN 1 ? 223 FLAGELLA BASAL BODY P-RING FORMATION
FT CHAIN 1 ? 223 PROTEIN FLGA.
FT CHAIN 1 ? 223 PROTEIN FLGA.
SQ SEQUENCE 223 AA; 26303 MW; 98C0A5189D8254CD CRC64;

Query Match 63.8%; Score 37; DB 1; Length 223;
Best Local Similarity 60.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGNSPKGFAY 10
Db 75 YKNSPRGFLH 84

RESULT 5
PHY_PSEAE STANDARD; PRT; 394 AA.
AC P20586;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE P-hydroxybenzoate hydroxylase (EC 1.14.13.2) (4-hydroxybenzoate 3-
DE monooxygenase) (PHEH).
GN POBA OR PA0247.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89138003; PubMed=2465205;
RA Entsch B., Nan Y., Weaich K., Scott K.F.;
RT "Sequence and organization of poBa, the gene coding for p-
RT hydroxybenzoate hydroxylase, an inducible enzyme from Pseudomonas
RT aeruginosa.";
RL Gene 71:279-291(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

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RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=95025875; PubMed=7939628;
RA Gatti D.L., Palfey B.A., Lah M.S., Entsch B., Massey V., Ballou D.P.,
RA Ludwig M.L.;
RT "The mobile flavin of 4-OH benzoate hydroxylase.";
RL Science 266:110-114(1994).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=96140232; PubMed=8555229;
RA Gatti D.L., Entsch B., Ballou D.P., Ludwig M.L.;
RT "pH-dependent structural changes in the active site of
RT p-hydroxybenzoate hydroxylase point to the importance of proton and
RT water movements during catalysis.";
RL Biochemistry 35:567-578(1996).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF MUTANTS.
RX MEDLINE=94146010; PubMed=8312276;
RA Lah M.S., Palfey B.A., Schreuder H.A., Ludwig M.L.;
RT "Crystal structures of mutant Pseudomonas aeruginosa
RT p-hydroxybenzoate hydroxylases: the Tyr201Phe, Tyr385Phe, and
RT Asn300Asp variants.";
RL Biochemistry 33:1555-1564(1994).
CC CC -1- CATALYTIC ACTIVITY: 4-hydroxybenzoate + NADPH + O(2) =
CC -1- protocatechuate + NADP(+) + H(2)O.
CC CC -1- COFACTOR: FAD.
CC CC -1- PATHWAY: Degradation of benzoate to succinate and acetyl-CoA.
CC CC -1- SUBUNIT: Homodimer.
CC CC -1- SIMILARITY: TO P.PUTIDA SALICYLATE HYDROXYLASE.
CC CC -----
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CC -----
DR EMBL: M23173; AAA88455.1; -.
DR EMBL: AE004463; BAG03636.1; -.
DR F1R: J70384; WHPSEA.
DR PDB: 1DOB; 30-NOV-94.
DR PDB: 1DOC; 30-NOV-94.
DR PDB: 1DOD; 30-NOV-94.
DR PDB: 1DOE; 30-NOV-94.
DR PDB: 1IUS; 03-APR-96.
DR PDB: 1IUT; 03-APR-96.
DR PDB: 1IUU; 03-APR-96.
DR PDB: 1IUV; 20-JUN-96.
DR PDB: 1IUX; 11-JUL-96.
DR PDB: 1PXA; 27-FEB-95.
DR PDB: 1PXB; 27-FEB-95.
DR PDB: 1PXC; 27-FEB-95.
DR PDB: 1D7L; 21-JAN-00.
DR PDB: 1K01; 27-FEB-02.
DR PDB: 1K0J; 27-FEB-02.
DR PDB: 1K0L; 27-FEB-02.
DR InterPro: IPR000733; Flav_monooxygenase.
DR InterPro: IPR002938; Mox_FAD_binding.
DR InterPro: IPR003042; Rng_monooxygenase.
DR Pfam: PF01494; FAD_binding_3; 1.
DR Pfam: PF01360; Monooxygenase; 1.
DR PRINTS: PR00420; RINGMONOXGNASE.
KW Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase;
KW Flavoprotein; FAD; NADP; 3D-structure; Complete proteome.
FT NP_BIND 4 32 FAD (POTENTIAL).
FT STRAND 2 2
FT STRAND 5 5

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FT HELIX 12 23
 FT TURN 24 25
 FT STRAND 28 31
 FT HELIX 36 40
 FT TURN 41 41
 FT STRAND 47 49
 FT HELIX 50 58
 FT TURN 59 60
 FT HELIX 63 68
 FT STRAND 70 72
 FT STRAND 74 79
 FT TURN 80 81
 FT STRAND 82 87
 FT HELIX 88 91
 FT TURN 92 93
 FT STRAND 97 99
 FT HELIX 102 116
 FT TURN 117 117
 FT STRAND 119 121
 FT TURN 122 123
 FT STRAND 125 130
 FT TURN 132 133
 FT STRAND 138 143
 FT TURN 144 145
 FT STRAND 146 151
 FT STRAND 154 157
 FT TURN 161 162
 FT HELIX 164 167
 FT TURN 168 168
 FT HELIX 171 173
 FT STRAND 175 190
 FT TURN 200 202
 FT TURN 205 206
 FT STRAND 209 215
 FT TURN 216 217
 FT STRAND 218 225
 FT TURN 227 228
 FT HELIX 231 233
 FT HELIX 236 246
 FT HELIX 249 252
 FT TURN 253 254
 FT STRAND 260 274
 FT STRAND 277 278
 FT TURN 279 280
 FT STRAND 281 283
 FT HELIX 285 287
 FT TURN 288 288
 FT STRAND 289 290
 FT STRAND 293 295
 FT HELIX 298 319
 FT STRAND 322 327
 FT HELIX 328 350
 FT HELIX 358 373
 FT HELIX 375 386
 SQ SEQUENCE 394 AA; 44323 MW; 1E7232854D9EC792 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 394;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGNPKGFA 9
 Db 201 YANHPRGFA 209

RESULT 6
 PHHY PSEFL STANDARD; PRT; 394 AA.
 AC P00436;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P-hydroxybenzoate hydroxylase (EC 1.14.13.2) (4-hydroxybenzoate 3-

DE monooxygenase).
 GN FOBA.
 OS Pseudomonas fluorescens.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=294;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93092974; PubMed=1459126;
 RA van Berkel W., Westphal A., Eschrich K., Eppink M., de Kok A.;
 RT "Substitution of Arg214 at the substrate-binding site of p-
 RT hydroxybenzoate hydroxylase from Pseudomonas fluorescens.";
 RL Eur. J. Biochem. 210:411-419(1992).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=82257502; PubMed=6809053;
 RA Weijer W.J., Hofsteenge J., Vereijken J.M., Jekel P.A., Beintema J.J.;
 RT "Primary structure of p-hydroxybenzoate hydroxylase from Pseudomonas
 RT fluorescens.";
 RL Biochim. Biophys. Acta 704:385-388(1982).
 RN [3]
 RP SEQUENCE OF 111-138 AND 270-280.
 RX MEDLINE=81114230; PubMed=6780352;
 RA Hofsteenge J., Vereijken J.M., Weijer W.J., Beintema J.J.,
 RA Wierenga R.K., Drenth J.;
 RT "Primary and tertiary structure studies of p-hydroxybenzoate
 RT hydroxylase from Pseudomonas fluorescens. Isolation and alignment of
 RT the CNBr peptides; interactions of the protein with flavin adenine
 RT dinucleotide.";
 RL Eur. J. Biochem. 113:141-150(1980).
 RN [4]
 RP SEQUENCE OF 1-52; 53-65 AND 66-110.
 RX MEDLINE=81114232; PubMed=6780353;
 RA Vereijken J.M., Hofsteenge J., Bak H.J., Beintema J.J.;
 RT "The amino-acid sequence of the three smallest CNBr peptides from p-
 RT hydroxybenzoate hydroxylase from Pseudomonas fluorescens.";
 RL Eur. J. Biochem. 113:151-157(1980).
 RN [5]
 RP SEQUENCE OF CNBR PEPTIDES AND TERTIARY STRUCTURE.
 RX MEDLINE=83209654; PubMed=6406229;
 RA Hofsteenge J., Weijer W.J., Jekel P.A., Beintema J.J.;
 RT "p-hydroxybenzoate hydroxylase from Pseudomonas fluorescens. 1.
 RT Completion of the elucidation of the primary structure.";
 RL Eur. J. Biochem. 133:91-108(1983).
 RN [6]
 RP SEQUENCE OF CNBR PEPTIDES AND STRUCTURE OF ACTIVE SITE.
 RX MEDLINE=83209623; PubMed=6406227;
 RA Weijer W.J., Hofsteenge J., Beintema J.J., Wierenga R.K., Drenth J.;
 RT "p-hydroxybenzoate hydroxylase from Pseudomonas fluorescens. 2.
 RT Fitting of the amino-acid sequence to the tertiary structure.";
 RL Eur. J. Biochem. 133:109-118(1983).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=80029705; PubMed=40036;
 RA Wierenga R.K., de Jong R.J., Kalk K.H., Hol W.G.J., Drenth J.;
 RT "Crystal structure of p-hydroxybenzoate hydroxylase.";
 RL J. Mol. Biol. 131:55-73(1979).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=88172509; PubMed=3351945;
 RA Schreuder H.A., van der Laan J.M., Hol W.G.J., Drenth J.;
 RT "Crystal structure of p-hydroxybenzoate hydroxylase complexed with
 RT its reaction product 3,4-dihydroxybenzoate.";
 RL J. Mol. Biol. 199:637-648(1988).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF REDUCED FORM.
 RX MEDLINE=93028353; PubMed=1409567;
 RA Schreuder H.A., van der Laan J.M., Swarte M.B.A., Kalk K.H.,
 RA Hol W.G.J., Drenth J.;
 RT "Crystal structure of the reduced form of p-hydroxybenzoate
 RT hydroxylase refined at 2.3-A resolution.";
 RL Proteins 14:178-190(1992).
 RN [10]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT LYS-44.
 RX MEDLINE=95354684; PubMed=7628466;
 RA Eppink M.H., Schreuder H.A., van Berkel W.J.;
 RT "Structure and function of mutant Arg44Lys of 4-hydroxybenzoate
 hydroxylase implications for NADPH binding.";
 RL Eur. J. Biochem. 231:157-165 (1995).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT LYS-42 AND SER-42.
 RX MEDLINE=98237589; PubMed=9578477;
 RA Eppink M.H., Schreuder H.A., van Berkel W.J.;
 RT "Lys42 and Ser42 variants of p-hydroxybenzoate hydroxylase from
 Pseudomonas fluorescens reveal that Arg42 is essential for NADPH
 binding.";
 RL Eur. J. Biochem. 253:194-201 (1998).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF VARIANTS.
 RX MEDLINE=99148809; PubMed=10025942;
 RA Eppink M.H., Buntol C., Schreuder H.A., van Berkel W.J.;
 RT "Phe161 and Arg166 variants of p-hydroxybenzoate hydroxylase.
 Implications for NADPH recognition and structural stability.";
 RL FEBS Lett. 443:251-255 (1999).
 CC -!- CATALYTIC ACTIVITY: 4-hydroxybenzoate + NADPH + O(2) =
 product + CO₂; FAD.
 CC -!- COFACTOR: FAD.
 CC -!- PATHWAY: Degradation of benzoate to succinate and acetyl-CoA.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SIMILARITY: TO E. COLI UBIIH/VISB AND VISC.
 CC -----
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 CC -----
 CC EMBL; X68438; CAA48483.1; --
 DR PIR; A90643; WHPSBF.
 DR PDB; 1PHH; 15-JAN-93.
 DR PDB; 2PHH; 15-APR-92.
 DR PDB; 1PBB; 30-SEP-94.
 DR PDB; 1PBC; 30-SEP-94.
 DR PDB; 1PBD; 30-SEP-94.
 DR PDB; 1PBE; 30-SEP-94.
 DR PDB; 1PBF; 30-SEP-94.
 DR PDB; 1PDH; 31-MAR-95.
 DR PDB; 1BF3; 12-AUG-98.
 DR PDB; 1BGJ; 12-AUG-98.
 DR PDB; 1BGN; 12-AUG-98.
 DR PDB; 1BKW; 22-JUL-98.
 DR PDB; 1CC4; 12-MAR-99.
 DR PDB; 1CC6; 12-MAR-99.
 DR PDB; 1CJ2; 30-APR-99.
 DR PDB; 1CJ3; 30-APR-99.
 DR PDB; 1CJ4; 30-APR-99.
 DR PDB; 1CJ5; 30-APR-99.
 DR InterPro; IPR000733; Flav_monooxygenase.
 DR InterPro; IPR002938; MoxF_FAD_binding.
 DR InterPro; IPR003042; Rug_moxxygenase.
 DR Pfam; PF01494; FAD_binding_3; 1.
 DR Pfam; PF01360; Monooxygenase; 1.
 DR PRINTS; PR00420; RNMNMOXGNASE.
 KW Aromatic hydrocarbons catabolism; Oxidoreductase; Monooxygenase;
 Flavoprotein; FAD; NADP; 3D-structure.
 FT NP_BIND 4 33 FAD (POTENTIAL).
 FT NP_BIND 276 286 FAD (POTENTIAL).
 FT CONFLICT 344 344 W -> Y (IN REF. 2).
 FT STRAND 2 2
 FT STRAND 5 8
 FT HELIX 12 23
 FT TURN 24 25
 FT STRAND 28 31
 FT STRAND 36 40
 FT HELIX 36 41
 FT TURN 41 41

FT STRAND 47 49
 FT HELIX 50 58
 FT TURN 59 60
 FT HELIX 63 68
 FT STRAND 70 72
 FT STRAND 74 79
 FT TURN 80 81
 FT STRAND 82 87
 FT HELIX 88 91
 FT TURN 92 93
 FT STRAND 97 99
 FT HELIX 102 116
 FT TURN 117 117
 FT STRAND 119 121
 FT TURN 122 123
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 FT STRAND 138 143
 FT TURN 144 145
 FT STRAND 146 151
 FT STRAND 154 157
 FT TURN 161 162
 FT HELIX 164 167
 FT TURN 168 168
 FT STRAND 171 173
 FT HELIX 175 190
 FT STRAND 200 203
 FT TURN 205 206
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 FT HELIX 293 295
 FT STRAND 298 318
 FT HELIX 322 327
 FT HELIX 328 350
 FT HELIX 358 371
 FT TURN 372 373

Query Match 63.8%; Score 37; DB 1; Length 394;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFA 9
 DB 201 YANHPRGFA 209

RESULT 7
 ID RNT1 DROME STANDARD; PRT; 1180 AA.
 AC Q9VIE3; Q9SRG9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Regulator of nonsense transcripts 1 homolog.
 GN UPE1 OR CG1559.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RN [1]


```

OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-12.
RX STRAIN=FI;
RX MEDLINE=89359301; PubMed=2670929;
RA Zylstra G.J., Gibson D.T.;
RT "Toluene degradation by Pseudomonas putida Fl. Nucleotide sequence of
RT the tdcC2BADE genes and their expression in Escherichia coli.";
RL J. Biol. Chem. 264:114940-14946(1989).
CC -1- CATALYTIC ACTIVITY: 3-methylnocatechol + O(2) = 2-hydroxy-6-oxo-
CC 2,4-heptadienoate.
CC -1- COFACTOR: Ferrous ion.
CC -1- PATHWAY: Toluene degradation; third step.
CC -1- SUBUNIT: Homooctamer.
CC -1- SIMILARITY: Belongs to the extradiol ring-cleavage dioxygenase
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J04996; AAA26010.1; -.
CC FIR: P36516; F36516.
CC HSP: P17297; LDHY.
CC InterPro: IPR004360; Gly_bleo_diox.
CC ProDom: IPR000486; Xdiol_dioxygns.
CC Pfam: PF00903; Glyoxalase; 1.
CC ProDom: PD000977; Xdiol_dioxygns; 1.
CC PROSITE: PS00082; EXTRADIOL_DIOXYGENAS; 1.
CC Oxidoreductase; Dioxygenase; Aromatic hydrocarbons catabolism; Iron.
CC INIT.MET 0
CC METAL 145 145 IRON (BY SIMILARITY).
CC METAL 209 209 IRON (BY SIMILARITY).
CC METAL 259 259 IRON (BY SIMILARITY).
CC SEQUENCE 290 AA; 32078 MW; 4752380FA5C249A9 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 290;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGNSPKGFA 9
||:|:|
Db 249 YGATPSGFA 257

RESULT 13
BHCL RHOG
ID BHCL RHOG STANDARD; PRT; 291 AA.
AC P47231;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 39, Last annotation update)
DE BiPhenyl-2,3-diol 1,2-dioxygenase I (EC 1.13.11.39) (23OHPB
DE oxygenase I) (2,3-dihydroxybiphenyl dioxygenase I) (DHBD I).
GN BHCL.
OS Rhodococcus globerulus.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=33008;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=P6;
RX MEDLINE=94171820; PubMed=8126007;
RA Asturias J.A., Eltis L.D., Prucha M., Timmis K.N.;
RT "Analysis of three 2,3-dihydroxybiphenyl 1,2-dioxygenases found in
RT Rhodococcus globerulus P6. Identification of a new family of
RT extradiol dioxygenases.";
RL J. Biol. Chem. 269:7807-7815(1994).

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CC -1- CATALYTIC ACTIVITY: Biphenyl-2,3-diol + O(2) = 2-hydroxy-6-oxo-6-
CC phenylhexa-2,4-dienoate + H(2)O.
CC -1- COFACTOR: Ferrous ion.
CC -1- PATHWAY: Degradation of biphenyls and polychlorobiphenyls (PCB) to
CC benzoic acid and chlorobenzoic acids.
CC -1- SIMILARITY: Belongs to the extradiol ring-cleavage dioxygenase
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X75633; CAA53297.1; -.
CC FIR: B53419; B53419.
CC HSP: P47228; LHAN.
CC InterPro: IPR004360; Gly_bleo_diox.
CC ProDom: IPR000486; Xdiol_dioxygns.
CC Pfam: PF00903; Glyoxalase; 1.
CC ProDom: PD000977; Xdiol_dioxygns; 1.
CC PROSITE: PS00082; EXTRADIOL_DIOXYGENAS; 1.
CC Oxidoreductase; Dioxygenase; Aromatic hydrocarbons catabolism; Iron.
CC METAL 146 146 IRON (BY SIMILARITY).
CC METAL 210 210 IRON (BY SIMILARITY).
CC METAL 260 260 IRON (BY SIMILARITY).
CC SEQUENCE 291 AA; 32081 MW; 104F189FE1EDDA6A CRC64;

Query Match 60.3%; Score 35; DB 1; Length 291;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGNSPKGFA 9
||:|:|
Db 250 YGATPSGFA 258

RESULT 14
CLC3 CAVPO
ID CLC3 CAVPO STANDARD; PRT; 332 AA.
AC Q9QX76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE T-cell surface glycoprotein CD1c3 precursor (CD1-c3 antigen).
GN CD1C3.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Hartley, and NIH 2; TISSUE=Thymus;
RX MEDLINE=20021845; PubMed=10553074;
RA Dascher C.C., Hiromatsu K., Naylor J.W., Brauer P.P., Brown K.A.,
RA Storey J.R., Behar S.M., Kawasaki E.S., Porcelli S.A., Brenner M.B.,
RA Leclair K.P.;
RT "Conservation of a CD1 multigene family in the guinea pig.";
RL J. Immunol. 163:5478-5488(1999).
CC -1- FUNCTION: Not known.
CC -1- SUBUNIT: Associates non-covalently with beta-2-microglobulin (By
CC similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
DR EMBL; AF145489; AAF12744.1; -.
DR HSSP; P11609; IC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGc1; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Glycoprotein; Signal; Transmembrane; Immunoglobulin domain;
KW Multigene family.
FT SIGNAL 1 17
FT CHAIN 18 332
FT DOMAIN 18 300
FT TRANSMEM 301 321
FT DOMAIN 322 332
FT DOMAIN 205 292
FT DISULFID 120 184
FT CARBOHYD 25 25
FT CARBOHYD 38 38
FT CARBOHYD 75 75
FT CARBOHYD 146 146
FT SEQUENCE 332 AA; 37437 MW; 19DA52E30CC05DFC CRC64;
Query Match 60.3%; Score 35; DB 1; Length 332;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 2 GNSPKGFAY 10
DB 125 GEPPKGFY 133
RESULT 15
RNFD_PASMU
ID RNFD_PASMU STANDARD; PRT; 349 AA.
AC Q9CNP3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Electron transport complex protein rnfd.
GN RNFD OR PM0384
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Pm70;
EX MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Faustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida Pm70."
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
CC -!- FUNCTION: May be part of a membrane complex involved in electron
CC transport (By similarity).
CC -!- SUBUNIT: Composed of at least six subunits; rnfa, rnfb, rnfc,
CC rnfd, rnfe and rnfg (By similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -!- SIMILARITY: Belongs to the nqrB/rnfd family.
CC -----
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CC -----
DR EMBL; AE006074; AA02468.1; -.
DR HAMAP; MF_00462; 1.
DR InterPro; IPR004338; NOR2_Rnfd_Rnfe.
```

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DR Pfam; PF03116; NOR2_Rnfd_Rnfe; 1.
KW Electron transport; Transmembrane; Inner membrane; Complete proteome.
FT TRANSMEM 21 38
FT TRANSMEM 42 64
FT TRANSMEM 69 88
FT TRANSMEM 98 118
FT TRANSMEM 125 145
FT TRANSMEM 214 234
FT TRANSMEM 237 257
FT TRANSMEM 269 289
FT TRANSMEM 299 319
FT TRANSMEM 320 340
SQ SEQUENCE 349 AA; 38470 MW; DE45D6E3370FC6BE CRC64;
Query Match 60.3%; Score 35; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 43;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 YGNSPKGFAY 10
DB 315 YGNYPDGVAF 324
Search completed: July 29, 2004, 08:47:34
Job time : 2.6658 secs
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 2.0235 Seconds
(without alignments)
1559.271 Million cell updates/sec

Title: US-09-661-992B-5
Perfect score: 58
Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: SPTEMBL_25.*
 - 2: sp_archaea.*
 - 3: sp_bacteria.*
 - 4: sp_fungi.*
 - 5: sp_human.*
 - 6: sp_invertebrate.*
 - 7: sp_mammal.*
 - 8: sp_mhc.*
 - 9: sp_organelle.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	75.9	120	11 Q920E8	Q920E8 mus musculus
2	43	74.1	294	16 Q8XN61	Q8XN61 clostridium
3	42	72.4	160	3 Q9UTU1	Q9UTU1 schizosacch
4	42	72.4	583	16 Q7TXM1	Q7TXM1 mycobacteri
5	42	72.4	833	3 Q13620	Q13620 schizosacch
6	41	70.7	389	8 Q98R27	Q98R27 guillardi
7	41	70.7	453	16 P74064	P74064 synecocyst
8	41	70.7	467	16 Q832Q1	Q832Q1 enterococc
9	41	70.7	1044	10 Q84UN0	Q84UN0 oryza sativ
10	41	70.7	2515	5 Q9W2J8	Q9W2J8 drosophila
11	40	69.0	203	3 Q875X7	Q875X7 saccharomyc
12	40	69.0	291	5 Q9VTH9	Q9VTH9 drosophila
13	40	69.0	1312	16 Q98NH6	Q98NH6 rhizobium 1
14	39	67.2	401	16 Q9KRK6	Q9KRK6 vibrio chol
15	39	67.2	491	4 Q9BZB7	Q9BZB7 homo sapien
16	39	67.2	559	13 Q9DED5	Q9DED5 carassius a

17	39	67.2	559	13 Q9YGX5	Q9YGX5 brachydanio
18	39	67.2	561	11 P70166	P70166 mus musculu
19	39	67.2	566	4 Q9BZB8	Q9BZB8 homo sapien
20	39	67.2	568	13 Q91572	Q91572 xenopus lae
21	39	67.2	600	13 Q93386	Q93386 brachydanio
22	38	65.5	183	12 Q7T4G5	Q7T4G5 spring vire
23	38	65.5	183	12 Q7T4F0	Q7T4F0 spring vire
24	38	65.5	203	16 Q7VGF8	Q7VGF8 helicobacte
25	38	65.5	241	16 Q7WHG5	Q7WHG5 bordetella
26	38	65.5	241	16 Q7W9A2	Q7W9A2 bordetella
27	38	65.5	241	16 Q7VYQ9	Q7VYQ9 bordetella
28	38	65.5	248	13 Q7SZS0	Q7SZS0 brachydanio
29	38	65.5	258	13 Q7ZTU8	Q7ZTU8 xenopus lae
30	38	65.5	402	16 Q99RS8	Q99RS8 staphylococ
31	38	65.5	402	16 Q9NV56	Q9NV56 staphylococ
32	38	65.5	488	10 Q9LNG1	Q9LNG1 arabidopsis
33	38	65.5	488	16 Q8Z7V6	Q8Z7V6 salmomella
34	38	65.5	488	16 Q8Z622	Q8Z622 salmomella
35	38	65.5	488	16 Q83LM6	Q83LM6 shigella fl
36	38	65.5	489	16 Q83T15	Q83T15 salmomella
37	38	65.5	583	16 Q9Z5K5	Q9Z5K5 mycobacteri
38	38	65.5	588	3 Q9P982	Q9P982 lentinula e
39	37	63.8	205	5 Q93233	Q93233 caenorhabdi
40	37	63.8	255	3 Q9P4V6	Q9P4V6 candida boi
41	37	63.8	258	5 Q9W086	Q9W086 drosophila
42	37	63.8	292	11 Q8CC96	Q8CC96 mus musculu
43	37	63.8	298	4 Q86U42	Q86U42 homo sapien
44	37	63.8	302	11 Q35935	Q35935 mus musculu
45	37	63.8	306	4 Q43484	Q43484 homo sapien

ALIGNMENTS

RESULT 1

Q920E8 PRELIMINARY; PRT; 120 AA.
ID Q920E8
AC Q920E8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
in Mammalian Cells";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307936; AAL09420.1; -;
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON_TER 1
FT NON_TER 120
SQ SEQUENCE 120 AA; 13204 MW; DC4834ABIDE56F3C CRC64;

Query Match 75.9%; Score 44; DB 11; Length 120;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10

DB 101 YGNSPAWFAY 110

RESULT 2

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Q8XN61
ID Q8XN61 PRELIMINARY; PRT; 294 AA.
AC Q8XN61;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Probable beta-glycosyltransferase.
GN CPE0477.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
CX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003186; BAB80183.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001173; Glyco_transf.2.
DR Pfam; PF00535; Glycos_transf.2; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 294 AA; 34356 MW; 390BF593B712CA35 CRC64;

Query Match 74.1%; Score 43; DB 16; Length 294;
Best Local Similarity 70.0%; Pred. No. 7.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
|:|||||
DB 222 YKNNPKGFAY 231

Query Match 72.4%; Score 42; DB 16; Length 583;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 9
|:|||||
DB 30 YGSDPKGFAY 38

RESULT 3
Q8XN61 PRELIMINARY; PRT; 160 AA.
AC Q8XN61;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN 2257512.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
CX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=968 h30;
RX MEDLINE=20223868; PubMed=10759689;
RA Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
RA Hiraoka Y.;
RT "Large-scale screening of intracellular protein localization in living
RT fission yeast cells by the use of a GFP-fusion genomic DNA library.";
RL Genes Cells 3:169-180(2000).
DR EMBL; AB028003; BAA87307.1; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 160
SQ SEQUENCE 160 AA; 18116 MW; 168A1F1D5D5A94F5 CRC64;

Query Match 72.4%; Score 42; DB 3; Length 160;

Q8XN61 PRELIMINARY; PRT; 294 AA.
AC Q8XN61;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Probable beta-glycosyltransferase.
GN CPE0477.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
CX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / Type A;
RX MEDLINE=21664373; PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003186; BAB80183.1; -.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR001173; Glyco_transf.2.
DR Pfam; PF00535; Glycos_transf.2; 1.
KW Transferase; Complete proteome.
SQ SEQUENCE 294 AA; 34356 MW; 390BF593B712CA35 CRC64;

Query Match 74.1%; Score 43; DB 16; Length 294;
Best Local Similarity 70.0%; Pred. No. 7.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
|:|||||
DB 222 YKNNPKGFAY 231

Query Match 72.4%; Score 42; DB 16; Length 583;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 9
|:|||||
DB 30 YGSDPKGFAY 38

RESULT 4
Q7TXM1 PRELIMINARY; PRT; 583 AA.
AC Q7TXM1;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Fatty-acid-CoA ligase FADD26 (Fatty-acid-CoA synthetase)
DE (Fatty-acid-CoA synthase) (EC 6.2.1.1.-).
GN FADD26 OR MB2955.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
CX NCBI_TaxID=1765;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Carrier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Iacroix C., Monsemp C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
DR EMBL; BX248344; CAD96642.1; -.
KW Ligase; Complete proteome.
SQ SEQUENCE 583 AA; 63011 MW; 9DCD9DF3F5A416CB CRC64;

Query Match 72.4%; Score 42; DB 16; Length 583;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 9
|:|||||
DB 30 YGSDPKGFAY 38

RESULT 5
Q13620 PRELIMINARY; PRT; 833 AA.
AC Q13620;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein (RNA binding protein, 5 RRM RNA recognition
DE MOTIFS).
GN F1029 OR SBP22H7.02C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
CX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972 H-;
RA Kushida N., Yamazaki S., Tanaka T., Jinno K., Haikawa Y., Yamazaki J.,
RA Yamamoto S., Sekine M., Oguchi A., Nagai Y., Sakai M., Aoki K.,
RA Ogura K., Otsuka R., Kudo Y., Yanagida M., Machida M., Zhang M.Q.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Murphy L., Harris D., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB004535; BAA21408.1; -.

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DR EMBL; AL590883; CAC37370.1; -.
DR GeneDB SPombe; GFBP22H7.02c; -.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 5.
DR SMART; SM00360; RRM; 5.
DR PROSITE; PS50102; RRM; 5.
DR PROSITE; PS00030; RRM_RNP_1; 2.
KW Hypothetical protein.
SQ SEQUENCE 833 AA; 93676 MW; 64FE767D43E02FE4 CRC64;

Query Match 72.4%; Score 42; DB 3; Length 833;
Best Local Similarity 87.5%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NSPKGFAY 10
:|||||
Db 361 NNPKGFAY 368

RESULT 6
Q98RZ7 PRELIMINARY; PRT; 389 AA.
AC Q98RZ7;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Polyadenylate-binding protein.
GN PAB1.
OS Guillardia theta (Cryptomonas phi).
OC Nucleomorph.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OC NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2123349; PubMed=11323671;
RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,
RA Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
RT "The highly reduced genome of an enslaved algal nucleus.";
RL Nature 410:1091-1096(2001).
DR EMBL; AF165818; AAK39803.1; -.
DR FIR; H90083; H90083.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 3.
DR SMART; SM00360; RRM; 3.
DR PROSITE; PS50102; RRM; 3.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 389 AA; 45171 MW; 7214503D3D37FE40D CRC64;

Query Match 70.7%; Score 41; DB 8; Length 389;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 YGNSPKGFAY 10
:|||||
Db 222 YNSPKGFAY 231

RESULT 7
P74064 PRELIMINARY; PRT; 453 AA.
AC P74064;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein sll0804.
GN SLL0804.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OC NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nanno K., Okumura S.,
RA Shimpō S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL; D90911; BAA18140.1; -.
DR FIR; S75579; S75579.
DR InterPro; IPR005225; Small_GTP.
DR TIGRFAMs; TIGR00231; small_GTP; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 453 AA; 49154 MW; 4CFDFAED77536F59 CRC64;

Query Match 70.7%; Score 41; DB 16; Length 453;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNSPKG 7
:|||||
Db 224 YGNSPKG 230

RESULT 8
Q832Q1 PRELIMINARY; PRT; 467 AA.
AC Q832Q1;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Membrane protein, putative.
DE EF2169.
GN EF2169.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OC NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan M.,
RA Daugherty S., Deboy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Utterback T., Radune D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis.";
RL Science 299:2071-2074(2003).
DR EMBL; AF016953; AAO81901.1; -.
DR TIGR; EF2189; -.
DR InterPro; IPR007016; Wzy_C.
DR Pfam; PF04932; Wzy_C; 1.
KW Complete proteome.
SQ SEQUENCE 467 AA; 53562 MW; D122B0FDC63B0AF CRC64;

Query Match 70.7%; Score 41; DB 16; Length 467;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 YGNSPKGFA 9
:|||||
Db 341 FGTSKGF 349

RESULT 9
Q84UN0 PRELIMINARY; PRT; 1044 AA.
AC Q84UN0;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

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DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE B1027A11.31 protein.
 GN B1027A11.31.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriactoidae; Oryzaceae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Nipponbare;
 RA Sasaki T., Matsumoto T., Katayose Y.;
 RT "Oryza sativa nipponbare (GA3) genomic DNA, chromosome 8, BAC
 clone: B1027A11.31";
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP005464; BAC66751.1; -;
 DR InterPro; IPR004242; Transposase 21.
 DR Pfam; PF02992; Transposase 21; 1_
 SQ SEQUENCE 1044 AA; 117074 MW; D383E61C5D5C0B7A CRC64;

 Query Match 70.7%; Score 41; DB 10; Length 1044;
 Best Local Similarity 77.8%; Pred. No. 69;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

 QY 2 GNSPKGRAY 10
 I:|||||:
 DB 959 GSSPKGRAH 967

 RESULT 10
 Q9W2J8
 ID Q9W2J8 PRELIMINARY; PRT; 2515 AA.
 AC Q9W2J8;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE TUD protein.
 GN TUD OR CG9450.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 EX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Sidon-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195 (2000).
 DR EMBL; AE003453; AAF46693.1; -;
 DR HSSP; Q16637; IG5V.
 DR Flybase; FBgn003891; tud.
 DR GO; GO:0019090; P:mitochondrial rRNA, mitochondrial export; IMP.
 DR GO; GO:0007315; P:pole plasm assembly; IMP.
 DR InterPro; IPR008191; Maternal_tudor.
 DR InterPro; IPR002999; Tudor.
 DR Pfam; PF00567; TUDOR; 10.
 DR SMART; SM00333; TUDOR; 9.
 DR PROSITE; PS0304; TUDOR; 9.
 SQ SEQUENCE 2515 AA; 285264 MW; 1218700174D66701 CRC64;

 Query Match 70.7%; Score 41; DB 5; Length 2515;
 Best Local Similarity 87.5%; Pred. No. 1.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 YGNSPKGF 8
 I:|||||:
 DB 2171 YGNSPKSF 2178

 RESULT 11
 Q875X7
 ID Q875X7 PRELIMINARY; PRT; 203 AA.
 AC Q875X7;
 DT 01-JUN-2003 (Tremblrel. 24, Created)
 DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE LYPI (fragment).
 OS Saccharomyces castellii (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=27288;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS4309;
 RX MEDLINE=22482865; PubMed=12594514;
 RA Langkjaer R.B., Clifton P.F., Johnston M., Piskur J.;
 RT "Yeast genome duplication was followed by asynchronous differentiation
 of duplicated genes.";
 RL Nature 421:848-852 (2003).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS4309;
 RX Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AY144938; AAC032501.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.
 DR GO; GO:0005865; P:amino acid transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR002293; AA/rel_permease.
 DR InterPro; IPR004841; Permease_region.
 DR Pfam; PF00324; aa_permeases; 1.
 FT NON TER 1
 SQ SEQUENCE 203 AA; 23238 MW; 3FPB5C870A618156 CRC64;

 Query Match 69.0%; Score 40; DB 3; Length 203;
 Best Local Similarity 77.8%; Pred. No. 18;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;


```

QY 2 GNSPKGFAY 10
DB 21 GNAPKGFAY 29

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10
DB 119 GKPKGFAY 127

RESULT 12
Q9VTH9 PRELIMINARY; PRT; 291 AA.
AC Q9VTH9;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE CG11726 protein.
GN CG11726
OS Drosophila melanogaster (Fruit fly).
OC Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.Y.,
RA Brandon R.C., Rogers J.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Buseam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.G., Ketchum K.A.,
RA Kimmel P.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko B., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Furi V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AB003545; AAP0069.1;
DR FlyBase; FBgn036156; CG11726.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rim; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS00102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 291 AA; 32307 MW; 65A1P6D3407AA699 CRC64;

Query Match 69.0%; Score 40; DB 5; Length 291;
Best Local Similarity 77.8%; Pred. No. 26;

QY 2 GNSPKGFAY 9
DB 1183 GNEPKGFA 1190

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 9
DB 1183 GNEPKGFA 1190

RESULT 14
Q9KXK6 PRELIMINARY; PRT; 401 AA.
AC Q9KXK6;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Multidrug resistance protein.
GN VC1634.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

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RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.,
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 RT *cholerae*.";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004241; AAF94785.1; -.
 DR PIR; H82175; H82175.
 DR TIGR; VC1634; -.
 DR GO; GO:0016021; C: integral to membrane; IEA.
 DR GO; GO:0005215; P: transporter activity; IEA.
 DR GO; GO:0006810; P: transport; IEA.
 DR GO; GO:0006810; P: transport; IEA.
 DR InterPro; IPR004812; Eflux_Bor_CflA.
 DR InterPro; IPR007114; MFS.
 DR InterPro; IPR005828; Sub_transporter.
 DR Pfam; PF00083; sugar_tr; 1.
 DR TIGRFAMs; TIGR00710; efflux_Bor_CflA; 1.
 DR PROSITE; PS50850; MFS; 1.
 KW Complete proteome.
 SQ SEQUENCE 401 AA; 42914 MW; 814CD7A2A86E3BDB CRC64;

Query Match 67.2%; Score 39; DB 16; Length 401;
 Best Local Similarity 70.0%; Pred. No. 58;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 YGNSPKGFAY 10
 DB 251 YGVSPDGFY 260

RESULT 15
 Q3E2B7
 ID Q9B2B7 PRELIMINARY; PRT; 491 AA.
 AC Q9B2B7;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytoplasmic polyadenylation element-binding protein short form.
 GN CPB1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary and Brain;
 RA MEDLINE=2112522; PubMed=1123249;
 RA Welk J.F., Charlesworth A., Smith G.D., MacNicol A.M.;
 RT "Identification and characterization of the gene encoding human
 RT cytoplasmic polyadenylation element binding protein.";
 RL Gene 263:113-121(2001).
 DR EMBL; AF329403; AAK01240.1; -.
 DR GO; GO:0003676; P: nucleic acid binding; IEA.
 DR InterPro; IPR000504; RNA_rec_mot.
 DR PROSITE; PS50102; RRM; 2.
 SQ SEQUENCE 491 AA; 54162 MW; 561A40FED482262 CRC64;

Query Match 67.2%; Score 39; DB 4; Length 491;
 Best Local Similarity 66.7%; Pred. No. 72;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 GNSPKGFAY 10
 DB 280 GNMKGYYV 288

Search completed: July 29, 2004, 08:50:20
 Job time : 5.0235 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 3.08094 Seconds
(without alignments)
917.082 Million cell updates/sec

Title: US-09-661-992B-5

Perfect score: 58

Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62.

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	10	4 AAB20388	Aab20388 Anti-FIX/
2	58	100.0	16	4 AAB20444	Aab20444 Anti-FIX/
3	58	100.0	242	4 AAB20433	Aab20433 Anti-FIX/
4	42	72.4	583	6 ABR82455	AbR82455 FACULABE
5	42	72.4	583	7 ABR83540	AbR83540 M. tuberc
6	42	72.4	626	4 AAB66460	Aab66460 Protein e
7	41	70.7	2515	4 ABB64427	AbB64427 Drosophil
8	40	69.0	291	4 ABB63366	AbB63366 Drosophil
9	39	67.2	116	5 ABP08836	AbP08836 Human ORF
10	39	67.2	401	6 ABU49388	AbU49388 Protein e
11	38	65.5	129	3 AAY43866	Aay43866 Heavy cha
12	38	65.5	404	6 ABM72949	AbM72949 Staphyloc
13	37	63.8	151	5 ABJ01013	AbJ01013 Human bre
14	37	63.8	258	4 ABB68781	AbB68781 Drosophil
15	37	63.8	365	5 AAW59884	Aaw59884 Amino aci
16	37	63.8	365	5 ABG95556	AbG95556 Human nov
17	37	63.8	365	6 ABO34750	AbO34750 Fragment
18	36	62.1	92	3 AAG02102	AgO2102 Human sec
19	36	62.1	117	5 ABP03818	AbP03818 Human ORF
20	36	62.1	118	4 ABG00681	AbG00681 Novel hum
21	36	62.1	130	4 ABG55227	AbG55227 Novel hum
22	36	62.1	183	3 AAY70228	Aay70228 Human RNA
23	36	62.1	183	4 AAB92806	Aab92806 Human pro
24	36	62.1	198	4 ABG00682	AbG00682 Novel hum
25	36	62.1	216	3 AAY84429	Aay84429 Amino aci

26	36	62.1	216	3 AAY70220	Aay70220 Human RNA
27	36	62.1	238	4 ABG15228	AbG15228 Novel hum
28	36	62.1	261	4 AAB93180	Aab93180 Human pro
29	36	62.1	261	6 AAE36184	Aae36184 Human CGD
30	36	62.1	271	4 AAM41266	Aam41266 Human pol
31	36	62.1	280	6 ABU11773	AbU11773 Human MDD
32	36	62.1	287	4 AAM39480	Aam39480 Human pol
33	36	62.1	373	7 ADB94921	AdB94921 Programme
34	36	62.1	396	4 AAB65770	Aab65770 Cysteine
35	36	62.1	396	7 ADB94789	AdB94789 Programme
36	36	62.1	452	6 ABR52983	AbR52983 Protein s
37	36	62.1	484	5 ABP40557	AbP40557 Staphyloc
38	36	62.1	696	6 ABU17558	AbU17558 Protein e
39	36	62.1	710	3 AAW90940	Aaw90940 Pyrococcu
40	36	62.1	767	4 ABB67398	AbB67398 Drosophil
41	36	62.1	969	4 ABB63009	AbB63009 Drosophil
42	36	62.1	1928	7 ADD48254	AdD48254 Rat Prote
43	35	60.3	13	7 ABR61868	AbR61868 Mouse Mab
44	35	60.3	63	3 AAG49954	Aag49954 Arabidops
45	35	60.3	63	3 AAG10161	Aag10161 Arabidops

ALIGNMENTS

RESULT 1

AAB20388

ID AAB20388 standard; peptide; 10 AA.

XX AAB20388;

XX AC

XX 21-JUN-2001 (first entry)

XX DE Anti-FIX/FIXa antibody 193/AD3 CDR3.

XX XX

Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;
Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
complementarity determining region; CDR.

XX OS Mus musculus.

XX XX WO200119992-A2.

XX XX 22-MAR-2001.

XX PF 13-SEP-2000; 2000WO-EP008936.

XX PR 14-SEP-1999; 99AT-00001576.

XX XX (BAXT) BAXTER AG.

XX PI Scheiflinger F, Kerschbaumer R, Falkner F, Dörner F;

XX DR WPI; 2001-290358/30.

XX XX New factor IX/factor IXa antibodies and their derivatives useful for
increasing amidolytic activity of factor IXa, and for treating blood
coagulation disorders such as hemophilia A and hemorrhagic diathesis.

XX PS Claim 7; Page 74; 138pp; English.

XX CC The present sequence is that of complementarity determining region 3
(CDR3) of the heavy chain of an antibody expressed by mouse hybridoma
193/AD3. This antibody has anti-Factor IX (FIX) or anti-activated Factor
IX (FIXa) activity. It is an example of anti-FIX/FIXa antibodies of the
CC invention. Such antibodies and their derivatives (including those that
comprise the present CDR3 peptide) have factor VIIa (FVIIa) cofactor
activity or FIXa activating activity. Administration of the antibodies or
their derivatives leads to an increase in the procoagulant activity of
CC FIXa, even in the presence of FVIIa inhibitors. This allows for rapid
CC blood coagulation even in the absence of FVIII or FVIIa, and in the case
of FVIII inhibitor patients. The antibodies or their derivatives are used

CC in a claimed pharmaceutical composition for treating patients with blood
 CC coagulation disorders, especially haemophilia A and haemorrhagic
 CC diathesis
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 58; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YGNSPKGFAY 10
 |||||
 DB 1 YGNSPKGFAY 10
 |||||
 RESULT 2
 AAB20444
 ID AAB20444 standard; peptide; 16 AA.
 AC AAB20444;
 XX
 DT 21-JUN-2001 (first entry)
 XX
 DE Anti-FIX/FIXa antibody CDR3.
 XX
 KW Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
 KW complementarity determining region; CDR.
 XX
 OS Mus musculus.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 2 /note= "any amino acid"
 FT
 FT Misc-difference 3 /note= "any amino acid"
 FT
 FT Misc-difference 14 /note= "any amino acid"
 FT
 FT Misc-difference 15 /note= "any amino acid"
 FT
 FT
 XX WO200119992-A2.
 XX
 XX
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000WO-EP008936.
 XX
 PR 14-SEP-1999; 99AT-00001576.
 XX
 PA (BAXT) BAXTER AG.
 XX
 PI Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
 XX
 DR WPI; 2001-290358/30.
 XX
 PT New factor IX/factor IXa antibodies and their derivatives useful for
 PT increasing amidolytic activity of factor IXa, and for treating blood
 PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
 XX
 PS Claim 7; Page 74; 138pp; English.
 XX
 CC The present sequence is that of complementarity determining region 3
 CC (CDR3) of an antibody having anti-Factor IX (FIX) or anti-activated
 CC Factor IX (FIXa) activity. Such antibodies and their derivatives
 CC (including those that comprise the present CDR3 peptide) have Factor
 CC VIIIa (FVIIIa) cofactor activity or FIXa activating activity.
 CC Administration of the antibodies or their derivatives leads to an
 CC increase in the procoagulant activity of FIXa, even in the presence of
 CC FVIIIa inhibitors. This allows for rapid blood coagulation even in the
 CC absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients.
 CC The antibodies or their derivatives are used in a claimed pharmaceutical
 CC composition for treating patients with blood coagulation disorders,

CC especially haemophilia A and haemorrhagic diathesis
 XX
 SQ Sequence 16 AA;
 Query Match 100.0%; Score 58; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 YGNSPKGFAY 10
 |||||
 DB 4 YGNSPKGFAY 13
 |||||
 RESULT 3
 AAB20433
 ID AAB20433 standard; protein; 242 AA.
 XX
 AC AAB20433;
 XX
 DT 21-JUN-2001 (first entry)
 XX
 DE Anti-FIX/FIXa antibody 193/AD3 scFv.
 XX
 KW Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
 XX
 OS Mus musculus.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Protein 1..119
 FT /label= VH
 FT Region 98..108
 FT /label= CDR3
 FT Peptide 120..134
 FT /label= Linker
 FT Protein 135..242
 FT /label= VL
 FT Region 223..231
 FT /label= CDR3
 XX
 PN WO200119992-A2.
 XX
 XX
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000WO-EP008936.
 XX
 PR 14-SEP-1999; 99AT-00001576.
 XX
 PA (BAXT) BAXTER AG.
 XX
 PI Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
 XX
 DR WPI; 2001-290358/30.
 XX
 PT New factor IX/factor IXa antibodies and their derivatives useful for
 PT increasing amidolytic activity of factor IXa, and for treating blood
 PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
 XX
 PS Claim 8; Fig 14; 138pp; English.
 XX
 CC The present sequence is that of a single chain Fv (scFv) derivative of
 CC antibody 193/AD3, comprising the heavy (VH) and light (VL) chain variable
 CC regions of 193/AD3 joined by an artificial, flexible linker peptide. The
 CC scFv was obtained by PCR amplification of cDNAs for 193/AD3 VH and VL
 CC regions and cloning in vector pDAP2. 193/AD3 is an example of anti-human
 CC Factor IX (FIX)/activated factor IX (FIXa) antibodies of the invention.
 CC Anti-FIX/FIXa and their derivatives, including scFv and CDR3 fragments,
 CC have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity.
 CC Administration leads to an increase in the procoagulant activity of FIXa,

Query Match 72.4%; Score 42; DB 7; Length 583;
 Best Local Similarity 77.8%; Pred. No. 83;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFA 9
 ||: |||||
 Db 30 YGSDPKGFA 38

RESULT 6
 AAB66460
 ID AAB66460 standard; protein; 626 AA.
 XX
 AC AAB66460;
 XX
 DT 09-APR-2001 (first entry)
 XX
 DE Protein encoded by Mycobacterium tuberculosis fad26 (Rv2930) gene.
 XX
 KW Mycobacterium tuberculosis; attenuated microorganism; fad26; Rv2930;
 KW signature tagged transposon mutant; mutant library;
 KW mycobacterial infection; actinomycetales; antibacterial; immunostimulant;
 KW vaccine.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200102555-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 06-JUL-2000; 2000WO-IB000950.
 XX
 PR 06-JUL-1999; 99US-0142982P.
 PR 08-JUL-1999; 99US-0142833P.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Gicquel B, Guilhot C, Camacho L;
 XX
 DR WPI; 2001-091804/10.
 DR N-PSDB; AAF31627.
 XX
 PT Screening a mutant library for mutants unable to grow under specific
 PT conditions and for identifying loci involved in pathogenicity, comprises
 PT using signature tagged transposon mutagenesis.
 XX
 PS Example 8; Fig 5A; 159pp; English.
 XX
 CC The present sequence is given in a specification relating to a method for
 CC screening a library of mutants. The method comprises constructing a
 CC library with insertions in genes and/or regulatory regions of the
 CC organisms of interest, where the insertion contains a tag and/or a
 CC transposon associated with a tag. The mutants are identified by
 CC hybridisation of the tags to known sequences. The method is useful for
 CC treating an individual suffering from a mycobacterial infection,
 CC suspected of being infected with a Mycobacterium, or having been exposed
 CC to an infectious Mycobacterium. It is also useful for identifying and
 CC isolating mutants of actinomycetales and for identifying compounds that
 CC have antibiotic activity. The method is used to identify mutants of
 CC microorganisms, preferably an actinomycetales, such as M. tuberculosis,
 CC M. bovis, M. leprae, M. avium, M. intracellulare and M.
 CC paratuberculosis, that is unable to grow under specific conditions. It is
 CC especially useful for identifying loci involved in pathogenicity. It is
 CC useful in constructing vaccines. The method can be used to screen
 CC multiple libraries concurrently. It can screen libraries of different
 CC organisms or different strains of the same organism. The present protein
 CC is encoded by a gene which is disrupted by the insertion of the IS 1096
 CC transposon to produce an attenuated mutant of Mycobacterium tuberculosis
 XX
 SQ Sequence 626 AA;

Query Match 72.4%; Score 42; DB 4; Length 626;
 Best Local Similarity 77.8%; Pred. No. 89;

QY 1 YGNSPKGFA 9
 ||: |||||
 Db 30 YGSDPKGFA 38

RESULT 6
 AAB66460
 ID AAB66460 standard; protein; 626 AA.
 XX
 AC AAB66460;
 XX
 DT 09-APR-2001 (first entry)
 XX
 DE Protein encoded by Mycobacterium tuberculosis fad26 (Rv2930) gene.
 XX
 KW Mycobacterium tuberculosis; attenuated microorganism; fad26; Rv2930;
 KW signature tagged transposon mutant; mutant library;
 KW mycobacterial infection; actinomycetales; antibacterial; immunostimulant;
 KW vaccine.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN WO200102555-A1.
 XX
 PD 11-JAN-2001.
 XX
 PF 06-JUL-2000; 2000WO-IB000950.
 XX
 PR 06-JUL-1999; 99US-0142982P.
 PR 08-JUL-1999; 99US-0142833P.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Gicquel B, Guilhot C, Camacho L;
 XX
 DR WPI; 2001-091804/10.
 DR N-PSDB; AAF31627.
 XX
 PT Screening a mutant library for mutants unable to grow under specific
 PT conditions and for identifying loci involved in pathogenicity, comprises
 PT using signature tagged transposon mutagenesis.
 XX
 PS Example 8; Fig 5A; 159pp; English.
 XX
 CC The present sequence is given in a specification relating to a method for
 CC screening a library of mutants. The method comprises constructing a
 CC library with insertions in genes and/or regulatory regions of the
 CC organisms of interest, where the insertion contains a tag and/or a
 CC transposon associated with a tag. The mutants are identified by
 CC hybridisation of the tags to known sequences. The method is useful for
 CC treating an individual suffering from a mycobacterial infection,
 CC suspected of being infected with a Mycobacterium, or having been exposed
 CC to an infectious Mycobacterium. It is also useful for identifying and
 CC isolating mutants of actinomycetales and for identifying compounds that
 CC have antibiotic activity. The method is used to identify mutants of
 CC microorganisms, preferably an actinomycetales, such as M. tuberculosis,
 CC M. bovis, M. leprae, M. avium, M. intracellulare and M.
 CC paratuberculosis, that is unable to grow under specific conditions. It is
 CC especially useful for identifying loci involved in pathogenicity. It is
 CC useful in constructing vaccines. The method can be used to screen
 CC multiple libraries concurrently. It can screen libraries of different
 CC organisms or different strains of the same organism. The present protein
 CC is encoded by a gene which is disrupted by the insertion of the IS 1096
 CC transposon to produce an attenuated mutant of Mycobacterium tuberculosis
 XX
 SQ Sequence 626 AA;

Query Match 70.7%; Score 41; DB 4; Length 2515;
 Best Local Similarity 87.5%; Pred. No. 5.8e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8
 ||: |||||
 Db 2171 YGNSPKSF 2178

RESULT 8
 ABB63366
 ID ABB63366 standard; protein; 231 AA.
 XX
 AC ABB63366;
 XX
 DT 26-MAR-2002 (first entry)

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFA 9
 ||: |||||
 Db 73 YGSDPKGFA 81

RESULT 7
 ABB64427
 ID ABB64427 standard; protein; 2515 AA.
 XX
 AC ABB64427;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 20073.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US009231.
 XX
 PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL08530.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX
 PS Disclosure; SEQ ID NO 20073; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 2515 AA;

XX Drosophila melanogaster polypeptide SEQ ID NO 16890.
 XX Drosophila; developmental biology; cell signalling; insecticide;
 KW Pharmaceutical.
 XX Drosophila melanogaster.
 OS WO200171042-A2.
 XX WO200171042-A2.
 FN 27-SEP-2001.
 PD 23-MAR-2001; 2001WO-US009231.
 XX 23-MAR-2001; 2000US-0191637P.
 XX 23-MAR-2000; 2000US-00614150.
 PR 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 PA Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 FI N-PSDB; ABL07469.
 DR New isolated nucleic acid detection reagent for detecting 1000 or more
 XX genes from Drosophila and for elucidating cell signalling and cell-cell
 XX interactions.
 PT Disclosure; SEQ ID NO 16890; 21pp + Sequence Listing; English.
 PS The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABP57737-
 CC ABP72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 291 AA;
 Query Match 69.0%; Score 40; DB 4; Length 291;
 Best Local Similarity 77.8%; Pred. No. 88;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 GNSPKGFAY 10
 Db 119 GKRPKGFAY 127
 RESULT 9
 ABP08836
 ID ABP08836 standard; protein; 116 AA.
 XX AC ABP08836;
 XX 25-JUN-2002 (first entry)
 DT Human ORFX protein sequence SEQ ID NO:17654.
 DE Human; open reading frame; ORFX; Gene therapy; cancer; cirrhosis;
 XX hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.
 XX Homo sapiens.
 OS
 XX

PN WO200192523-A2.
 XX 06-DEC-2001.
 XX 29-MAY-2001; 2001WO-US010836.
 XX 30-MAY-2000; 2000US-0206132P.
 XX 29-AUG-2000; 2000US-0228716P.
 XX (CURA-) CURAGEN CORP.
 XX Shimkets RA, Leach MD;
 PI WPI; 2002-106308/14.
 DR N-PSDB; ABN24588.
 XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders.
 XX Disclosure; SEQ ID NO 17654; 1037pp; English.
 XX The present invention describes substantially purified human proteins
 CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP0010 to ABP1500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage. N.B. The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 116 AA;
 Query Match 67.2%; Score 39; DB 5; Length 116;
 Best Local Similarity 77.8%; Pred. No. 50;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 YGNSPKGFA 9
 Db 65 YGNSPDGFA 73
 RESULT 10
 ABU49388
 ID ABU49388 standard; protein; 401 AA.
 XX AC ABU49388;
 XX 19-JUN-2003 (first entry)
 DT Protein encoded by Prokaryotic essential gene #34915.
 DE Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW Vibrio cholerae.
 XX
 OS
 XX WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX DR WPI; 2003-029926/02.

XX DR N-PSDB; ACA53258.

XX PT New antisense nucleic acids, useful for identifying proteins or screening

XX PT for homologous nucleic acids required for cellular proliferation to

XX PT isolate candidate molecules for rational drug discovery programs.

XX PS Claim 25; SEQ ID NO 77312; 1766pp; English.

XX CC The invention relates to an isolated nucleic acid comprising any one of

XX CC the 6213 antisense sequences given in the specification where expression

XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:

XX CC (1) a vector comprising a promoter operably linked to the nucleic acid

XX CC encoding a polypeptide whose expression is inhibited by the antisense

XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

XX CC polypeptide or its fragment whose expression is inhibited by the

XX CC antisense nucleic acid; (4) an antibody capable of specifically binding

XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

XX CC proliferation or the activity of a gene in an operon required for

XX CC proliferation; (7) identifying a compound that influences the activity of

XX CC the gene product or that has an activity against a biological pathway

XX CC required for proliferation, or that inhibits cellular proliferation; (8)

XX CC identifying a gene required for cellular proliferation or the biological

XX CC pathway in which a proliferation-required gene or its gene product lies

XX CC or a gene on which the test compound that inhibits proliferation of an

XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

XX CC compound's activity; (11) a culture comprising strains in which the gene

XX CC product is overexpressed or underexpressed; (12) determining the extent

XX CC to which each of the strains is present in a culture or collection of

XX CC strains; or (13) identifying the target of a compound that inhibits the

XX CC proliferation of an organism. The antisense nucleic acids are useful for

XX CC identifying proteins or screening for homologous nucleic acids required

XX CC for cellular proliferation to isolate candidate molecules for rational

XX CC drug discovery programs, or for screening homologous nucleic acids

XX CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,

XX CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of

XX CC the target prokaryotic essential genes. Note: The sequence data for this

XX CC patent did not form part of the printed specification, but was obtained

XX CC in electronic format directly from WIPO at

XX CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 401 AA;

Query Match 67.2%; Score 39; DB 6; Length 401;

Best Local Similarity 70.0%; Pred. No. 1.9e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10

DB 251 YGVSPDGFY 260

RESULT 11

RAY43866

ID AAY43866 standard; peptide; 129 AA.

XX AC AAY43866;

XX DT 11-FEB-2000 (first entry)

XX DE Heavy chain (VH) gene sequence of *Bacillus anthracis* antibody 7-1.

XX KW Heavy chain; VH; IGG; monoclonal antibody; spore; *Bacillus*;

XX KW VH gene usage; anthrax.

XX OS Mus sp.

XX PN WO9355842-A1.

XX PD 04-NOV-1999.

XX PF 27-APR-1999; 99WO-US009122.

XX PR 29-APR-1998; 98US-00069628.

XX PA (UABR-) UAB RES FOUND.

XX PI Kearney JF;

XX DR WPI; 2000-013435/01.

XX PT Monoclonal antibody specific for *Bacillus* spores, used to detect anthrax.

XX PS Example 13; Page 53-54; 64pp; English.

XX CC AAY43862-75 represent the amino acid sequences of the heavy chain (VH)

XX CC gene sequences from antibodies against *Bacillus anthracis* spores. The

XX CC antibodies are produced by different hybridomas. The specification

XX CC describes monoclonal antibodies (especially IGG antibodies) which are

XX CC highly specific and can discriminate between the spores of the *Bacillus*

XX CC family. The antibodies are produced by exposing mice to *Bacillus* spores.

XX CC The humoral immune response to *Bacillus* spores shows a conservation of VH

XX CC gene usage which is distinct for each spore. Peptide fragments derived

XX CC from the antibodies are also capable of binding spores. The monoclonal

XX CC antibody, and peptide fragments of it, can be used to detect *Bacillus*

XX CC spores in a field sample. It is particularly useful for detecting anthrax

XX CC in a field sample

XX SQ Sequence 129 AA;

Query Match 65.5%; Score 39; DB 3; Length 129;

Best Local Similarity 70.0%; Pred. No. 84;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10

DB 77 YGNYPWFAY 86

RESULT 12

ABM72949

ID ABM72949 standard; protein; 404 AA.

XX AC ABM72949;

XX DT 20-NOV-2003 (first entry)

XX DE *Staphylococcus aureus* protein #2189.

XX KW Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;

XX KW enzymatic assay; antibiotic target.

XX OS *Staphylococcus aureus*.

XX PN WO200294868-A2.

XX PD 28-NOV-2002.

XX PF 27-MAR-2002; 2002WO-IB002637.

XX AC

PR 27-MAR-2001; 2001GB-00007661.
XX (CHIR-) CHIRON SPA.
XX
XX Masignani V, Mora M, Scarselli M;
XX WPI; 2003-120786/11.
XX N-PSDB; ACF74509.
XX
XX New Staphylococcus aureus protein, useful as a vaccine for treating or
XX preventing Staphylococcal infection, specifically an infection caused by
XX S. aureus, e.g. sepsis.
XX
XX Claim 1; SEQ ID NO 4378; 49pp; English.
XX
XX The invention relates to novel genes and encoded proteins from
XX Staphylococcus aureus. A composition comprising the S. aureus protein, a
XX nucleic acid encoding the protein, or an antibody to the protein, is
XX useful as a pharmaceutical, particularly as a vaccine for treating or
XX preventing infection due to Staphylococcus bacteria, specifically an
XX infection caused by S. aureus. The composition is particularly useful for
XX treating or preventing sepsis in a patient. The composition can also be
XX used for diagnostics. The protein is also used in an assay for enzymatic
XX studies and as a target for antibiotics. This sequence represents one of
XX the novel S. aureus proteins of the invention.
XX
XX Sequence 404 AA;
SQ
Query Match 65.5%; Score 38; DB 6; Length 404;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YGNSPKGF 8
Db ||||| :
370 YGNSPKAY 377
RESULT 13
ID ABJ01013 standard; protein; 151 AA.
XX
XX ABJ01013;
XX
XX 05-SEP-2002 (first entry)
XX Human breast specific protein SEQ ID NO: 96.
XX
XX Human; breast specific gene; breast cancer; gene therapy; breast disease;
XX cystostatic.
XX Homo sapiens.
XX WO200240672-A2.
XX
XX 23-MAY-2002.
XX
XX 20-NOV-2001; 2001WO-US045079.
XX
XX 20-NOV-2000; 2000US-0249998P.
XX 22-NOV-2000; 2000US-0252563P.
XX
XX (DIAD-) DIADEXUS INC.
XX
XX Salceda S, Macina RA, Recipon H, Cafferkey R, Sun Y, Liu C;
XX WPI; 2002-500220/53.
XX
XX Novel breast-specific polypeptides and polynucleotides encoding
XX polypeptide, useful for identifying, diagnosing, monitoring, staging,
XX imaging and treating breast cancer and non-cancerous disease states in
XX breast.
XX
XX Claim 11; Page 219; 243pp; English.

XX The present invention provides human breast specific coding sequences and
XX proteins. These are useful for detecting breast tissue and for detecting
XX and treating breast cancer and other breast diseases. The present
XX sequence is a breast specific polypeptide of the invention
SQ Sequence 151 AA;
Query Match 63.8%; Score 37; DB 5; Length 151;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 GNSPKGFA 9
Db ||||| :
6 GNGPRGFA 13
RESULT 14
ID ABB68781 standard; protein; 258 AA.
XX
XX ABB68781;
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 33135.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US009231.
XX
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-656960/75.
XX N-PSDB; ABL12884.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 33135; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16196-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 258 AA;
Query Match 63.8%; Score 37; DB 4; Length 258;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YGNSPKGF 8
Db ||||| :
1 YGNSPKGF 8

Db 188 YGNAPVGF 195

RESULT 15
AAW59884

ID AAW59884 standard; protein; 365 AA.
XX
AC AAW59884;
XX
XX 20-NOV-1998 (first entry)
XX
XX Amino acid sequence of the cDNA clone Bcl-like (HAICH29).
XX
XX Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
KW immunological disorder; autoimmune disease; anti-infectious agent.
XX
XX Homo sapiens.
OS
XX
PN WO9831800-A2.
XX
PD 23-JUL-1998.
XX
PF 21-JAN-1998; 98WO-US000960.
XX
PR 21-JAN-1997; 97US-0034204P.
PR 21-JAN-1997; 97US-0034205P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (AUCK-) AUCKLAND UNISERVICES LTD.
XX
PI Ni J, Rosen CA, Gentz RL, Feng P, Krissansen GW, Su JY;
XX
DR WPI; 1998-414099/35.
DR N-PSDB; AAV41925.
XX
XX New isolated polynucleotides and encoded polypeptides - used to develop
PT products for treating e.g. inflammatory diseases, infections,
PT immunological disorders, autoimmune diseases, allergies or tumours.
XX
PS Claim 1; Fig 12A-12D; 120pp; English.
XX
CC This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29),
CC used in the method of the invention. The products of the clone can be
CC used for treating conditions associated with abnormal expression of the
CC polypeptides. They can be used for e.g. treating chronic inflammatory
CC diseases, immunological disorders, autoimmune diseases, inflammatory
CC diseases, various allergies, and as anti-infectious agents. The products
CC can also be used for detection and diagnosis
XX
SQ Sequence 365 AA;

Query Match 63.8%; Score 37; DB 2; Length 365;
Best Local Similarity 60.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 YGNAPVGF 10
:
Db 267 FSGHPKGFAY 276

Search completed: July 29, 2004, 08:46:32
Job time : 5.08094 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:50:28 ; Search time 2.45431 Seconds

(without alignments)
1278.091 Million cell updates/sec

Title: US-09-661-992B-5

Perfect score: 58

Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	39	67.2	401	12	US-10-282-122A-77312
3	39	67.2	503	16	US-10-349-852-4
4	39	67.2	566	16	US-10-349-852-3
5	37	63.8	151	13	US-10-001-887-96
6	37	63.8	249	14	US-10-153-668-118
7	37	63.8	306	14	US-10-153-668-120
8	37	63.8	365	10	US-09-809-391-696
9	37	63.8	365	10	US-09-882-171-696
10	37	63.8	365	12	US-10-164-861-696
11	36	62.1	63	12	US-10-424-599-160543
12	36	62.1	229	12	US-10-425-114-62168
13	36	62.1	244	12	US-10-425-114-50501
14	36	62.1	245	12	US-10-425-114-49293
15	36	62.1	373	14	US-10-219-220-285

Sequence 153, App
Sequence 21911, A
Sequence 38308, A
Sequence 1947, Ap
Sequence 45482, A
Sequence 13515, A
Sequence 184117,
Sequence 274743,
Sequence 275965,
Sequence 232910,
Sequence 279854,
Sequence 140039,
Sequence 142198,
Sequence 47876, A
Sequence 59653, A
Sequence 73029, A
Sequence 65458, A
Sequence 126595,
Sequence 63048, A
Sequence 227299,
Sequence 250381,
Sequence 52135, A
Sequence 140042,
Sequence 279857,
Sequence 46096, A
Sequence 229389,
Sequence 162915,
Sequence 8711, Ap
Sequence 2151, Ap
Sequence 20626, A

396 14 US-10-219-220-153
452 15 US-10-369-493-21911
596 12 US-10-425-114-38308
611 15 US-10-369-493-1947
696 12 US-10-282-122A-45482
1038 14 US-10-156-761-13515
69 12 US-10-424-599-184117
95 12 US-10-424-599-274743
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243 12 US-10-425-114-52135
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358 12 US-10-424-599-229389
402 16 US-10-437-963-162915
410 15 US-10-369-493-8711
438 12 US-10-276-774-2151
457 15 US-10-369-493-20626

ALIGNMENTS

RESULT 1
US-10-437-963-115600
; Sequence 115600, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53221)B

; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14

; NUMBER OF SEQ ID NOS: 204966

; SEQ ID NO 115600

; LENGTH: 86

; TYPE: PRT

; ORGANISM: Oryza sativa

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT4530_19181C.1.pep

US-10-437-963-115600

Query Match 67.2%; Score 39; DB 16; Length 86;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10

Db 57 WGNSPQDFSY 66

RESULT 2

US-10-282-122A-77312

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; Sequence 77312, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77312
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Vibrio cholerae
; US-10-282-122A-77312

Query Match          67.2%; Score 39; DB 12; Length 401;
Best Local Similarity 70.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
Db 251 YGVSPDGFY 260

RESULT 3
US-10-349-852-4
; Sequence 4, Application US/10349852
; Publication No. US20040076970A1
; GENERAL INFORMATION:
; APPLICANT: MacNicol, Angus, M.
; TITLE OF INVENTION: Human Cytoplasmic Polyadenylation Element Binding
; FILE REFERENCE: D6443
; CURRENT APPLICATION NUMBER: US/10/349,852
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,121
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 4
; LENGTH: 503
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARSPLIC
; OTHER INFORMATION: sequence of the short form of cytoplasmic
; OTHER INFORMATION: polyadenylation element binding protein
; US-10-349-852-4

Query Match          67.2%; Score 39; DB 16; Length 503;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10
Db 292 GNMFKGYV 300

RESULT 4
US-10-349-852-3
; Sequence 3, Application US/10349852
; Publication No. US20040076970A1
; GENERAL INFORMATION:
; APPLICANT: MacNicol, Angus, M.
; TITLE OF INVENTION: Human Cytoplasmic Polyadenylation Element Binding
; FILE REFERENCE: D6443
; CURRENT APPLICATION NUMBER: US/10/349,852
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,121
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARSPLIC
; OTHER INFORMATION: sequence of the long form of cytoplasmic
; OTHER INFORMATION: polyadenylation element binding protein
; US-10-349-852-3

Query Match          67.2%; Score 39; DB 16; Length 566;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10
Db 355 GNMFKGYV 363

RESULT 5
US-10-001-887-96
; Sequence 96, Application US/10001887
; Publication No. US20020155464A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
; FILE REFERENCE: DEX-0269
; CURRENT APPLICATION NUMBER: US/10/001,887
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,998
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/252,563
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 151
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARSPLIC
; OTHER INFORMATION: sequence of the short form of cytoplasmic
; OTHER INFORMATION: polyadenylation element binding protein
; US-10-349-852-4

Query Match          67.2%; Score 39; DB 16; Length 503;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10
Db 292 GNMFKGYV 300

RESULT 4
US-10-349-852-3
; Sequence 3, Application US/10349852
; Publication No. US20040076970A1
; GENERAL INFORMATION:
; APPLICANT: MacNicol, Angus, M.
; TITLE OF INVENTION: Human Cytoplasmic Polyadenylation Element Binding
; FILE REFERENCE: D6443
; CURRENT APPLICATION NUMBER: US/10/349,852
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: 60/351,121
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: VARSPLIC
; OTHER INFORMATION: sequence of the long form of cytoplasmic
; OTHER INFORMATION: polyadenylation element binding protein
; US-10-349-852-3

Query Match          67.2%; Score 39; DB 16; Length 566;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10
Db 355 GNMFKGYV 363

RESULT 5
US-10-001-887-96
; Sequence 96, Application US/10001887
; Publication No. US20020155464A1
; GENERAL INFORMATION:
; APPLICANT: Salceda, Susana
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Cafferey, Robert
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific Genes and Pr
; FILE REFERENCE: DEX-0269
; CURRENT APPLICATION NUMBER: US/10/001,887
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/249,998
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: 60/252,563
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 137
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 151
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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-001-887-96

Query Match      63.8%; Score 37; DB 13; Length 151;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGFA 9
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Db 6 GNGPRGFA 13

RESULT 6
US-10-153-668-118
; Sequence 118, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-118

Query Match      63.8%; Score 37; DB 14; Length 249;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
   : |||||
Db 151 FSGHPKGFAY 160

RESULT 7
US-10-153-668-120
; Sequence 120, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR APPLICATION NUMBER: US 60/328,403

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-120

Query Match      63.8%; Score 37; DB 13; Length 151;
Best Local Similarity 75.0%; Pred. No. 94;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGFA 9
   |||:||||
Db 6 GNGPRGFA 13

RESULT 6
US-10-153-668-118
; Sequence 118, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 118
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-118

Query Match      63.8%; Score 37; DB 14; Length 249;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
   : |||||
Db 151 FSGHPKGFAY 160

RESULT 7
US-10-153-668-120
; Sequence 120, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR APPLICATION NUMBER: US 60/328,403

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-120

Query Match      63.8%; Score 37; DB 14; Length 365;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
   : |||||
Db 267 FSGHPKGFAY 276

RESULT 9
US-09-882-171-696
; Sequence 696, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
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1 PRIOR FILING DATE: 1997-03-07
2 PRIOR APPLICATION NUMBER: 60/040,626
3 PRIOR FILING DATE: 1997-03-07
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5 PRIOR FILING DATE: 1997-03-07
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8 PRIOR APPLICATION NUMBER: 60/040,163
9 PRIOR FILING DATE: 1997-03-07
10 PRIOR APPLICATION NUMBER: 60/047,600
11 PRIOR FILING DATE: 1997-05-23
12 PRIOR APPLICATION NUMBER: 60/047,615
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;; PRIOR APPLICATION NUMBER: 60/056,862
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,887
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/056,908
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/048,964
;; PRIOR FILING DATE: 1997-06-06
;; PRIOR APPLICATION NUMBER: 60/057,650
;; PRIOR FILING DATE: 1997-09-05
;; PRIOR APPLICATION NUMBER: 60/056,884
;; PRIOR FILING DATE: 1997-08-22
;; PRIOR APPLICATION NUMBER: 60/057,669
;; PRIOR FILING DATE: 1997-09-05

Query Match 63.8%; Score 37; DB 10; Length 365;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
: |||||
Db 267 PSHPKGFAY 276

RESULT 10
US-10-164-861-696
; Sequence 696, Application US/10164861
; Publication No. US200302248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-861-696

Query Match 63.8%; Score 37; DB 12; Length 365;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
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Db 267 PSHPKGFAY 276

RESULT 11
US-10-424-599-160543
; Sequence 160543, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 160543
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_11598C.1.pep
US-10-424-599-160543

Query Match 62.1%; Score 36; DB 12; Length 63;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
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Db 46 FGNHVKGFY 55

RESULT 12
US-10-425-114-62168
; Sequence 62168, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62168
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3354-003-B5_FLI.pep
US-10-425-114-62168

Query Match 62.1%; Score 36; DB 12; Length 229;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
: |||||
Db 204 YGYSPYGYGY 213

RESULT 13
US-10-425-114-50501
; Sequence 50501, Application US/10425114
; Publication No. US2004003488A1

; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 50501
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3150-100-E6_FLI.pap
US-10-425-114-50501

Query Match 62.1%; Score 36; DB 12; Length 244;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10
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Db 220 GSSPRGVAY 228

RESULT 14
US-10-425-114-49293
; Sequence 49293; Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 49293
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4742-010-C3_FLI.pap
US-10-425-114-49293

Query Match 62.1%; Score 36; DB 12; Length 245;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKGFAY 10
|:|:|:|
Db 220 GSSPRGVAY 228

RESULT 15
US-10-219-220-285
; Sequence 285; Application US/10219220
; Publication No. US20030082724A1
; GENERAL INFORMATION:
; APPLICANT: Flinn, Barry
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of plant development

; FILE REFERENCE: 11000.1022c1
; CURRENT APPLICATION NUMBER: US/10/219,220
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: U.S. No. US20030082724A1 09/325,932
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 290
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 285
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-219-220-285

Query Match 62.1%; Score 36; DB 14; Length 373;
Best Local Similarity 60.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
|:|:|:|
Db 305 YGKSPEGINY 314

Search completed: July 29, 2004, 09:12:25
Job time: 3.45431 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:27 ; Search time 0.900783 Seconds
(without alignments)
573.123 Million cell updates/sec

Title: US-09-661-992B-5

Perfect score: 58

Sequence: 1 YGNSPKGFAY 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	70.7	415	4	US-09-134-000C-6391
2	37	63.8	62	4	US-09-621-976-4459
3	37	63.8	365	4	US-09-149-476-696
4	37	63.8	365	4	US-09-010-147B-24
5	37	63.8	426	4	US-09-252-991A-32215
6	36	62.1	69	4	US-09-621-976-6307
7	36	62.1	149	4	US-09-252-991A-19973
8	36	62.1	396	4	US-09-325-932A-153
9	36	62.1	484	4	US-09-134-001C-5402
10	35	60.3	474	4	US-09-252-991A-29391
11	35	60.3	1197	3	US-08-836-567-12
12	35	60.3	1197	4	US-09-606-304-12
13	35	60.3	1230	2	US-08-968-542C-35
14	35	60.3	1230	4	US-08-554-467A-35
15	35	60.3	1257	4	US-08-750-152A-2
16	34	58.6	9	3	US-08-467-472C-12
17	34	58.6	9	3	US-08-384-061-12
18	34	58.6	9	4	US-08-852-207A-12
19	34	58.6	111	4	US-08-858-207A-464
20	34	58.6	166	4	US-09-543-681A-5529
21	34	58.6	263	5	PT-US94-00844-11
22	34	58.6	324	4	US-09-648-004-18
23	34	58.6	334	4	US-09-107-532A-6336
24	34	58.6	402	4	US-09-134-001C-4138
25	34	58.6	688	4	US-09-489-039A-9813
26	33	56.9	128	4	US-09-530-139-16
27	33	56.9	236	4	US-09-530-139-46

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28      33      56.9      238      4      US-09-530-139-36      Sequence 36, Appl
29      33      56.9      239      4      US-09-530-139-40      Sequence 40, Appl
30      33      56.9      250      4      US-09-530-139-44      Sequence 44, Appl
31      33      56.9      410      4      US-09-252-991A-21004      Sequence 21004, A
32      33      56.9      413      4      US-09-540-236-3494      Sequence 3494, Ap
33      33      56.9      434      4      US-09-198-452A-118      Sequence 118, App
34      33      56.9      510      4      US-09-134-000C-6635      Sequence 6635, Ap
35      33      56.9      849      4      US-09-489-039A-10225      Sequence 27, Appl
36      32      55.2      34      3      US-08-441-507-27      Sequence 27, Appl
37      32      55.2      34      4      US-07-969-875A-27      Sequence 27, Appl
38      32      55.2      74      3      US-08-441-507-11      Sequence 11, Appl
39      32      55.2      74      4      US-07-969-875A-11      Sequence 11, Appl
40      32      55.2      78      3      US-08-441-507-13      Sequence 13, Appl
41      32      55.2      78      3      US-08-441-507-14      Sequence 14, Appl
42      32      55.2      78      4      US-07-969-875A-13      Sequence 13, Appl
43      32      55.2      78      4      US-07-969-875A-14      Sequence 14, Appl
44      32      55.2      109      4      US-09-025-769B-16      Sequence 16, Appl
45      32      55.2      134      4      US-09-252-991A-31838      Sequence 31838, A

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ALIGNMENTS

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RESULT 1
US-09-134-000C-6391
; Sequence 6391, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6391
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6391

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Query Match      70.7%; Score 41; DB 4; Length 415;
Best Local Similarity 77.8%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 YGNSPKGFA 9
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Db      353 FGTSRKGFA 361

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RESULT 2
US-09-621-976-4459
; Sequence 4459, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4459
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4459

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Query Match 63.8%; Score 37; DB 4; Length 62;
Best Local Similarity 60.0%; Pred. No. 9.2;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 YGNSPKGFAY 10
Db 48 FSGHPKGFAY 57

RESULT 3
US-09-149-476-696
; Sequence 696 Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
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; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
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; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
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; EARLIER APPLICATION NUMBER: 60/043,674
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
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; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
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; EARLIER APPLICATION NUMBER: 60/056,874
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/057,761
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/047,595
EARLIER FILING DATE: 1997-08-23
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EARLIER FILING DATE: 1997-08-23
EARLIER APPLICATION NUMBER: 60/047,588
EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER FILING DATE: 1997-05-23
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EARLIER APPLICATION NUMBER: 60/056,908
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EARLIER APPLICATION NUMBER: 60/048,964
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EARLIER APPLICATION NUMBER: 60/057,650
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EARLIER APPLICATION NUMBER: 60/056,884
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EARLIER APPLICATION NUMBER: 60/057,669
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/049,610
EARLIER FILING DATE: 1997-06-13
EARLIER APPLICATION NUMBER: 60/061,060
EARLIER FILING DATE: 1997-10-02

Query Match 63.8%; Score 37; DB 4; Length 365;
Best Local Similarity 60.0%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 YGNSPKGFAY 10
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Db 267 FSGHPKGFAY 276

RESULT 4

US-09-010-147B-24
; Sequence 24, Application US/09010147B
; Patent No. 6653445
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,147B
; FILING DATE: 12-No. 6653445-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997
; APPLICATION NUMBER: US 60/034,204
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jonathan L. Klein
; REGISTRATION NUMBER: 41,119
; REFERENCE/DOCKET NUMBER: PF353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-010-147B-24

Query Match 63.8%; Score 37; DB 4; Length 365;
Best Local Similarity 60.0%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YGNSPKGFAY 10
: |||||
Db 267 FSGHPKGFAY 276

RESULT 5

US-09-252-991A-32215
; Sequence 32215, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142

```
; SEQ ID NO 32215
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32215

Query Match      63.8%; Score 37; DB 4; Length 426;
Best Local Similarity 66.7%; Pred. No. 71;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFPA 9
   |||||
Db 233 YANHPRGFA 241

RESULT 6
US-09-621-976-6307
; Sequence 6307, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621.976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 6307
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-6307

Query Match      62.1%; Score 36; DB 4; Length 69;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
   |||||
Db 46 YTRPRGFAY 55

RESULT 7
US-09-252-991A-19973
; Sequence 19973, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19973
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19973

Query Match      62.1%; Score 36; DB 4; Length 149;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGFPA 9
   |||||
Db 141 YQNPKGFA 149

RESULT 8
US-09-325-932A-153
; Sequence 153, Application US/09325932A
; Patent No. 6451604
; GENERAL INFORMATION:
; APPLICANT: Lasham, Annette
; APPLICANT: Flinn, Barry
; TITLE OF INVENTION: Compositions affecting programmed cell
; TITLE OF INVENTION: death and their use in the modification of forestry plant develop
; FILE REFERENCE: 1022
; CURRENT APPLICATION NUMBER: US/09/325.932A
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 206
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 153
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-325-932A-153

Query Match      62.1%; Score 36; DB 4; Length 396;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
   |||||
Db 328 YGKSPEGINY 337

RESULT 9
US-09-134-001C-5402
; Sequence 5402, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134.001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5402
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5402

Query Match      62.1%; Score 36; DB 4; Length 484;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YGNSPKGEA 9
   :|||||
Db 353 FGNSPSGIA 361

RESULT 10
US-09-252-991A-29391
; Sequence 29391, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
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;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 29391
;; LENGTH: 474
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29391

Query Match 60.3%; Score 35; DB 4; Length 474;
Best Local Similarity 85.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 NSPKGFA 9
|:|||||
Db 245 NAPKGA 251

RESULT 11
US-08-836-567-12
; Sequence 12, Application US/08836567
; Patent No. 6130367
; GENERAL INFORMATION:

;; APPLICANT: Kossmann, Jens
;; APPLICANT: Springer, Franziska
;; APPLICANT: Abel, Gernot
;; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
;; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
;; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FISH & NEAVE
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10020

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/836,567
;; FILING DATE: 24-JUL-1997
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/EP95/04415
;; FILING DATE: 09-NOV-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: DE P 44 41 408.0
;; FILING DATE: 10-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haley Jr., James F.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: Agrevo-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-596-9000
;; TELEFAX: 212-596-9090
;; INFORMATION FOR SEQ ID NO: 12:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1197 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-836-567-12

Query Match 60.3%; Score 35; DB 3; Length 1197;
Best Local Similarity 85.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSPKGF 8
|:|||||
Db 45 GSSPKGF 51

RESULT 12
US-09-606-304-12
; Sequence 12, Application US/09606304
; Patent No. 6483010
; GENERAL INFORMATION:

;; APPLICANT: Kossmann, Jens
;; APPLICANT: Springer, Franziska
;; APPLICANT: Abel, Gernot
;; TITLE OF INVENTION: DNA MOLECULES THAT CODE FOR ENZYMES
;; TITLE OF INVENTION: INVOLVED IN STARCH SYNTHESIS VECTORS BACTERIA TRANSGENIC
;; TITLE OF INVENTION: PLANT CELLS AND PLANTS CONTAINING SAID MOLECULES
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FISH & NEAVE
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10020

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/606,304
;; FILING DATE: 28-Jun-2000
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/836,567
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: DE P 44 41 408.0
;; FILING DATE: 10-NOV-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Haley Jr., James F.
;; REGISTRATION NUMBER: 27,794
;; REFERENCE/DOCKET NUMBER: Agrevo-4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 212-596-9000
;; TELEFAX: 212-596-9090
;; INFORMATION FOR SEQ ID NO: 12:

;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1197 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-606-304-12

Query Match 60.3%; Score 35; DB 4; Length 1197;
Best Local Similarity 85.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSPKGF 8
|:|||||
Db 45 GSSPKGF 51

RESULT 13
US-08-968-542C-35
; Sequence 35, Application US/08968542C
; Patent No. 5981728
; GENERAL INFORMATION:

;; APPLICANT: Myers, et al.
;; TITLE OF INVENTION: dult1 Codes For A No. 5981728el Starch
;; TITLE OF INVENTION: Synthase
;; NUMBER OF SEQUENCES: 35
;; CORRESPONDENCE ADDRESS:

ADDRESS: McGregor & Adler, LLP
STREET: 8011 Candle Lane
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 6.0.1 for Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,542C
FILING DATE: No. 5981728ember 12, 1997
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benjamin Aaron Adler, Ph.D., J.D.
REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D6036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (713) 777-2321
TELEFAX: (713) 777-6908
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 1230 amino acid residues
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: amino acid
DESCRIPTION: amino acid
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE:
US-08-968-542C-35
Query Match 60.3%; Score 35; DB 2; Length 1230;
Best Local Similarity 85.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 GNSPKGF 8
|:|||||
Db 78 GSSPKGF 84
RESULT 14
US-09-554-467A-35
; Sequence 35, Application US/09554467A
; Patent No. 6639125
; GENERAL INFORMATION:
; APPLICANT: Myers, Alan M.
; TITLE OF INVENTION: gull1 Coding for a No. 6639125el Starch Synthase and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: D6036PCT
; CURRENT APPLICATION NUMBER: US/09/554,467A
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: PCT/US98/24225
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 08/062,102
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 37
; SEQ ID NO 35
; LENGTH: 1230
; TYPE: PRT
; ORGANISM: potato
; FEATURE:
; OTHER INFORMATION: Deduced amino acid sequence of potato starch synthase
; OTHER INFORMATION: SSIII.
US-09-554-467A-35
Query Match 60.3%; Score 35; DB 4; Length 1230;

Best Local Similarity 85.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 2 GNSPKGF 8
|:|||||
Db 78 GSSPKGF 84
RESULT 15
US-08-750-152A-2
; Sequence 2, Application US/08750152A
; Patent No. 5977331
; GENERAL INFORMATION:
; APPLICANT: ASAKURA, YOKO
; APPLICANT: KIMURA, EIICHIRO
; APPLICANT: ABE, CHIZU YOSHIO
; APPLICANT: KAWAHARA, TSUYOSHI
; TITLE OF INVENTION: ALPHA-KETOGLUTARATE DEHYDROGENASE GENE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22152
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,152A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: NORMAN F. OBLON
; REGISTRATION NUMBER: 24,618
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1257 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-750-152A-2
Query Match 60.3%; Score 35; DB 2; Length 1257;
Best Local Similarity 50.0%; Pred. No. 5.2e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY 1 YGNSPKGFAY 10
|:|||||
Db 883 FANTPEGFNY 892
Search completed: July 29, 2004, 08:53:06
JOB time : 1.90078 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 09:09:13 ; Search time 16 seconds
(without alignments)
60.120 Million cell updates/sec

Title: US-09-661-992B-5
Perfect score: 58
Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1101

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	39.7	9	2 A28495	conopressin G - co
2	23	39.7	9	2 G41946	T-cell receptor ga
3	23	39.7	9	2 S39040	lysine-conopressin
4	21	36.2	8	2 FQ0701	unidentified 6.5/3
5	20	34.5	9	2 B28495	conopressin S - co
6	20	34.5	9	2 A29477	diuretic neuropept
7	20	34.5	9	2 S06375	arginine vasotocin
8	20	34.5	9	2 B61364	vasotocin - common
9	20	34.5	9	2 P20027	pev-tachykinin - p
10	20	34.5	10	2 A61131	Hydrin 2 - bullfro
11	19	32.8	9	2 A61363	bradykinin - commo
12	19	32.8	9	2 S65433	bradykinin - horn
13	19	32.8	9	2 A43065	hydroxyproline-3-b
14	19	32.8	10	2 S70721	heat shock protein
15	19	32.8	10	2 I40032	trpE protein - Bac
16	19	32.8	10	2 A40753	aldhyde ferredoxi
17	19	32.8	10	2 PH0944	T-cell receptor be
18	18	31.0	8	2 A39892	P element, P cytot
19	18	31.0	9	2 A61358	bradykinin-like pe
20	18	31.0	9	2 A61057	Thr-6 bradykinin -
21	18	31.0	9	2 A26744	bradykinin-like pe
22	18	31.0	9	2 B60579	bradykinin-like pe
23	18	31.0	9	2 B60246	ornitho-kinin - ch
24	18	31.0	10	2 A24196	acetylcholinestera
25	17	29.3	7	2 A60139	fatty-acid synthas
26	17	29.3	9	2 S35538	ribosomal protein
27	17	29.3	9	2 S66607	quinoline 2-oxidor
28	17	29.3	9	2 PC2021	oxytocin-related p
29	17	29.3	9	2 PT0324	19 heavy chain CRD

30	17	29.3	10	1 RHAQ1	gonadoliberin I -
31	16	27.6	4	2 A32480	achatin-I - giant
32	16	27.6	6	2 S14159	paraspinal crystal
33	16	27.6	8	2 F60588	sperm-activating p
34	16	27.6	8	2 F60588	sperm-activating p
35	16	27.6	8	2 G60588	sperm-activating p
36	16	27.6	9	2 A91466	oxytocin - hippopo
37	16	27.6	9	2 A92774	oxytocin - spotted
38	16	27.6	9	2 A93147	oxytocin - finback
39	16	27.6	9	2 A93408	oxytocin - Austral
40	16	27.6	9	2 B90667	oxytocin - rabbit
41	16	27.6	9	2 S15850	vitamin D3 26-mono
42	16	27.6	9	2 S10784	enamelin I - bovin
43	16	27.6	10	1 RHFGG	gonadoliberin - pi
44	16	27.6	10	1 RHSHG	gonadoliberin - sh
45	16	27.6	10	2 E60788	sperm-activating p

ALIGNMENTS

RESULT 1

A28495
N: conopressin G - cone shell (Conus geographus)
N: Alternate names: Lys-conopressin-G
C: Species: Conus geographus (geography cone)
C: Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 25-Apr-1997
C: Accession: A28495
R: Cruz, L.J.; de Santos, V.; Zafaralla, G.C.; Ramilo, C.A.; Zeikus, R.; Gray, W.R.; Oli,
J. Biol. Chem. 262, 15821-15824, 1987
A: Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from
A: Reference number: A92617; MUID:88058932; PMID:3680228
A: Accession: A28495
A: Molecule type: protein
A: Residues: 1-9 <CRU>
C: Superfamily: oxytocin-neurophysin
C: Keywords: amidated carboxyl end; venom
F: 1-6/Disulfide bonds: #status experimental
F: 9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 39.7%; Score 23; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NSPKG 7
DB 5 NCPKG 9

RESULT 2

G41946
T-cell receptor gamma chain (2t.23) - mouse (fragment)
C: Species: Mus musculus (house mouse)
C: Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C: Accession: G41946
R: Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A: Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma g
A: Reference number: A41946; MUID:92049316; PMID:1658619
A: Accession: G41946
A: Status: preliminary; not compared with conceptual translation
A: Molecule type: DNA
A: Residues: 1-9 <WHE>
C: Keywords: T-cell receptor

Query Match 39.7%; Score 23; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKGF 8
DB 2 YGSYSGF 9

```

RESULT 3
S39040
Lysine-conopressin - Erpobdella octoculata
C:Species: Erpobdella octoculata
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-1999
C:Accession: S39040
R:Salzer, M.; Bulet, P.; van Dorsselaer, A.; Malecha, J.
Eur. J. Biochem. 217, 897-903, 1993
A:Title: Isolation, structural characterization and biological function of a lysine-conopressin
A:Reference number: S39040; MUID:94039146; PMID:8223646
A:Accession: S39040
A:Molecule type: protein
A:Residues: 1-9 <SAL>

Query Match      39.7%; Score 23; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 NSPKG 7
DB      5 NCPKG 9

RESULT 4
PQ0701
unidentified 6.5/31K protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PQ0701
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimensional
A:Reference number: PQ0696
A:Accession: PQ0701
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-8 <KOM>

Query Match      36.2%; Score 21; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 YGNSPKG 7
DB      1 YGNPVTG 7

RESULT 5
B28495
conopressin S - cone shell (Conus striatus)
N:Alternate names: Arg-vasopressin-S
C:Species: Conus striatus (striated cone)
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 25-Apr-1997
C:Accession: B28495
R:Cruz, L.J.; de Santos, V.; Zafaralla, G.C.; Ramilo, C.A.; Zeikus, R.; Gray, W.R.; Oliv
J. Biol. Chem. 262, 15821-15824, 1987
A:Title: Invertebrate vasopressin/oxytocin homologs. Characterization of peptides from C
A:Reference number: A92617; MUID:88058932; PMID:3680228
A:Accession: B28495
A:Molecule type: protein
A:Residues: 1-9 <CRU>
C:Superfamily: oxytocin-neurophysin
C:Keywords: amidated carboxyl end; venom
F:1-6/Disulfide bonds: #status experimental
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match      34.5%; Score 20; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 NSPKG 7
DB      5 NCPKG 9

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DB      5 NCPRG 9

RESULT 6
A29477
diuretic neuropeptide F1 - migratory locust
C:Species: Locusta migratoria (migratory locust)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 31-Dec-1993
C:Accession: A29477
R:Proux, J.P.; Miller, C.A.; Li, J.P.; Carney, R.L.; Girardie, A.; Delaage, M.; Schooley
Biochem. Biophys. Res. Commun. 149, 180-186, 1987
A:Title: Identification of an arginine vasopressin-like diuretic hormone from Locusta mi
A:Reference number: A29477; MUID:88077077; PMID:3689410
A:Accession: A29477
A:Molecule type: protein
A:Residues: 1-9 <PRO>
A>Note: two neuroptides, F1 and F2, were identified. F2 is an antiparallel dimer of F1
C:Keywords: neuropeptide

Query Match      34.5%; Score 20; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 NSPKG 7
DB      5 NCPRG 9

RESULT 7
S06375
arginine vasotocin - sea lamprey
C:Species: Petromyzon marinus (sea lamprey)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 31-Mar-1997
C:Accession: S06375
R:Lane, T.F.; Sower, S.A.; Kawauchi, H.
Gen. Comp. Endocrinol. 70, 152-157, 1988
A:Title: Arginine vasotocin from the pituitary gland of the lamprey (Petromyzon marinus)
A:Reference number: S06375; MUID:88225976; PMID:3371648
A:Accession: S06375
A:Molecule type: protein
A:Residues: 1-9 <LAN>
C:Keywords: amidated carboxyl end; hormone; neuropeptide; pituitary
F:1-6/Disulfide bonds: #status experimental
F:9/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match      34.5%; Score 20; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 NSPKG 7
DB      5 NCPRG 9

RESULT 8
B61364
vasotocin - common carp
C:Species: Cyprinus carpio (common carp)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 20-Jun-2000
C:Accession: B61364
R:Acher, R.; Chauvet, J.; Chauvet, M.T.; Crepy, D.
Comp. Biochem. Physiol. A 14, 245-254, 1965
A:Title: Caracterisation des hormones neurohypophysaires d'un poisson osseux d'eau douce
A:Reference number: A61364
A:Accession: B61364
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <ACH>
C:Keywords: amidated carboxyl end; neuropeptide; posterior pituitary

Query Match      34.5%; Score 20; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```


Qy 3 NSPKG 7
| | |
Db 5 NCPKG 9

RESULT 9
PD0027
Dev-tachykinin - pensaeid shrimp (Panaeus vannamei) (fragment)
C/Species: Panaeus vannamei
C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 19-May-2000
C/Accession: PD0027
R/Nieto, J.; Veelaert, D.; Derru, R.; Waelkens, E.; Cerstiaens, A.; Coast, G.; Devreese, Biochem. Biophys. Res. Commun. 248, 406-411, 1998
A/Title: Identification of one tachykinin- and two kinin-related peptides in the brain of Rana temporaria
A/Reference number: PD0027; MUID:98342103; PMID:9675150
A/Accession: PD0027
A/Molecule type: protein
A/Residues: 1-9 <NIE>
C/Comment: This peptide belongs to myotropic neuropeptides.

Query Match 34.5%; Score 20; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SPKGF 8
: | |
Db 1 APSGF 5

RESULT 10
A61131
hydrin 2 - bullfrog
N/Alternate names: AVT-related peptide
N/Contains: Arg-vasotocin
C/Species: Rana catesbeiana (bullfrog)
C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Jul-1997
C/Accession: A61131
R/Iwamuro, S.; Hayashi, H.; Yamashita, M.; Kikuyama, S. Gen. Comp. Endocrinol. 84, 412-418, 1991
A/Title: Arginine vasotocin (AVT) and AVT-related peptide are major aldosterone-releasing factors in the bullfrog
A/Reference number: A61131; MUID:92225310; PMID:1806022
A/Accession: A61131
A/Molecule type: protein
A/Residues: 1-10 <IWA>
C/Comment: Both the decapeptide (hydrin 2) and the amidated nonapeptide (Arg-vasotocin) are released from the bullfrog brain
C/Suprafamily: oxytocin-neurophysin
C/Keywords: amidated carboxyl end; neuropeptide; pituitary
F/1-9/Product: Arg-vasotocin #status experimental <RVAS>
F/9/Modified site: amidated carboxyl end (Gly) (amide in mature form from following glycosylation)

Query Match 34.5%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.3e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NSPKG 7
| | |
Db 5 NCPKG 9

RESULT 11
A61363
bradykinin - common frog
C/Species: Rana temporaria (common frog)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 18-Aug-2000
C/Accession: A61363
R/Anastasi, A.; Erspamer, V.; Bertaccini, G. Comp. Biochem. Physiol. A 14, 43-52, 1965
A/Title: Occurrence of bradykinin in the skin of Rana temporaria.
A/Reference number: A61363
A/Accession: A61363
A/Status: preliminary
A/Molecule type: protein

A/Residues: 1-9 <ANA>
C/Suprafamily: unassigned animal peptides
C/Keywords: skin

Query Match 32.8%; Score 19; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PKGFA 9
| | |
Db 2 PPGFS 6

RESULT 12
S65433
bradykinin - horn fly (fragment)
C/Species: Haematobia irritans (horn fly)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C/Accession: S65433
R/Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, I.; Eur. J. Biochem. 237, 414-423, 1996
A/Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran Haematobia irritans
A/Reference number: S65433; MUID:96215437; PMID:8647080
A/Accession: S65433
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <WIJ>
A/Note: the source is designated as Haematobia irritans exigua

Query Match 32.8%; Score 19; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PKGFA 9
| | |
Db 2 PPGFS 6

RESULT 13
A43065
hydroxyproline-3-bradykinin - frog (Helleophryne purcellii)
C/Species: Helleophryne purcellii
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C/Accession: A43065
R/Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Visser, J. Experientia 35, 1133, 1979
A/Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of the South American frog Helleophryne purcellii
A/Reference number: A43065; MUID:80024576; PMID:468255
A/Accession: A43065
A/Molecule type: protein
A/Residues: 1-9 <NAK>
C/Keywords: bradykinin; hydroxyproline; skin
F/3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 32.8%; Score 19; DB 2; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PKGFA 9
| | |
Db 2 PPGFS 6

RESULT 14
S70721
heat shock protein C62.5 homolog - Salmonella typhimurium (fragment)
N/Alternate names: high temperature protein G
C/Species: Salmonella typhimurium
C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C/Accession: S70721
R/Qi, S.Y.; Li, Y.; Szyroki, A.; Giles, I.G.; Moir, A.; O'Connor, C.D. Mol. Microbiol. 17, 523-531, 1995
A/Title: Salmonella typhimurium responses to a bactericidal protein from human neutrophils

A;Reference number: S70719; MUID:96100451; PMID:8559071
A;Accession: S70721
A;Molecule type: Protein
A;Residues: 1-10 <QIS>
A;Experimental source: strain SL1344
C;Keywords: ATP binding; heat shock; molecular chaperone

Query Match 32.8%; Score 19; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 GNSPKGF 8
| :||
Db 3 GQETRGF 9

RESULT 15
I40032
trpE protein - Bacillus amyloliquefaciens (fragment)
C;Species: Bacillus amyloliquefaciens
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 15-Oct-1999
C;Accession: I40032
R;Yoshimura, K.; Uemura, J.; Seki, T.; Oshima, Y.
J. Bacteriol. 159, 905-912, 1984
A;Title: Construction of a promoter-probe vector for Bacillus subtilis host by using the
A;Reference number: I40032; MUID:85006754; PMID:6090398
A;Accession: I40032
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <RES>
A;Cross-references: GB:K02661; NID:g143775; PIDN:AB05353.1; PID:g143776

Query Match 32.8%; Score 19; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 NSPKGFAY 10
| :||
Db 1 NSQSFLE 8

Search completed: July 29, 2004, 09:15:03
Job time : 17 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:53:13 ; Search time 13 Seconds
(without alignments)
40.054 Million cell updates/sec

Title: US-09-661-992B-5
Perfect score: 58
Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 371

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	41.4	7	1 UN06_PINPS	P81675 pinus pinas
2	23	39.7	9	1 CONO_CONGE	P05486 conus geogr
3	20	34.5	9	1 CONO_CONST	P05487 conus stria
4	20	34.5	9	1 DNF1_LOCM1	P16339 locusta mig
5	20	34.5	9	1 OXYT_CYPCA	P23879 cyprinus ca
6	20	34.5	9	1 TEPA_LEUMA	P81736 leucophaea
7	19	32.8	9	1 OXYF_SCYCA	P42937 scyllorhinu
8	19	32.8	9	1 OXYT_RAUCJL	P42934 raja clavav
9	19	32.8	9	1 TKL1_LOCM1	P16223 locusta mig
10	18	31.0	9	1 KNL3_BOMVA	P83058 bombina var
11	18	31.0	10	1 PPCK_FAGHE	P80525 fasciola he
12	17	29.3	8	1 RS7_MYCIT	P33564 mycobacteri
13	17	29.3	8	1 UF07_MOUSE	P38644 mus musculu
14	17	29.3	9	1 AL10_CARMA	P81813 carcinus ma
15	17	29.3	9	1 OXYT_EISFO	P42938 eisenia foe
16	17	29.3	10	1 GON1_ALLMI	P37041 alligator m
17	17	29.3	10	1 Q2OB_COMTE	P80465 comamonas t
18	16	27.6	4	1 ACH1_ACHFU	P35904 achatina fu
19	16	27.6	9	1 OXYA_SCYCA	P42936 scyllorhinu
20	16	27.6	9	1 OXYA_SQAC	P42939 squalus aca
21	16	27.6	9	1 OXYT_OCRVU	P80027 octopus vul
22	16	27.6	9	1 OXYT_RABIT	P32878 oryctolagus
23	16	27.6	9	1 OXYV_SQAC	P43000 squalus aca
24	16	27.6	10	1 GON1_CLUPA	P81749 clupea pall
25	15	25.9	8	1 ALL7_CARMA	P81809 carcinus ma
26	15	25.9	9	1 ISOT_CYPECA	P42933 cyprinus ca
27	15	25.9	10	1 UH05_RAT	P56573 rattus norv
28	14.5	25.0	10	1 FNEU_RAT	P21996 rattus norv
29	14	24.1	8	1 RSI_ERWCH	P37985 erwinia chr
30	14	24.1	9	1 FAR3_MACRS	P83276 macrobrachi
31	14	24.1	9	1 NSK1_SABBU	P41492 sarcophaga
32	14	24.1	9	1 SAP_STOVA	P24047 stomopneute
33	14	24.1	10	1 AMPN_HELAM	P81731 helicoverpa

34 14 24.1 10 1 BPP8_BOTIN
35 14 24.1 10 1 BRK_ONCMY
36 14 24.1 10 1 COX2_THUOB
37 14 24.1 10 1 FAR7_MACRS
38 14 24.1 10 1 GON3_ONCRE
39 14 24.1 10 1 HTF_HELZE
40 14 24.1 10 1 LSK2_LEUMA
41 14 24.1 10 1 RL16_ACHLA
42 14 24.1 10 1 RLC2_ACHLA
43 14 24.1 10 1 TKNC_RANCA
44 13 22.4 5 1 PAP2_PARMA
45 13 22.4 5 1 TPIS_CANFA

ALIGNMENTS

RESULT 1

UN06_PINPS STANDARD; PRT; 7 AA.
ID P81675;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of needles (N141) (Fragment).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.6, its MW is: 25 kDa.
FT NON_TER 1
FT NON_TER 7
SQ SEQUENCE 7 AA; 823 MW; 69D76724486B5740 CRC64;

Query Match 41.4%; Score 24; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.4e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSP 5
|||
Db 2 YGNLP 6

RESULT 2

CONO_CONGE STANDARD; PRT; 9 AA.
ID P05486;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Lys-conopressin G.
OS Conus geographus (Geography cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=6491;
RN [1]
RP SEQUENCE.

RX MEDLINE=88058932; PubMed=3680228;
RA Cruz L.J., de Santos V., Zafaralla G.C., Ramilo C.A., Zeikus R.D.,
RA Gray W.R., Olivera B.M.;
RT "Invertebrate vasopressin/oxytocin homologs. Characterization of
RT peptides from Conus geographus and Conus straitus venoms.";

RL J. Biol. Chem. 262:15821-15824 (1987).

RN [2]

RP REVIEW.

RX MEDLINE=89024586; PubMed=3052286;

RA Gray W.R., Olivera B.M., Cruz L.J.;

RT "Peptide toxins from venomous Conus snails."

RL Annu. Rev. Biochem. 57:665-700 (1988).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.

DR PIR; A28495; A28495.

DR InterPro: IPR000981; Neurhyp_horm.

DR Pfam; PF00220; hormone4; 1.

DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.

KW Hormone; Amidation.

FT DISULFID 1 6

FT MOD RES 9 9

FT SEQUENCE 9 AA; 1037 MW; D4FC276EB4540059 CRC64;

Query Match 39.7%; Score 23; DB 1; Length 9;

Best Local Similarity 80.0%; Pred. No. 1.4e+05;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 NSPKG 7

DB 5 NCPKG 9

RESULT 3

CONO_CONST

ID CONO_CONST STANDARD; PRT; 9 AA.

AC P05487;

DT 01-NOV-1988 (Rel. 09, Created)

DT 01-NOV-1988 (Rel. 09, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Arg-conopressin S.

OS Conus striatus (Striated cone).

OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;

OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;

OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI_TaxID=6493;

RN [1]

RP SEQUENCE.

RX MEDLINE=88058932; PubMed=3680228;

RA Cruz L.J., de Santos V., Zafrazalla G.C., Ramilo C.A., Zeikus R.D.,

RA Gray W.R., Olivera B.M.;

RT "Invertebrate vasopressin/oxytocin homologs. Characterization of

RT peptides from Conus geographus and Conus striatus venoms."

RL J. Biol. Chem. 262:15821-15824 (1987).

RN [2]

RP REVIEW.

RX MEDLINE=89024586; PubMed=3052286;

RA Gray W.R., Olivera B.M., Cruz L.J.;

RT "Peptide toxins from venomous Conus snails."

RL Annu. Rev. Biochem. 57:665-700 (1988).

CC -!- FUNCTION: Targets vasopressin-oxytocin related receptors.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom duct.

CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.

DR PIR; B28495; B28495.

DR InterPro: IPR000981; Neurhyp_horm.

DR Pfam; PF00220; hormone4; 1.

DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.

KW Hormone; Amidation.

FT DISULFID 1 6

FT MOD RES 9 9

FT SEQUENCE 9 AA; 1031 MW; 17EB176EB4540050 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 9;

Best Local Similarity 60.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NSPKG 7

DB 5 NCPKG 9

Db 5 NCPKG 9

RESULT 4

DNFI_LOCFI

ID DNFI_LOCFI STANDARD; PRT; 9 AA.

AC P16339;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Locupressin (Diuretic neurotensin F1/F2).

OS Locusta migratoria (Migratory locust).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;

OC Acridoidea; Acrididae; Oedipodinae; Locusta.

OX NCBI_TaxID=7004;

RN [1]

RP SEQUENCE.

RC TISSUE=Suboesophageal ganglion, and Thoracic ganglion;

RX MEDLINE=88077077; PubMed=3689410;

RA Proulx J.P., Miller C.A., Li J.P., Carney R.L., Girardie A.,

RA Delaage M., Schooley D.A.;

RT "Identification of an arginine vasopressin-like diuretic hormone from

RT Locusta migratoria."

RL Biochem. Biophys. Res. Commun. 149:180-186 (1987).

CC -!- FUNCTION: DIURETIC HORMONE.

CC -!- SUBUNIT: Monomer (F1) and homodimer (F2); disulfide-linked.

CC -!- SIMILARITY: Belongs to the vasopressin/oxytocin family.

DR PIR; A29477; A29477.

DR InterPro: IPR000981; Neurhyp_horm.

DR Pfam; PF00220; hormone4; 1.

DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.

KW Hormone; Neuropeptide; Amidation.

FT DISULFID 1 6

FT DISULFID 1 1

FT DISULFID 6 6

FT MOD RES 9 9

FT SEQUENCE 9 AA; 976 MW; 56EB176EB451A057 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 9;

Best Local Similarity 60.0%; Pred. No. 1.4e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NSPKG 7

DB 5 NCPKG 9

RESULT 5

OXYT_CYPCA

ID OXYT_CYPCA STANDARD; PRT; 9 AA.

AC P23879;

DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 01-NOV-1995 (Rel. 32, Last annotation update)

DE Vasotocin.

OS Cyprinus carpio (Common carp), and

OS Petromyzon marinus (Sea lamprey).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Cyprinus.

OX NCBI_TaxID=7962; 7757;

RN [1]

RP SEQUENCE.

RC SPECIES=C. carpio; TISSUE=Pituitary;

RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;

RT "Characterization of neurohypophyseal hormones from a fresh water bony

RT fish, the carp (Cyprinus carpio). Comparison with hormones from sea

RT water bony fish."

RL Comp. Biochem. Physiol. 14:245-254 (1965).

RN [2]

RP SEQUENCE.

RC SPECIES=P. marinus; TISSUE=Pituitary;

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RX MEDLINE=88225976; PubMed=3371648;
RA Lane T.F., Sower S.A., Kawauchi H.;
RT "Arginine vasotocin from the pituitary gland of the lamprey
(Petromyzon marinus): isolation and amino acid sequence.";
RL Gen. Comp. Endocrinol. 70:152-157(1988).
CC -1- FUNCTION: ANTIDIURETIC HORMONE.
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
DR PIR; B61364; B61364.
DR PIR; S06375; S06375.
DR InterPro; IPR000981; Neurhyp_horm.
DR Pfam; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9
SQ SEQUENCE 9 AA; 1053 MW; 17EB176EB456D04B CRC64;

Query Match 34.5%; Score 20; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NSPKG 7
DB 5 NCPQG 9

RESULT 6
TRP4 LEUMA
ID TRP4 LEUMA STANDARD; PRT; 9 AA.
AC P81736;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tachykinin-related peptide 4 (LentRP 4).
OS Leucophaea maderae (Madeira cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP SEQUENCE.
RT TISSUE=Midgut;
RX MEDLINE=97053012; PubMed=8897641;
RA Muren J.E., Naessel D.R.;
RT "Isolation of five tachykinin-related peptides from the midgut of
the cockroach Leucophaea maderae: existence of N-terminally extended
isoforms.";
RL Regul. Pept. 65:185-196(1996).
CC -1- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
of spontaneous contractions and tonus of hindgut muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Midgut.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 953 MW; 2403987699C865A7 CRC64;

Query Match 34.5%; Score 20; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPKGF 8
DB 1 APSGF 5

RESULT 7
OXYF SCYCA
ID OXYF SCYCA STANDARD; PRT; 9 AA.
AC P42997;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)

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DE Phasvatocin.
OS Scyllorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharniiformes;
OC Scyllorhinidae; Scyllorhinus.
OX NCBI_TaxID=7830;
RN [1]
RP SEQUENCE.
RC TISSUE=Pituitary;
RX MEDLINE=95062247; PubMed=7972045;
RA Chauvet J., Rouille Y., Chauvet C., Chauvet M.-T., Acher R.;
RT "Special evolution of neurohypophysial hormones in cartilaginous
fishes: asvatocin and phasvatocin, two oxytocin-like peptides
isolated from the spotted dogfish (Scyllorhinus canicula).";
RL Proc. Natl. Acad. Sci. U.S.A. 91:11266-11270(1994).
CC -1- FUNCTION: DISPLAYS OXYTOCIC ACTIVITY ON RAT UTERUS.
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
CC InterPro; IPR000981; Neurhyp_horm.
DR PIR; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9
SQ SEQUENCE 9 AA; 1016 MW; 17EDD76EB4449DB CRC64;

Query Match 32.8%; Score 19; DB 1; Length 9;
Best Local Similarity 42.9%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 YGNSPKG 7
DB 3 FNCPVG 9

RESULT 8
OXYT RAJCL
ID OXYT RAJCL STANDARD; PRT; 9 AA.
AC F42994;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Glumitocin.
OS Raja clavata (Thornback ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hymnosqualea; Pristiograja; Batoidae;
OC Rajiformes; Rajidae; Raja.
OX NCBI_TaxID=7781;
RN [1]
RP SEQUENCE.
RX MEDLINE=66123415; PubMed=5880565;
RA Acher R., Chauvet J., Chauvet M.-T., Crepy D.;
RT "Phylogeny of neurohypophysal peptides: isolation of a new hormone,
glumitocin (Ser 4-Gln 8-oxytocin) present in a cartilaginous fish,
the ray (Raja clavata).";
RL Biochim. Biophys. Acta 107:393-396(1965).
CC -1- FUNCTION: ANTIDIURETIC HORMONE.
CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
CC InterPro; IPR000981; Neurhyp_horm.
DR PIR; PF00220; hormone4; 1.
DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; 1.
KW Hormone; Amidation.
FT DISULFID 1 6
FT MOD RES 9
SQ SEQUENCE 9 AA; 984 MW; 17E9C76EB455B04B CRC64;

Query Match 32.8%; Score 19; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 NSPKG 7
DB 5 NCPQG 9

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Db          2 PGPF 5

RESULT 9
TKL1_L0CMI
ID TKL1_L0CMI STANDARD; PRT; 9 AA.
AC P16223;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Locustatachykinin I (TK-I).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]_TaxID=7004;
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=90184489; PubMed=2311766;
RA Schoofs L., Holman G.M., Hayes T.K., Nachman R.J., de Loof A.;
RT "Locustatachykinin I and II, two novel insect neuropeptides with
RT homology to peptides of the vertebrate tachykinin family.";
RL FEBS Lett. 261:397-401(1990)
CC -!- FUNCTION: Myocactive peptide. Stimulates the contraction of the
CC oviduct and foregut.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
DR PIR; S08265; ECLQ1M.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD RES 9
SQ SEQUENCE 9 AA; 939 MW; 2389C86B59C865A7 CRC64;

Query Match 32.8%; Score 19; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PKGF 8
DB 2 PSGF 5

RESULT 10
KNL3_BOMVA
ID KNL3_BOMVA STANDARD; PRT; 9 AA.
AC P83058;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE [Thr6]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., Orr D.F., Boursion A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to Swiss-Prot.
CC -!- FUNCTION: [Thr6]bradykinin produces in vitro relaxation of rat
CC arterial smooth muscle and constriction of intestinal smooth
CC muscle.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the bradykinin family.
KW Amphibian defense peptide; Vasodilator; Bradykinin.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

Query Match 31.0%; Score 18; DB 1; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.4e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PKGF 8
DB 2 PSGF 5

RESULT 11
PPCK_FASHE
ID PPCK_FASHE STANDARD; PRT; 10 AA.
AC P80525;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Putative phosphoenolpyruvate carboxylase [GTP] (EC 4.1.1.32)
DE (Phosphoenolpyruvate carboxylase) (PEPCK) (Newly excysted juvenile
DE protein 1) (Fragment).
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomata; Fasciolidae; Fasciola.
OX NCBI_TaxID=6192;
RN [1]
RP SEQUENCE.
RX MEDLINE=95366993; PubMed=7639732;
RA Tkalecic J., Ashman K., Meusen B.;
RT "Fasciola hepatica: rapid identification of newly excysted juvenile
RT proceins.";
RL Biochem. Biophys. Res. Commun. 213:169-174(1995).
CC -!- CATALYTIC ACTIVITY: GTP + oxaloacetate = GDP + phosphoenolpyruvate
CC + CO(2).
CC -!- SIMILARITY: Belongs to the phosphoenolpyruvate carboxylase [GTP]
CC family.
DR InterPro; IPR008209; PEP carboxykin.
DR PROSITE; PS00505; PEPCK_GTP; PARTIAL.
KW Lyase; Decarboxylase; GTP-Binding.
FT NON TER 10
SQ SEQUENCE 10 AA; 1069 MW; 8393A6187AA9C87A CRC64;

Query Match 31.0%; Score 18; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PKGF 8
DB 2 PGPF 5

RESULT 12
RS7_MYCIT
ID RS7_MYCIT STANDARD; PRT; 8 AA.
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 3CS ribosomal protein S7 (Fragment).
GN RPSG.
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1767;
RN [1]_TaxID=1767;
RP SEQUENCE FROM N.A.
RX MEDLINE=93197130; PubMed=8451173;
RA Nair J., Rouse D.A., Morris S.L.;
RT "Nucleotide sequence analysis of the ribosomal S12 gene of
RT Mycobacterium intracellulare.";
RL Nucleic Acids Res. 21:1039-1039(1993).
CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
CC directly to 16S rRNA where it nucleates assembly of the head
CC domain of the 30S subunit. Is located at the subunit interface
CC close to the decoding center, probably blocks exit of the E-site
CC tRNA (By similarity).
CC -!- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
CC and S11 (By similarity).
CC -!- SIMILARITY: Belongs to the S7P family of ribosomal proteins.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration

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 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; L08171; AAA25376.1; -
 DR PIR; S35538; S35538.
 DR HAVAP; WP_00480; -; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; rRNA-binding; trRNA-binding.
 FT INIT MET 0
 FT NON TER 8
 FT BY SIMILARITY.
 SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 8;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPK 6
 | : | |
 Db 4 GPAPK 8

RESULT 13

UF06 MOUSE STANDARD; PRT; 8 AA.
 AC P38644;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 15-MAR-2004 (Rel. 43, Last sequence update)
 DE Unknown protein from 2D-page of fibroblasts (P50) (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]

RP SEQUENCE.
 RC TISSUE=Fibroblast; PubMed=7523108;
 RX MEDLINE=95009907; Wichter L.L., He C., Selkirk J.K.;
 RA Merrick B.A., Patterson R.M.; Wichter L.L., He C., Selkirk J.K.;
 RT "Separation and sequencing of familial and novel murine proteins
 using preparative two-dimensional gel electrophoresis."
 RL Electrophoresis 15:735-745(1994).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 protein is: 5.2, its MW is: 50 kDa.
 FT NON TER 8
 FT

SQ SEQUENCE 8 AA; 817 MW; A35DD878676B05B1 CRC64;
 Query Match 29.3%; Score 17; DB 1; Length 8;
 Best Local Similarity 50.0%; Pred. No. 1.4e+05;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 NSPKGFAY 10
 | : | | | |
 Db 1 HSEPGGAY 8

RESULT 14

AL10 CARMA STANDARD; PRT; 9 AA.
 AC P81813;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Carcinustatin 10.
 OS Carcinus maenas (Common shore crab) (Green crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 CC Eubrachyura; Portunoidae; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;

RN SEQUENCE.
 RP TISSUE=Cerebral ganglion, and Thoracic ganglion;
 RX MEDLINE=98121193; PubMed=9461295;
 RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
 RA Thorpe A.;
 RT "Isolation and identification of multiple neuropeptides of the
 RT allatostatin superfamily in the shore crab Carcinus maenas."
 RL Eur. J. Biochem. 250:727-734(1997).
 CC -1- FUNCTION: May act as a neurotransmitter or neuromodulator.
 CC -1- SIMILARITY: Belongs to the allatostatin family.
 KW Neuropeptide; Amidation; Multigene family.
 FT MOD_RES 9
 FT AMIDATION.
 SQ SEQUENCE 9 AA; 963 MW; 372D79CDCB4776C7 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 9;
 Best Local Similarity 28.6%; Pred. No. 1.4e+05;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPKGRAY 10
 | : | |
 Db 1 APQYAF 7

RESULT 15

OXYT EISFO STANDARD; PRT; 9 AA.
 AC P42958;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Annetocin.
 OS Eisenia foetida (Common brandling worm) (Common dung-worm).
 CC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 CC Lumbricina; Lumbricidae; Eisenia.
 OX NCBI_TaxID=6396;
 [1]

RP SEQUENCE.
 RC TISSUE=Pituitary; PubMed=8292046;
 RX MEDLINE=94121660; Matsushima O., Ikeda T., Fujita T., Minakata H.,
 RA Cumi T., Ukena K., Matsushima O., Ikeda T., Fujita T., Minakata H.,
 RA Nomoto K.;
 RT "Annetocin: an oxytocin-related peptide isolated from the earthworm,
 RT Eisenia foetida."
 RL Biochem. Biophys. Res. Commun. 198:393-399(1994).
 CC -1- FUNCTION: POTENTIATES SPONTANEOUS CONTRACTIONS OF THE GUT AND ALSO
 CC PULSATORY CONTRACTIONS AND BLADDER-SHAKING MOVEMENT OF THE
 CC NEPHRIDIA. MAY BE INVOLVED IN OSMOREGULATION OF THE ANIMAL THROUGH
 CC NEPHRIDIAL FUNCTION.
 CC -1- SIMILARITY: Belongs to the vasopressin/oxytocin family.
 CC PIR; PC2021; PC2021.
 DR InterPro; IPR000981; Neurhyp_horm.
 DR Pfam; PF00220; hormone4; 1.
 DR PROSITE; PS00264; NEUROHYPOPHYS_HORM; FALSE_NEG.
 KW Hormone; Amidation.
 FT DISULFID 1
 FT MOD_RES 9
 FT AMIDATION.
 SQ SEQUENCE 9 AA; 996 MW; D4EEB76EB45412C9 CRC64;

Query Match 29.3%; Score 17; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.4e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 NSPKG 7
 | : | |
 Db 5 NCPGTG 9

Search completed: July 29, 2004, 09:13:51
 Job time : 14 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 09:07:33 ; Search time 33 seconds
(without alignments)
95.612 Million cell updates/sec

Title: US-09-661-992B-5
Perfect score: 58
Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1443

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archaea:
2: sp_bacteria:
3: sp_fungi:
4: sp_human:
5: sp_invertebrate:
6: sp_mammal:
7: sp_mhc:
8: sp_organelle:
9: sp_phage:
10: sp_plant:
11: sp_rodent:
12: sp_virus:
13: sp_vertebrate:
14: sp_unclassified:
15: sp_virus:
16: sp_bacterioph:
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	22	37.9	9	15 Q7ZPK1	Q7zpk1 human immun
2	22	37.9	9	15 Q7ZPK1	Q7zpk1 human immun
3	21	36.2	10	6 Q8MJ78	Q8mj78 bos mutus g
4	21	36.2	10	11 Q9QVJ7	Q9qvj7 mus sp. mep
5	19	32.8	10	2 Q44693	Q44693 bacillus am
6	19	32.8	10	13 Q90V93	Q90v93 gallus gall
7	18	31.0	9	12 Q92766	Q92766 canine dist
8	18	31.0	10	2 Q47561	Q47561 escherichia
9	18	31.0	10	4 Q9UNF2	Q9unf2 homo sapien
10	17	29.3	9	15 Q7ZP19	Q7zp19 human immun
11	17	29.3	10	2 Q9AE19	Q9ae19 streptococc
12	16	27.6	9	8 Q9SDS5	Q9sds5 magnolia sa
13	16	27.6	9	8 Q9SDS0	Q9sds0 manglietia
14	16	27.6	9	8 Q9TNE0	Q9tnf0 magnolia tr
15	16	27.6	9	8 Q9SDS1	Q9sds1 manglietia
16	16	27.6	9	8 Q9TNE9	Q9tnf9 magnolia co

17	16	27.6	9	8 Q9TNE4	Q9tnf4 magnolia sc
18	16	27.6	9	8 Q9THL7	Q9thl7 magnolia si
19	16	27.6	9	8 Q9TNE0	Q9tnf0 michelia co
20	16	27.6	9	8 Q9TNE4	Q9tnf4 magnolia sa
21	16	27.6	9	8 Q9SDS6	Q9sds6 magnolia wi
22	16	27.6	9	8 Q9TNE6	Q9tnf6 magnolia gr
23	16	27.6	9	8 Q9THL5	Q9thl5 magnolia li
24	16	27.6	9	8 Q9TNE1	Q9tnf1 magnolia he
25	16	27.6	9	8 Q9SDT3	Q9sdt3 magnolia il
26	16	27.6	9	8 Q9THM0	Q9thm0 magnolia fr
27	16	27.6	9	8 Q9SDS2	Q9sds2 magnolia ov
28	16	27.6	9	8 Q9T3P4	Q9t3p4 magnolia ma
29	16	27.6	9	8 Q9THL8	Q9thl8 magnolia of
30	16	27.6	9	8 Q9TNE2	Q9tnf2 magnolia ac
31	16	27.6	9	8 Q9TNE5	Q9tnf5 magnolia gu
32	16	27.6	9	8 Q9TNE5	Q9tnf5 magnolia ko
33	16	27.6	9	8 Q9TNE1	Q9tnf1 magnolia li
34	16	27.6	9	8 Q9TNE3	Q9tnf3 magnolia fi
35	16	27.6	9	8 Q9TND9	Q9tnf9 michelia fi
36	16	27.6	9	8 Q9THL6	Q9thl6 magnolia si
37	16	27.6	9	8 Q9SDS4	Q9sds4 magnolia sh
38	16	27.6	9	8 Q9TNE3	Q9tnf3 magnolia de
39	16	27.6	9	8 Q9SDS7	Q9sds7 magnolia si
40	16	27.6	9	8 Q9THL9	Q9thl9 magnolia fr
41	16	27.6	9	8 Q9TNE6	Q9tnf6 magnolia de
42	16	27.6	9	8 Q9TNE2	Q9tnf2 magnolia ta
43	16	27.6	9	8 Q9T3P3	Q9t3p3 magnolia vi
44	16	27.6	9	8 Q9TNE7	Q9tnf7 magnolia ni
45	16	27.6	9	8 Q9TNE7	Q9tnf7 magnolia ni

ALIGNMENTS

RESULT 1

Q7ZPK1 PRELIMINARY; PRT; 9 AA.
AC Q7ZPK1; STRAIN=3-022877;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3-022877;
RA Agwale S.M., Zeh C., Paxinos E., Odama L., Pienazek D., Wambebe C.,
RA Kalish M.L., Ziermann R.;
RT "Genotypic and Phenotypic Analyses of Human Immunodeficiency Virus
RT Type-1 in Antiretroviral Drug-Naive Nigerian Patients."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY181068; AAO16649.1; -;
FT NON_TER
SQ SEQUENCE 9 AA; 990 MW; 5E16A4489C735B3 CRC64;

Query Match 37.9%; Score 22; DB 15; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSP 5
Db 5 FGNDP 9

RESULT 2

Q7ZP17 PRELIMINARY; PRT; 9 AA.
ID Q7ZP17
AC Q7ZP17
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)

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DN 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3-022879;
RA Agwale S.M., Zeh C., Paxinos E., Odama L., Pienazek D., Wanabebe C.,
RA Kalish M.D., Ziermann R.;
RT "Genotypic and Phenotypic Analyses of Human Immunodeficiency Virus
RT Type-1 in Antiretroviral Drug-Naive Nigerian Patients.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY181070; AA016653.1; -.
RT NON_TER 1
SQ SEQUENCE 9 AA; 990 MW; 5E16A44879C735B3 CRC64;

Query Match 37.9%; Score 22; DB 15; Length 9;
Best Local Similarity 60.0%; Pred. No. 1e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSP 5
DB 5 FGNDP 9

RESULT 3
Q8MJ78 PRELIMINARY; PRT; 10 AA.
AC Q8MJ78;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Prolactin (Fragment).
GN PRL.
OS Bos mutus grunniens (Yak).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=30521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood.
RA Ou J.T. Jr., Zhong J.C. Sr., Chen Z.H. III, Zhao S.J. IV, Bai W.L. V.;
RT "Cloning, sequencing and polymorphism analysis on prolactin gene of
RT yak.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF516697; AA061895.1; -.
RT NON_TER 10
SQ SEQUENCE 10 AA; 1024 MW; 93781FC5A5B87325 CRC64;

Query Match 36.2%; Score 21; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKG 7
DB 5 GSSQKG 10

RESULT 4
Q9QVJ7 PRELIMINARY; PRT; 10 AA.
AC Q9QVJ7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Meprin-B (Fragment).
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;

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RN [1]
RP SEQUENCE.
RX MEDLINE=91373354; PubMed=1894622;
RA Kounnas M.Z.; Wolz E.L.; Gorbea C.M.; Bond J.S.;
RT "Meprin-A and -B. Cell surface endopeptidases of the mouse kidney.";
RL J. Biol. Chem. 266:17350-17357(1991).
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 1031 MW; DAFBDEC9C87B076D CRC64;

Query Match 36.2%; Score 21; DB 11; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPKGF 8
DB 3 APEGF 7

RESULT 5
Q44693 PRELIMINARY; PRT; 10 AA.
AC Q44693;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Amylolyquefaciens trpE gene (3' end) and trpD gene (5' end)
DE (Fragment).
OS Bacillus amylolyquefaciens.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1390;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85006754; PubMed=6090398;
RA Yoshimura K., Uemura J., Seki T., Oshima Y.;
RT "Construction of a promoter-probe vector for Bacillus subtilis host by
RT using the trpD+ gene of Bacillus amylolyquefaciens.";
RL J. Bacteriol. 159:905-912(1984).
DR EMBL: X02861; AA805353.1; -.
DR F01R; I40032; I40032.1
FT NON_TER 1
SQ SEQUENCE 10 AA; 1266 MW; D5121FC729D5A416 CRC64;

Query Match 32.8%; Score 19; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 6.1e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 NSPKGFAY 10
DB 1 NSQSRFLF 8

RESULT 6
Q90Y93 PRELIMINARY; PRT; 10 AA.
AC Q90Y93;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Growth hormone (Fragment).
GN GH.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kansaku N., Nakada A., Yagi E., Okabayashi H., Guemene D.;
RT "Genetic variation of chicken growth hormone gene.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB061722; BAB69037.1; -.
FT NON_TER 1

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FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1155 MW; 6841751775A40AAB CRC64;

Query Match 32.8%; Score 19; DB 13; Length 10;
Best Local Similarity 75.0%; Pred. No. 6.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPKG 7
DB 6 SPRG 9

RESULT 7
ID O92766 PRELIMINARY; PRT; 9 AA.
AC O92766;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Fusion protein (Fragment).
GN F.
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dog H5526/89;
RA Liemann H., Harder T., Haas L.;
RT "Genetic analysis of the central untranslated genome region and the
RT proximal coding part of the F gene of wild-type and vaccine distemper
RT morbilliviruses."
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026237; AAC09167.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1011 MW; F281732760533441 CRC64;

Query Match 31.0%; Score 18; DB 12; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKG 7
DB 6 PKG 8

RESULT 8
ID Q47561 PRELIMINARY; PRT; 10 AA.
AC Q47561;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Hypothetical protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=94162733; PubMed=7764507;
RA Yamada M., Yanai S., Talkuder A.;
RT "Analysis of products of the Escherichia coli genomic genes and
RT regulation of their expressions: an applicable procedure for genomic
RT analysis of other microorganisms."
RL Biosci. Biotechnol. Biochem. 58:117-120(1994).
DR EMBL; D21143; BAA04679.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1109 MW; 2D1B58B1E67DD733 CRC64;

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Query Match 31.0%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNPS 5
DB 6 GHSP 9

RESULT 9
ID Q9UNF2 PRELIMINARY; PRT; 10 AA.
AC Q9UNF2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE Alpha 1 collagen (Fragment).
GN COL1A1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RA Ratcliffe F.A., Vitz J.R., Ray D.B.;
RT "SNP located within intron 32 of human pro-alpha 1 (I) collagen gene
RT at 10,828 bp: cytosine replaces adenine."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF128441; AAD32608.1; -.
KW Collagen.
FT NON_TER 1
FT NON_TER 10
SQ SEQUENCE 10 AA; 953 MW; 364F91A873276867 CRC64;

Query Match 31.0%; Score 18; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PKG 7
DB 5 PKG 7

RESULT 10
ID Q7ZPI9 PRELIMINARY; PRT; 9 AA.
AC Q7ZPI9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE Gag protein (Fragment).
GN GAG.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3-022883;
RA Agwale S.M., Zeh C., Paxinos E., Odama L., Pienazek D., Wambebe C.,
RA Kallish M.L., Ziermann R.;
RT "Genotypic and Phenotypic Analyses of Human Immunodeficiency Virus
RT Type-1 in Antiretroviral Drug-Naive Nigerian Patients."
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY181074; AAO16661.1; -.
FT NON_TER 1
SQ SEQUENCE 9 AA; 963 MW; 5E16B5B879C735B3 CRC64;

Query Match 29.3%; Score 17; DB 15; Length 9;
Best Local Similarity 40.0%; Pred. No. 1e+06;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNP 5

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Db      5 FGSDP 9
RESULT 11
Q9AE19 PRELIMINARY; PRT; 10 AA.
ID Q9AE19
AC Q9AE19
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE Laminin-binding surface protein (Fragment).
GN LMB.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A5;
RA MEDLINE=21172873; PubMed=11274116;
RA Granlund M., Michel F., Norgren M.;
RT "Mutually exclusive distribution of IS1548 and GBS11, an active group
RT II intron identified in human isolates of group b streptococci.";
RL J. Bacteriol. 183:2560-2569(2001).
DR EMBL; AJ290953; CAC35987.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1204 MW; 4965EF9729C9C873 CRC64;

Query Match 29.3%; Score 17; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 KGF 8
   |||
Db 3 KGF 5

RESULT 12
Q9SDS5 PRELIMINARY; PRT; 9 AA.
ID Q9SDS5
AC Q9SDS5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RbCL protein (Fragment).
GN RbCL.
OS Magnolia sargentiana.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Magnoliales; Magnoliaceae;
OC Magnolia.
OX NCBI_TaxID=86736;
RN [1]
RP SEQUENCE FROM N.A.
RA Azuma H., Garcia-Franco J.G., Rico-Gray V., Thien L.B.;
RT "Molecular phylogeny of Magnolia (Magnoliaceae) inferred from cpDNA
RT sequence and evolutionary divergence of the floral scents.";
RL J. Plant Res. 112:291-306(1999).
DR EMBL; AB055577; BAB69567.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
FT NON TER 9
SQ SEQUENCE 9 AA; 992 MW; 9DEA21AB01A32775 CRC64;

Query Match 27.6%; Score 16; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPK 6
   |||
Db 2 SPK 4

RESULT 13
Q9SDSO PRELIMINARY; PRT; 9 AA.
ID Q9SDSO;
AC Q9SDSO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RbCL protein (Fragment).
GN RbCL.
OS Manglietia decudua.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Magnoliales; Magnoliaceae;
OC Manglietia.
OX NCBI_TaxID=152192;
RN [1]
RP SEQUENCE FROM N.A.
RA Azuma H., Garcia-Franco J.G., Rico-Gray V., Thien L.B.;
RT "Molecular phylogeny of Magnoliaceae.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB055583; BAB69578.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
FT NON TER 9
SQ SEQUENCE 9 AA; 992 MW; 9DEA21AB01A32775 CRC64;

Query Match 27.6%; Score 16; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPK 6
   |||
Db 2 SPK 4

RESULT 14
Q9TNF0 PRELIMINARY; PRT; 9 AA.
ID Q9TNF0;
AC Q9TNF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RbCL protein (Fragment).
GN RbCL.
OS Magnolia tripetala.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Magnoliales; Magnoliaceae;
OC Magnolia.
OX NCBI_TaxID=44926;
RN [1]
RP SEQUENCE FROM N.A.
RA Azuma H., Thien L.B., Kawano S.;
RT "Molecular phylogeny of Magnolia (Magnoliaceae) inferred from cpDNA
RT sequence and evolutionary divergence of the floral scents.";
RL J. Plant Res. 112:291-306(1999).
DR EMBL; AB01061; BAA83234.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
FT NON TER 9
SQ SEQUENCE 9 AA; 992 MW; 9DEA21AB01A32775 CRC64;

Query Match 27.6%; Score 16; DB 8; Length 9;
Best Local Similarity 100.0%; Pred. No. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SPK 6
   |||
Db 2 SPK 4

RESULT 15
Q9SDS1

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ID Q95DS1 PRELIMINARY; PRT; 9 AA.
AC Q95DS1,
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Rbcl protein (Fragment).
GN RBCL.
OS Manglietia confiera.
OG Chloroplast
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; magnoliids; Magnoliales; Magnoliaceae;
OC Manglietia.
OC NCBI_TaxID=86742;
OX NCBI_TaxID=86742;
RN [1]
RP SEQUENCE FROM N.A.
RA Azuma H.; Garcia-Franco J.G.; Rico-Gray V.; Thien L.B.;
RT "Molecular phylogeny of Magnoliaceae.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB055582; BAB69576.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON TER
SQ SEQUENCE 9 AA; 992 MW; 9DEA21AB01A32775 CRC64;

Query Match 27.6%; Score 16; DB 8; Length 9;
Best Local Similarity 100.0%; Pred.NO. 1e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPK 6
Db 2 SPK 4

Search completed: July 29, 2004, 09:14:37
Job time : 35 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:51:58 ; Search time 50 Seconds
(without alignments)
56.510 Million cell updates/sec

Title: US-09-661-992B-5
Perfect score: 58
Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 325896

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseq1980s.*
2: Geneseq1990s.*
3: Geneseq2000s.*
4: Geneseq2001s.*
5: Geneseq2002s.*
6: Geneseq2003as.*
7: Geneseq2003bs.*
8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	4 AAB20388	Ab20388 Anti-FIX/
2	34	58.6	9	3 ABB79021	Abb79021 Lanthioni
3	34	58.6	9	4 AAU07681	Aau07681 Synthetic
4	34	58.6	9	6 ABU61712	Abu61712 Lanthioni
5	31	53.4	9	3 ABB79022	Abb79022 Lanthioni
6	31	53.4	9	4 AAU07682	Aau07682 Synthetic
7	31	53.4	9	6 ABU61713	Abu61713 Lanthioni
8	30	51.7	9	3 ABB79023	Abb79023 Lanthioni
9	30	51.7	9	4 AAU07683	Aau07683 Synthetic
10	30	51.7	9	6 ABU61714	Abu61714 Lanthioni
11	30	51.7	9	7 ABR84746	Abr84746 Bovine po
12	30	51.7	10	5 ABP62399	Abp62399 Human imm
13	30	51.7	10	6 AAE38105	Aae38105 Human COU
14	29	50.0	9	2 AAU070576	Aau070576 Vasopress
15	29	50.0	9	5 ABP62425	Abp62425 Human imm
16	29	50.0	10	3 AAY94219	Aay94219 Murine 16
17	28	48.3	9	6 ABJ43365	Abj43365 151P3D4 c
18	28	48.3	9	6 ABJ46009	Abj46009 151P3D4 c
19	28	48.3	9	6 ABJ46653	Abj46653 151P3D4 c
20	28	48.3	9	6 ABJ45334	Abj45334 151P3D4 c
21	28	48.3	9	6 ABJ48704	Abj48704 151P3D4 c
22	28	48.3	9	6 ABJ43914	Abj43914 151P3D4 c
23	28	48.3	9	6 ABJ48034	Abj48034 151P3D4 c
24	28	48.3	9	6 ABJ49563	Abj49563 151P3D4 c
25	28	48.3	9	6 ABJ41100	Abj41100 151P3D4 c

26	28	48.3	9	6 ABJ42512	Abj42512 151P3D4 c
27	28	48.3	9	6 ABJ44636	Abj44636 151P3D4 c
28	28	48.3	9	6 ABJ47391	Abj47391 151P3D4 c
29	28	48.3	9	6 ABJ39487	Abj39487 151P3D4 c
30	28	48.3	9	6 ABJ41920	Abj41920 151P3D4 c
31	28	48.3	10	2 AAR12475	Aar12475 "Hydrophi
32	28	48.3	10	6 ABJ39722	Abj39722 151P3D4 c
33	28	48.3	10	6 ABJ51879	Abj51879 151P3D4 c
34	28	48.3	10	6 ABJ53928	Abj53928 151P3D4 c
35	28	48.3	10	6 ABJ52649	Abj52649 151P3D4 c
36	28	48.3	10	6 ABJ42118	Abj42118 151P3D4 c
37	28	48.3	10	6 ABJ52541	Abj52541 151P3D4 c
38	28	48.3	10	6 ABJ50213	Abj50213 151P3D4 c
39	28	48.3	10	6 ABJ41308	Abj41308 151P3D4 c
40	28	48.3	10	6 ABJ53226	Abj53226 151P3D4 c
41	28	48.3	10	6 ABJ50991	Abj50991 151P3D4 c
42	28	48.3	10	6 ABJ39768	Abj39768 151P3D4 c
43	28	48.3	10	6 ABJ53898	Abj53898 151P3D4 c
44	28	48.3	10	6 ABJ40130	Abj40130 151P3D4 c
45	28	48.3	10	6 ABJ42143	Abj42143 151P3D4 c

ALIGNMENTS

RESULT 1

AAB20388
ID AAB20388 standard; peptide; 10 AA.
XX
AC AAB20388;
XX
DT 21-JUN-2001 (first entry)
XX
DE Anti-FIX/FIXa antibody 193/AD3 CDR3.
XX
KW Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW complementarity determining region; CDR.
XX
OS Mus musculus.
XX
PN WO200119992-A2.
XX
PD 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-EP008936.
XX
PR 14-SEP-1999; 99AT-00001576.
XX
PA (BAXT) BAXTER AG.
XX
PI Schefflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX
DR WPI; 2001-290358/30.
XX
PT New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
PS Claim 7; Page 74; 138pp; English.
XX
CC The present sequence is that of complementarity determining region 3
CC (CDR3) of the heavy chain of an antibody expressed by mouse hybridoma
CC 193/AD3. This antibody has anti-Factor IX (FIX) or anti-activated Factor
CC IX (FIXa) activity. It is an example of anti-FIX/FIXa antibodies of the
CC invention. Such antibodies and their derivatives (including those that
CC comprise the present CDR3 peptide) have Factor VIIIa (FVIII) cofactor
CC activity or FIXa activating activity. Administration of the antibodies or
CC their derivatives leads to an increase in the procoagulant activity of
CC FIXa, even in the presence of FVIII inhibitors. This allows for rapid
CC blood coagulation even in the absence of FVIII or FVIIIa, and in the case
CC of FVIII inhibitor patients. The antibodies or their derivatives are used

CC in a claimed pharmaceutical composition for treating patients with blood
 CC coagulation disorders, especially haemophilia A and haemorrhagic
 CC diathesis
 XX
 XX Sequence 10 AA;

Query Match 100.0%; Score 58; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0018;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPKGFAY 10
 :|||||:
 Db 1 YGNSPKGFAY 10

RESULT 2
 ABB79021 standard; peptide; 9 AA.
 XX

AC ABB79021;

XX 01-AUG-2002 (first entry)

XX Lanthionine peptide SEQ ID NO:12.

DE Lanthionine; lanthionine bridge.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1..6
 FT /note= "forms a lanthionine bridge"

XX US6028168-A.

XX 22-FEB-2000.

XX 06-JUN-1995; 95US-00467472.

XX 09-AUG-1991; 91US-00742908.

PR 28-JAN-1993; 93US-00021606.

XX (KOLB/) KOLBECK W.

XX Osapay G, Goodman M;

XX WPI; 2000-348922/30.

XX New lanthionine bridged peptide compounds derived from naturally linear
 PT peptide e.g. virus related peptides.

XX Example; Col 57; 50pp; English.

XX The present invention describes lanthionine bridged peptide compounds
 CC (I). (i) Have improved biological activity compared to the corresponding
 CC linear peptide. The present sequence represents a peptide given in the
 CC exemplification of the present invention

XX Sequence 9 AA;

Query Match 58.6%; Score 34; DB 3; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPKG 7
 :|||||:
 Db 3 FGNSPRG 9

RESULT 3
 AAU07681 standard; peptide; 9 AA.
 ID AAU07681
 XX

AC AAU07681;
 XX 04-DEC-2001 (first entry)
 DT
 XX Synthetic lanthionine-vasopressin bridged peptide #1.
 DE
 XX Lanthionine bridged peptide; thioether bond; monosulphide bridge;
 KW hormone; neurotoxin; plant regulating agent; lanthionine-vasopressin.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1..6
 FT /label= OTHER
 FT /note= "OTHER= lanthionine bridge"

XX US6268339-B1.

XX 31-JUL-2001.

XX 26-AUG-1999; 99US-00384061.

XX 09-AUG-1991; 91US-00742908.

PR 28-JAN-1993; 93US-00021606.

PR 06-JUN-1995; 95US-00467472.

XX (KOLB/) KOLBECK W.

XX Goodman M, Osapay G;

XX WPI; 2001-549070/61.

XX New peptides comprising monosulfide bridges, are useful as

PT pharmacologically active agents such as hormones.

XX Disclosure; Col 53; 49pp; English.

XX The sequences represent synthetic lanthionine bridged peptides. The
 CC peptides of the invention all comprise a lanthionine bridge, a thioether
 CC bond also called a monosulphide bridge. The peptides can be used as
 CC pharmacologically active agents, for example, as hormones, as neurotoxins
 CC and as plant regulating agents. The sequences have a higher biological
 CC activity than their corresponding naturally occurring peptides. This
 CC sequence represents a lanthionine-vasopressin peptide

XX Sequence 9 AA;

Query Match 58.6%; Score 34; DB 4; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPKG 7
 :|||||:
 Db 3 FGNSPRG 9

RESULT 4
 ABU61712

ID ABU61712 standard; peptide; 9 AA.

XX ABU61712;

XX 13-AUG-2003 (first entry)

XX Lanthionine bridged peptide #12.

XX Lanthionine bridged peptide; monosulphide bridge; thioether bond;

XX improved biological activity; vasopressin; somatostatin; enkephalin;

XX endothelein; pharmaceutically active compound.

XX Synthetic.

XX key Location/Qualifiers

CC and as plant regulating agents. The sequences have a higher biological
 CC activity than their corresponding naturally occurring peptides. This
 CC sequence represents a lanthionine-oxytocin peptide

SQ Sequence 9 AA;

Query Match 53.4%; Score 31; DB 4; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSPKG 7
 Db 4 GNSPRG 9

RESULT 7
 ABU61713
 ID ABU61713 standard; peptide; 9 AA.

XX AC ABU61713;

XX DT 13-AUG-2003 (first entry)

XX DE Lanthionine bridged peptide #13.

XX KW Lanthionine bridged peptide; monosulphide bridge; thioether bond;
 KW improved biological activity; vasopressin; somatostatin; enkephalin;
 KW endothelin; pharmaceutically active compound.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1..6

XX FT /note= "Residues 1 and 6 linked by a lanthionine bridge"

XX FN US2002165132-A1.

XX PD 07-NOV-2002.

XX PF 10-MAY-2001; 2001US-00852870.

XX PR 09-AUG-1991; 91US-00742908.

XX PR 28-JAN-1993; 93US-00021606.

XX PR 06-JUN-1995; 95US-00467472.

XX PR 26-AUG-1999; 99US-00384061.

XX PA (GOOD/) GOODMAN M.

XX PA (OSAP/) OSAPAY G.

XX PI Goodman M, Osapay G;

XX DR WPI; 2003-391607/37.

XX PT Novel lanthionine-bridged biologically active peptides e.g. vasopressin,
 PT somatostatin or enkephalin, useful as pharmaceutically active compounds.

XX PS Disclosure; Page 15; 24pp; English.

XX CC The present invention relates to lanthionine bridged peptides which are
 CC analogues of peptide compounds comprising a disulphide bridge. The
 CC disulphide bridge is replaced by monosulphide bridge or thioether bond,
 CC designated a lanthionine bridge. Such analogues or lanthionine bridged
 CC peptides have improved biological activity compared to the original
 CC peptide compounds e.g. vasopressin, somatostatin, enkephalin, and
 CC endothelin. The lanthionine-bridged peptides are useful as
 CC pharmaceutically active compounds. ABU61701-ABU61724 represent
 CC lanthionine bridged peptides

XX SQ Sequence 9 AA;

Query Match 53.4%; Score 31; DB 6; Length 9;
 Best Local Similarity 83.3%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSPKG 7
 Db 4 GNSPRG 9

RESULT 8
 ABB79023

ID ABB79023 standard; peptide; 9 AA.

XX AC ABB79023;

XX DT 01-AUG-2002 (first entry)

XX DE Lanthionine peptide SEQ ID NO:14.

XX KW Lanthionine; lanthionine bridge.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Misc-difference 1..6

XX FT /note= "forms a lanthionine bridge"

XX FN US6028168-A.

XX PD 22-FEB-2000.

XX PF 06-JUN-1995; 95US-00467472.

XX PR 09-AUG-1991; 91US-00742908.

XX PR 28-JAN-1993; 93US-00021606.

XX PA (KOLB/) KOLBECK W.

XX PI Osapay G, Goodman M;

XX DR WPI; 2000-348922/30.

XX PT New lanthionine bridged peptide compounds derived from naturally linear
 PT peptide e.g. virus related peptides.

XX PS Example; Col 61; 50pp; English.

XX CC The present invention describes lanthionine bridged peptide compounds
 CC (I). (I) Have improved biological activity compared to the corresponding
 CC linear peptide. The present sequence represents a peptide given in the
 CC exemplification of the present invention

XX SQ Sequence 9 AA;

Query Match 51.7%; Score 30; DB 3; Length 9;
 Best Local Similarity 71.4%; Pred. No. 1.4e+06;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKG 7
 Db 3 FGNSPLG 9

RESULT 9
 AAU07683

ID AAU07683 standard; peptide; 9 AA.

XX AC AAU07683;

XX DT 04-DEC-2001 (first entry)

XX DE Synthetic lanthionine-vasopressin bridged peptide #2.

XX KW Lanthionine bridged peptide; thioether bond; monosulphide bridge;
 KW hormone; neurotoxin; plant regulating agent; lanthionine-vasopressin.

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OS Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1..6
FT /label= OTHER
FT /note= "OTHER= lanthionine bridge"
XX US6268339-B1.
XX 31-JUL-2001.
XX 26-AUG-1999; 99US-00384061.
XX 09-AUG-1991; 91US-00742908.
XX 28-JAN-1993; 93US-00021606.
XX 06-JUN-1995; 95US-00467472.
XX (XOLB/) KOLBECK W.
XX Goodman M, Osapay G;
XX WPI; 2001-549070/61.
XX New peptides comprising monosulfide bridges, are useful as
XX pharmacologically active agents such as hormones.
XX Disclosure; Col 59; 49pp; English.
XX The sequences represent synthetic lanthionine bridged peptides. The
XX peptides of the invention all comprise a lanthionine bridge, a thioether
XX bond also called a monosulphide bridge. The peptides can be used as
XX pharmacologically active agents, for example, as hormones, as neurotoxins
XX and as plant regulating agents. The sequences have a higher biological
XX activity than their corresponding naturally occurring peptides. This
XX sequence represents a lanthionine-vasopressin peptide
XX
XX Sequence 9 AA;
XX Query Match 51.7%; Score 30; DB 4; Length 9;
XX Best Local Similarity 71.4%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 YGNSPKG 7
XX :|||||
XX 3 FGNSPLG 9
XX
XX RESULT 10
XX ABU61714
XX ID ABU61714 standard; peptide; 9 AA.
XX AC
XX ABU61714;
XX 13-AUG-2003 (first entry)
XX DT
XX DE Lanthionine bridged peptide #14.
XX Lanthionine bridged peptide; monosulphide bridge; thioether bond;
XX improved biological activity; vasopressin; somatostatin; enkephalin;
XX endothelin; pharmaceutically active compound.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1..6
FT /note= "Residues 1 and 6 linked by a lanthionine bridge"
XX US2002165132-A1.
XX 07-NOV-2002.
XX 10-MAY-2001; 2001US-00852870.
XX

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PR 09-AUG-1991; 91US-00742908.
PR 28-JAN-1993; 93US-00021606.
PR 06-JUN-1995; 95US-00467472.
PR 26-AUG-1999; 99US-00384061.
XX (GOOD/) GOODMAN M.
XX PA (OSAP/) OSAPAY G.
XX Goodman M, Osapay G;
XX WPI; 2003-391607/37.
XX Novel lanthionine-bridged biologically active peptides e.g. vasopressin,
XX somatostatin or enkephalin, useful as pharmaceutically active compounds.
XX Disclosure; Page 15; 24pp; English.
XX The present invention relates to lanthionine bridged peptides which are
XX analogues of peptide compounds comprising a disulphide bridge. The
XX disulphide bridge is replaced by monosulphide bridge or thioether bond,
XX designated a lanthionine bridge. Such analogues or lanthionine bridged
XX peptides have improved biological activity compared to the original
XX peptide compounds e.g. vasopressin, somatostatin, enkephalin, and
XX endothelin. The lanthionine-bridged peptides are useful as
XX pharmaceutically active compounds. ABU61701-ABU61724 represent
XX lanthionine bridged peptides
XX
XX Sequence 9 AA;
XX Query Match 51.7%; Score 30; DB 6; Length 9;
XX Best Local Similarity 71.4%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX 1 YGNSPKG 7
XX :|||||
XX 3 FGNSPLG 9
XX
XX RESULT 11
XX ABR84746
XX ID ABR84746 standard; protein; 9 AA.
XX AC
XX ABR84746;
XX 18-DEC-2003 (first entry)
XX DT
XX DE Bovine polypyrimidine tract binding protein conserved nonapeptide.
XX Cow; polypyrimidine tract protein; isoform; RNA stability regulation;
XX immunosuppressive; allograft rejection; CD154; PTB.
XX Bos taurus.
XX WO2003061581-A2.
XX 31-JUL-2003.
XX 17-JAN-2003; 2003WO-US001623.
XX 17-JAN-2002; 2002US-0349869P.
XX 02-JAN-2003; 2003US-0437779P.
XX (DART-) DARTMOUTH COLLEGE.
XX Rigby WFC;
XX WPI; 2003-778776/73.
XX A new polypyrimidine tract protein isoform useful for finding agents
XX which modulate its activity and to prevent or treat allograft rejection
XX or CD40 activation.
XX Disclosure; Page 64; 0pp; English.
XX

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XX DT 14-JAN-1999 (first entry)
XX DE Vasopressin peptide used for peptide ligation.
XX KW Intervening protein sequence; IVPS; protein splicing; protein production.
XX OS Synthetic.
XX PH Key Location/Qualifiers
FT Modified-site 1
FT /note= "biotinylated"
XX PN US5834247-A.
XX PD 10-NOV-1998.
XX PF 05-MAR-1997; 97US-00811492.
XX PR 09-DEC-1992; 92US-00004139.
XX PR 03-NOV-1993; 93US-00146885.
XX PR 28-JUN-1995; 95US-00496247.
XX PR 29-DEC-1995; 95US-00580555.
XX PA (NEW ) NEW ENGLAND BIOLABS INC.
XX PI Hodges RA, Perlier FB, Comb DG, Southworth M, Adam E, Noren CJ;
XX PI Xu M, Chong SSC, Jack WE;
XX DR WPI; 1999-008713/01.
XX PT New modified target proteins - which have controllable intervening
XX PT protein sequence which can facilitate production, purification, labelling
XX PT or isolation of target proteins.
XX PS Example 19; Col 76; 123pp; English.
XX CC AAW0575-79 represent peptides used for peptide ligation, in the course
XX CC of the invention. The specification describes IVPS (intervening protein
XX CC sequence) regions which encode peptides which are removed via protein
XX CC splicing to form the native protein. The specification describes a
XX CC modified protein comprising a target protein or portion, fused either
XX CC internally or terminally to a IVPS, or to an amino- or carboxyl-terminal
XX CC element of a IVPS. The IVPS are capable of excision from or cleavage of
XX CC the modified protein upon predetermined conditions, in cis or trans, e.g.
XX CC temperature increase, deglycosylation, unblocking of amino acid residues,
XX CC treatment with chemical reagents. The methods can be used for modifying,
XX CC producing, purifying, labelling or isolating target proteins such as
XX CC enzymes, toxins, cytokines, glycoproteins and growth factors
XX SQ Sequence 9 AA;
XX Query Match 50.0%; Score 29; DB 2; Length 9;
XX Best Local Similarity 57.1%; Pred. No. 1.4e+06;
XX Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 YGNSPKG 7
XX DB 3 FGNCPRG 9
XX RESULT 15
XX ABP62425
XX ID ABP62425 standard; peptide; 9 AA.
XX AC ABP62425;
XX DT 10-OCT-2002 (first entry)
XX DE Human immunopeptide to HCV E2 glycoprotein light chain CDR #102.
XX KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
XX KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
```

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KW NS3 protein; viral infection.
XX OS Homo sapiens.
XX PN WO200259340-A1.
XX PD 01-AUG-2002.
XX PF 25-JAN-2002; 2002WO-US002303.
XX PR 26-JAN-2001; 2001US-0264451P.
XX PA (SCRI ) SCRIPPS RES INST.
XX PI Maruyama T, Jones JM, Burton DR, Fox RI;
XX DR WPI; 2002-599801/64.
XX PT New human immunopolypeptide with binding specificity for certain envelope
XX PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
XX PT diagnosing or treating patients having or suspected of having HCV
XX PT infection.
XX PS Claim 1; Fig 17; 308pp; English.
XX CC The present invention relates to human immunopolypeptides, produced by a
XX CC phage transfected cell library. The present sequence is one such
XX CC immunopolypeptide. The immunopolypeptides have binding specificity for
XX CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
XX CC virus (HCV). E2 glycoprotein is believed to be responsible for target
XX CC cell binding and contains neutralising epitopes, while NS3 is thought to
XX CC be involved in the replication of HCV. The immunopolypeptides are useful
XX CC for diagnosing and treating a patient having or suspected to be having
XX CC HCV infection
XX SQ Sequence 9 AA;
XX Query Match 50.0%; Score 29; DB 5; Length 9;
XX Best Local Similarity 71.4%; Pred. No. 1.4e+06;
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 YGNSPKG 7
XX DB 3 YGDSFVG 9
XX Search completed: July 29, 2004, 09:13:27
XX Job time : 51 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 09:14:44 ; Search time 41 Seconds
(without alignments)
76,508 Million cell updates/sec

Title: US-09-661-992B-5

Perfect score: 58

Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62

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Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 157453

Minimum DB seq length: 0

Maximum DB seq length: 10

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	58.6	9	9 US-09-852-870A-12	Sequence 12, Appl
2	31	53.4	9	9 US-09-852-870A-13	Sequence 13, Appl
3	30	51.7	9	9 US-09-852-870A-14	Sequence 14, Appl
4	29	50.0	10	13 US-10-140-555-7	Sequence 7, Appl
5	27	46.6	9	9 US-09-828-708-52	Sequence 52, Appl
6	27	46.6	9	9 US-09-828-708-56	Sequence 56, Appl
7	27	46.6	9	9 US-09-852-870A-15	Sequence 15, Appl
8	27	46.6	9	16 US-10-663-244-32	Sequence 32, Appl
9	26	44.8	9	10 US-09-977-797A-68	Sequence 68, Appl
10	26	44.8	10	8 US-08-986-140-15	Sequence 15, Appl
11	25	43.1	9	10 US-09-972-656-32	Sequence 32, Appl
12	25	43.1	9	12 US-09-948-939-35	Sequence 35, Appl
13	25	43.1	9	12 US-10-029-926B-191	Sequence 191, Appl
14	25	43.1	9	15 US-10-032-037B-191	Sequence 191, Appl
15	25	43.1	9	15 US-10-029-988B-191	Sequence 191, Appl

16 43.1 9 15 US-10-032-423A-191
17 43.1 9 15 US-10-338-366-24
18 43.1 10 10 US-09-572-404B-90
19 43.1 10 10 US-09-572-404B-828
20 43.1 10 10 US-09-572-404B-830
21 43.1 10 10 US-09-572-404B-832
22 43.1 10 10 US-09-572-404B-834
23 43.1 10 10 US-09-563-222-13
24 43.1 10 14 US-10-317-550-5
25 43.1 6 12 US-10-133-234A-15
26 41.4 8 9 US-09-828-708-55
27 41.4 8 14 US-10-193-768-46
28 41.4 8 14 US-10-193-788-52
29 41.4 9 9 US-09-834-765-48
30 41.4 9 12 US-10-013-312-318
31 41.4 9 12 US-10-013-312-319
32 41.4 9 12 US-10-013-312-331
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34 41.4 9 12 US-10-013-312-1544
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37 41.4 9 12 US-10-013-312-1849
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39 41.4 9 12 US-10-013-312-1938
40 41.4 9 12 US-10-013-312-1998
41 41.4 9 12 US-10-013-312-1999
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44 41.4 10 12 US-10-013-312-380
45 41.4 10 12 US-10-013-312-2336

ALIGNMENTS

RESULT 1
US-09-852-870A-12
; Sequence 12, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Geapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser Lanthionine bridge
US-09-852-870A-12

Query Match 58.6%; Score 34; DB 9; Length 9;
Best Local Similarity 71.4%; Pred.No. 1.2e+06;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPKG 7
:|||||:
Db 3 FGNSPRG 9

RESULT 2
US-09-852-870A-13
; Sequence 13, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray

; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-13

Query Match 53.4%; Score 31; DB 9; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GNSPKG 7
| | | | |
DB 4 GNSPRG 9

RESULT 3
US-09-852-870A-14
; Sequence 14, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-14

Query Match 51.7%; Score 30; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPKG 7
: | | | |
DB 3 FGNSPLG 9

RESULT 4
US-10-140-555-7
; Sequence 7, Application US/10140555
; Publication No. US2002012727A1
; GENERAL INFORMATION:
; APPLICANT: Julie A. Abrahamson
; APPLICANT: Stephen D. Holmes
; APPLICANT: Jeffrey R. Jackson
; TITLE OF INVENTION: RHAMM Antagonist Antibodies
; FILE REFERENCE: P50857
; CURRENT APPLICATION NUMBER: US/10/140,555
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: US/09/443,790
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 60/109,041

; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)...(10)
; OTHER INFORMATION: heavy chain CDR 3
US-10-140-555-7

Query Match 50.0%; Score 29; DB 13; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 GNSPKGAY 10
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DB 2 GSSLGAY 10

RESULT 5
US-09-828-708-52
; Sequence 52, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-52

Query Match 46.6%; Score 27; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPK 6
| | | | |
DB 3 YGSSPR 8

RESULT 6
US-09-828-708-56
; Sequence 56, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 56
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-56


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Query Match      46.6%; Score 27; DB 9; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPK 6
Db 3 YGSSPR 8

RESULT 7
US-09-852-870A-15
; Sequence 15, Application US/09852870A
; Patent No. US20020165132A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser Lanthionine bridge.
US-09-852-870A-15

Query Match      46.6%; Score 27; DB 9; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKG 7
Db 4 GNSPLG 9

RESULT 8
US-10-663-244-32
; Sequence 32, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-32

Query Match      46.6%; Score 27; DB 16; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 YGNSPK 6
Db 3 YGSSPR 8

RESULT 9
US-09-977-797A-68
; Sequence 68, Application US/0997797A
; Publication No. US2003004472A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Wu, Herren
; FILE REFERENCE: AME-06805
; TITLE OF INVENTION: Methods for Identifying Ligand Specific Binding Molecules
; CURRENT APPLICATION NUMBER: US/09/977,797A
; CURRENT FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 09/129,026
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 08/905,825
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-977-797A-68

Query Match      44.8%; Score 26; DB 10; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNSPK 6
Db 3 YGSSPR 8

RESULT 10
US-08-996-140-15
; Sequence 15, Application US/08996140
; Publication No. US20030190318A1
; GENERAL INFORMATION:
; APPLICANT: TORIGOE, Kakuji
; APPLICANT: USHIO, Shimppei
; APPLICANT: KUNIKATA, Toshio
; APPLICANT: KURIMOTO, Masashi
; TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,140
; FILING DATE: 22-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 356,426/1996
; FILING DATE: 26-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 52,526/1997
; FILING DATE: 21-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 163,490/1997
; FILING DATE: 6-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 215,490/1997
```

; FILING DATE: 28-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: TORIGOE=2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal fragment
US-08-996-140-15

Query Match 44.8%; Score 26; DB 8; Length 10;
Best Local Similarity 55.6%; Pred. No. 5.2e+02; Indels 0;
Matches 5; Conservative 0; Mismatches 4; Gaps 0;

QY 2 GNSPKGFAY 10
|||
Db 2 GNYGAGFGY 10

RESULT 11
US-09-972-656-32
; Sequence 32, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Wei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-32

Query Match 43.1%; Score 25; DB 10; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.2e+06; Indels 0;
Matches 4; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YGNSP 5
|||
Db 3 YGSSP 7

RESULT 12
US-09-948-939-35
; Sequence 35, Application US/09949393
; Publication No. US20020086014A1
; GENERAL INFORMATION:
; APPLICANT: Korman, Alan J.
; APPLICANT: Halk, Edward L.
; APPLICANT: Lonberg, Nils
; APPLICANT: Medarex, Inc.
; TITLE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
; FILE REFERENCE: 014643-010520US
; CURRENT APPLICATION NUMBER: US/09/948,939
; CURRENT FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: US 60/150,452
; PRIOR FILING DATE: 1999-08-24
; PRIOR APPLICATION NUMBER: 09/644,668
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: light chain CDR3 (HuMab 10D1, 4B6)
US-09-948-939-35

Query Match 43.1%; Score 25; DB 12; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.2e+06; Indels 0;
Matches 4; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YGNSP 5
|||
Db 3 YGSSP 7

RESULT 13
US-10-029-926B-191
; Sequence 191, Application US/10029926B
; Publication No. US20040073011A1
; GENERAL INFORMATION:
; APPLICANT: HAGAY, et al.
; TITLE OF INVENTION: SPECIFIC HUMAN ANTIBODIES FOR SELECTIVE CANCER THERAPY
; FILE REFERENCE: 10793/50
; CURRENT APPLICATION NUMBER: US/10/029,926B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 12/29/2000
; NUMBER OF SEQ ID NOS: 203
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-926B-191

Query Match 43.1%; Score 25; DB 12; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.2e+06; Indels 0;
Matches 4; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YGNSP 5
|||
Db 3 YGSSP 7

RESULT 14
US-10-032-037B-191
; Sequence 191, Application US/10032037B
; Publication No. US20040001822A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; FILE REFERENCE: 10793/44
; CURRENT APPLICATION NUMBER: US/10/032,037B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/258,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-037B-191

Query Match 43.1%; Score 25; DB 15; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.2e+06; Indels 0;
Matches 4; Conservative 1; Mismatches 0; Gaps 0;

QY 1 YGNSP 5

Db 3 YGSSP 7

RESULT 15
US-10-029-988B-191
; Sequence 191, Application US/10029988B
; Publication No. US20040001839A1
; GENERAL INFORMATION:
; APPLICANT: Bio-Technology General Corp.
; TITLE OF INVENTION: Y17-ISOLATED MOLECULES COMPRISING EPITOPES CONTAINING SULFATED
; TITLE OF INVENTION: MOIETIES, ANTIBODIES TO SUCH EPITOPES, AND USES THEREOF
; FILE REFERENCE: 10793/46
; CURRENT APPLICATION NUMBER: US/10/029,988B
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/238,948
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 191
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-029-988B-191

Query Match 43.1%; Score 25; DB 15; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 YGNSP 5
Db 3 YGSSP 7

Search completed: July 29, 2004, 09:19:53
Job time : 41 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 09:12:33 ; Search time 18 Seconds
(without alignments)
28.681 Million cell updates/sec

Title: US-09-661-992B-5
Perfect score: 58
Sequence: 1 YGNSPKGFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 103740

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	58.6	9	3	US-08-467-472C-12
2	34	58.6	9	3	US-09-384-061-12
3	34	58.6	9	3	US-09-852-870A-12
4	31	53.4	9	3	US-08-467-472C-13
5	31	53.4	9	3	US-09-384-061-13
6	31	53.4	9	4	US-09-852-870A-13
7	30	51.7	9	3	US-08-467-472C-14
8	30	51.7	9	3	US-09-384-061-14
9	30	51.7	9	4	US-09-852-870A-14
10	29	50.0	9	2	US-08-811-492-111
11	27	46.6	8	3	US-08-444-818-651
12	27	46.6	8	3	US-08-444-818-652
13	27	46.6	8	3	US-08-467-472C-15
14	27	46.6	9	3	US-09-384-061-15
15	27	46.6	9	4	US-09-852-870A-15
16	26	44.8	8	3	US-08-444-818-653
17	26	44.8	10	4	US-09-649-063-15
18	25	43.1	6	2	US-08-317-310A-21
19	25	43.1	6	5	PCT-US95-13041-21
20	25	43.1	8	1	US-08-421-702A-11
21	25	43.1	8	1	US-08-303-052A-11
22	25	43.1	8	1	US-08-421-696A-11
23	25	43.1	8	1	US-08-421-697A-11
24	25	43.1	8	1	US-08-421-698A-11
25	25	43.1	8	2	US-08-421-695A-11
26	25	43.1	8	5	PCT-US95-04741-11
27	25	43.1	9	1	US-07-714-167E-2

Sequence 503, App
Sequence 362, App
Sequence 210, App
Sequence 6, Appl
Sequence 503, App
Sequence 6, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 8, Appl
Sequence 47, Appl
Sequence 110, App
Sequence 47, Appl
Sequence 46, Appl
Sequence 52, Appl
Sequence 47, Appl
Sequence 47, Appl
Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-467-472C-12
; Sequence 12, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104

IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: GOODMAN, MURRAY
TITLE: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24

US-08-467-472C-12
Query Match 58.6%; Score 34; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YGNSPKG 7
Db 3 FGNSPRG 9

RESULT 2
US-09-384-061-12
Sequence 12, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
Zip: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384,061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE: PEPTIDE
DESCRIPTION: N/A
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.
IMMEDIATE SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986

DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: BY
TITLE: TANDEN MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 12: CYS-SER
RELEVANT RESIDUES IN SEQ ID NO: STRUCTURE
US-09-384-061-12

Query Match 58.6%; Score 34; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNSPKG 7
:||||:
Db 3 FGNSPRG 9

RESULT 3

US-09-852-870A-12
Sequence 12, Application US/09852870A
Patent No. 6673769
GENERAL INFORMATION:
APPLICANT: Goodman, Murray
APPLICANT: Oespay, George
TITLE OF INVENTION: Lanthionin Bridged Proteins
FILE REFERENCE: LKR 9122-D
CURRENT APPLICATION NUMBER: US/09/852.870A
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/384,601
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
SEQ ID NO 12
TYPE: PRT
LENGTH: 9
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-12

Query Match 58.6%; Score 34; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YGNSPKG 7
:||||:
Db 3 FGNSPRG 9

RESULT 4

US-08-467-472C-13
Sequence 13, Application US/08467472C
Patent No. 6028168
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES

NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HOFFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,472C
FILING DATE: 6-JUNE-1995
CLASSIFICATION: 514
PRIOR APPLICATION NUMBER: US 07/742,908
FILING DATE: 9-AUGUST-1991
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKR-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 9
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
VOLUME: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519

DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE: 443 - 445
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
US-08-467-472C-13

Query Match 53.4%; Score 31; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0

Qy 2 GNSPKG 7
Db 4 GNSPRG 9

RESULT 5
US-09-384-061-13
Sequence 13, Application US/09384061
Patent No. 6268339
GENERAL INFORMATION:
APPLICANT: GOODMAN, MURRAY
TITLE OF INVENTION: LANTHONINE BRIDGED PEPTIDES
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
STREET: 99 PARK AVENUE
CITY: NEW YORK
STATE: NY
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISC
COMPUTER: COMPAQ - IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS Version 6.2
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/384.061
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/467,472
FILING DATE:
APPLICATION NUMBER: US 08/021,606
FILING DATE: 28-JANUARY-1993
ATTORNEY/AGENT INFORMATION:
NAME: ROBINSON, WILLIAM R.
REGISTRATION NUMBER: 27,224
REFERENCE/DOCKET NUMBER: LKE-9122B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 697-3355
TELEFAX: (212) 557-5635
TELEX: NONE
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:

LENGTH: 9
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE: 865 - 869
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
TITLE: BY
TITLE: TANDEM MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE: 443 - 445
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 13: CYS-SER
US-09-384-061-13

Query Match 53.4%; Score 31; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GNSPKG 7
Db 4 GNSPRG 9

RESULT 6

US-09-852-870A-13
; Sequence 13, Application US/09852870A
; Patent No. 6673769
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Oespay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-13

Query Match 53.4%; Score 31; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GNSPKG 7

Db 4 GNSPRG 9

RESULT 7

US-08-467-472C-14
; Sequence 14, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:

LENGTH: 9
TYPE: AMINO ACID
TOPOLOGY: LINEAR
MOLECULE TYPE:
DESCRIPTION: PEPTIDE
HYPOTHETICAL: N/A
ANTI-SENSE: N/A
FRAGMENT TYPE: INTERNAL
ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
ORIGINAL SOURCE: INC.,
ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
POSITION IN GENOME: N/A
FEATURE:
NAME/KEY: N/A
LOCATION: N/A
IDENTIFICATION METHOD: N/A
OTHER INFORMATION: water is removed and
OTHER INFORMATION: thereby
OTHER INFORMATION: a -S- bridge is present between Cys and Ser
PUBLICATION INFORMATION:
AUTHORS: JUNG, GUNTHER
TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 865 - 869
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: SHIBA, TETSUO
TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
JOURNAL: BIOPOLYMERS
VOLUME: JOHN WILEY AND SONS, INC.
ISSUE: SUPPLEMENTARY
PAGES: 511 - 519
DATE: 1986
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
PUBLICATION INFORMATION:
AUTHORS: BEAN, MARK F.
TITLE: IDENTIFICATION OF A THIOETHER
TITLE: BY-PRODUCT
TITLE: BY
TITLE: BY
TITLE: TANDEN MASS SPECTROMETRY
JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
JOURNAL: PEPTIDE
JOURNAL: SYMPOSIUM
VOLUME: ESCOM (LEIDEN 1990)
ISSUE:
PAGES: 443 - 445
DATE: 1990
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
US-08-467-472C-14

Query Match 51.7%; Score 30; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 3e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 YGNSPKG 7
Db 3 FGNSPLG 9

RESULT 8
US-09-384-061-14
; Sequence 14, Application US/09384061
; Patent No. 6268339
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/384,061
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,472
; FILING DATE:
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE: PEPTIDE
; DESCRIPTION: N/A
; HYPOTHETICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: N/A
; LOCATION: N/A
; IDENTIFICATION METHOD: N/A
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:

; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK P.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: BY
; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
; JOURNAL: TANDEN MASS SPECTROMETRY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 14: CYS-SER
; US-09-384-061-14
; Query Match 51.7%; Score 30; DB 3; Length 9;
; Best Local Similarity 71.4%; Pred. No. 3e+05;
; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YGNSPKG 7
DB 3 FGNSPLG 9
RESULT 9
US-09-852-870A-14
; Sequence 14, Application US/09852870A
; Patent No. 6673769
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Osapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
; US-09-852-870A-14
; Query Match 51.7%; Score 30; DB 4; Length 9;
; Best Local Similarity 71.4%; Pred. No. 3e+05;
; Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YGNSPKG 7
DB 3 FGNSPLG 9

RESULT 10
US-08-811-492-111
; Sequence 111, Application US/08811492
; Patent No. 5834247
; GENERAL INFORMATION:
; APPLICANT: COMB, DONALD G.
; APPLICANT: PERLER, FRANCINE B.
; APPLICANT: JACK, WILLIAM E.
; APPLICANT: XU, MING-QUN
; APPLICANT: HODGES, ROBERT A.
; APPLICANT: NOREN, CHRISTOPHER J.
; APPLICANT: CHONG, SHAORONG S.C.
; APPLICANT: ADAM, ERIC
; APPLICANT: SOUTHWORTH, MAURICE
; TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR
; TITLE OF INVENTION: PRODUCTION AND METHODS FOR PURIFICATION OF TARGET
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 155
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC\ DOS/MS\ DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/811,492
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/580,555
; FILING DATE: 29-DEC-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,247
; FILING DATE: 28-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,885
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/004,139
; FILING DATE: 09-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-036C4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-927-5054
; TELEFAX: 509-927-1705
; TELEX:
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-811-492-111
Query Match 50.0%; Score 29; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YGNPFG 7
;|||:|
Db 3 FGNCPRG 9
RESULT 11
US-08-444-818-651
; Sequence 651, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANEV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608-2916
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,818
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/403,590
; FILING DATE: 14-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Harbin, Alisa A.
; REGISTRATION NUMBER: 33,895
; REFERENCE/DOCKET NUMBER: 0110.002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508)359-3876
; TELEFAX: (508)359-3885
; INFORMATION FOR SEQ ID NO: 651:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-444-818-651
Query Match 46.6%; Score 27; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPKGFRY 10
;|||:|
Db 2 TPMGFSY 8
RESULT 12
US-08-444-818-652
; Sequence 652, Application US/08444818
; Patent No. 6150087
; GENERAL INFORMATION:
; APPLICANT: Chien, David Y.
; APPLICANT: Rutter, William J.
; TITLE OF INVENTION: NANEV Diagnostics and Vaccines
; NUMBER OF SEQUENCES: 777
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Chiron Corporation
; STREET: 4560 Horton Street
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA

;; ZIP: 94608-2916
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/444,818
;; APPLICATION NUMBER: US/08/444,818
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/403,590
;; FILING DATE: 14-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hardin, Alisa A.
;; REGISTRATION NUMBER: 33,895
;; REFERENCE/DOCKET NUMBER: 0110.002
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (508)359-3876
;; TELEFAX: (508)359-3885
;; INFORMATION FOR SEQ ID NO: 652:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 8 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-444-818-652

Query Match 46.6%; Score 27; DB 3; Length 8;
Best Local Similarity 57.1%; Pred. No. 3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 SPKGFAY 10
DB 1 TPMGFSY 7

RESULT 13

US-08-467-472C-15
; Sequence 15, Application US/08467472C
; Patent No. 6028168
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,472C
; FILING DATE: 6-JUNE-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/742,908
; FILING DATE: 9-AUGUST-1991
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355

;; TELEFAX: (212) 557-5635
;; TELEX: NONE
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9
;; TYPE: AMINO ACID
;; TOPOLOGY: LINEAR
;; MOLECULE TYPE: PEPTIDE
;; DESCRIPTION: N/A
;; HYPOTHETICAL: N/A
;; ANTI-SENSE: N/A
;; FRAGMENT TYPE: INTERNAL
;; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
;; ORIGINAL SOURCE: INC., MARKET STREET, PHILADELPHIA, PA 19104
;; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
;; POSITION IN GENOME: N/A
;; FEATURE:
;; NAME/KEY: N/A
;; LOCATION: N/A
;; IDENTIFICATION METHOD: N/A
;; OTHER INFORMATION: water is removed and
;; OTHER INFORMATION: thereby
;; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
;; PUBLICATION INFORMATION:
;; AUTHORS: JUNG, GUNTHER
;; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
;; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
;; JOURNAL: PEPTIDE
;; JOURNAL: SYMPOSIUM
;; VOLUME: ESCOM (LEIDEN 1990)
;; ISSUE:
;; PAGES: 865 - 869
;; DATE: 1990
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO: 15: CYS-SER
;; PUBLICATION INFORMATION:
;; AUTHORS: SHIBA, TETSUO
;; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
;; JOURNAL: BIOPOLYMERS
;; VOLUME: JOHN WILEY AND SONS, INC.
;; ISSUE: SUPPLEMENTARY
;; PAGES: 511 - 519
;; DATE: 1986
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO: 15: CYS-SER
;; PUBLICATION INFORMATION:
;; AUTHORS: BEAN, MARK F.
;; TITLE: IDENTIFICATION OF A THIOETHER
;; TITLE: BY-PRODUCT
;; TITLE: IN THE SYNTHESIS OF A CYCLIC DISULFIDE PEPTIDE
;; TITLE: BY
;; JOURNAL: TANDEN MASS SPECTROMETRY
;; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
;; JOURNAL: PEPTIDE
;; JOURNAL: SYMPOSIUM
;; VOLUME: ESCOM (LEIDEN 1990)
;; ISSUE:
;; PAGES: 443 - 445
;; DATE: 1990
;; DOCUMENT NUMBER:
;; FILING DATE:
;; PUBLICATION DATE:
;; RELEVANT RESIDUES IN SEQ ID NO: 15: CYS-SER
US-08-467-472C-15

Query Match 46.6%; Score 27; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GNSPKG 7
| | | | |
Db 4 GNSPLG 9

RESULT 14

US-09-384-061-15
; Sequence 15, Application US/09384061
; Patent No. 6268339
; GENERAL INFORMATION:
; APPLICANT: GOODMAN, MURRAY
; TITLE OF INVENTION: LANTHIONINE BRIDGED PEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROOKS HAIDT HAPFNER & DELAHUNTY
; STREET: 99 PARK AVENUE
; CITY: NEW YORK
; STATE: NY
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" FLOPPY DISC
; COMPUTER: COMPAQ - IBM COMPATIBLE
; OPERATING SYSTEM: MS-DOS Version 6.2
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/384.061
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,472
; FILING DATE:
; APPLICATION NUMBER: US 08/021,606
; FILING DATE: 28-JANUARY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINSON, WILLIAM R.
; REGISTRATION NUMBER: 27,224
; REFERENCE/DOCKET NUMBER: LKR-9122B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 697-3355
; TELEFAX: (212) 557-5635
; TELEX: NONE
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9
; TYPE: AMINO ACID
; TOPOLOGY: LINEAR
; MOLECULE TYPE:
; DESCRIPTION: PEPTIDE
; HYPOTHEICAL: N/A
; ANTI-SENSE: N/A
; FRAGMENT TYPE: INTERNAL
; ORIGINAL SOURCE: AMINO ACIDS LISTED IN SEQUENCE -
; ORIGINAL SOURCE: INC.,
; ORIGINAL SOURCE: 3700 MARKET STREET, PHILADELPHIA, PA 19104
; IMMEDIATE SOURCE: SYNTHESIZED PEPTIDE
; POSITION IN GENOME: N/A
; FEATURE:
; NAME/KEY: N/A
; LOCATION: N/A
; IDENTIFICATION METHOD: N/A
; OTHER INFORMATION: water is removed and
; OTHER INFORMATION: thereby
; OTHER INFORMATION: a -S- bridge is present between Cys and Ser
; PUBLICATION INFORMATION:
; AUTHORS: JUNG, GUNTHER
; TITLE: PEPTIDES WITH SULFIDE BRIDGES AND
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:

; PAGES: 865 - 869
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 15: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: SHIBA, TETSUO
; TITLE: CHEMISTRY OF LANTHIONINE PEPTIDES
; JOURNAL: BIOPOLYMERS
; VOLUME: JOHN WILEY AND SONS, INC.
; ISSUE: SUPPLEMENTARY
; PAGES: 511 - 519
; DATE: 1986
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 15: CYS-SER
; PUBLICATION INFORMATION:
; AUTHORS: BEAN, MARK F.
; TITLE: IDENTIFICATION OF A THIOETHER
; TITLE: BY-PRODUCT
; TITLE: BY
; TITLE: TANDEN MASS SPECTROMETRY
; JOURNAL: PROCEEDINGS OF THE 11TH AMERICAN
; JOURNAL: PEPTIDE
; JOURNAL: SYMPOSIUM
; VOLUME: ESCOM (LEIDEN 1990)
; ISSUE:
; PAGES: 443 - 445
; DATE: 1990
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO: 15: CYS-SER
US-09-384-061-15
Query Match 46.6%; Score 27; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GNSPKG 7
| | | | |
Db 4 GNSPLG 9
RESULT 15
US-09-852-870A-15
; Sequence 15, Application US/09852870A
; Patent No. 6673769
; GENERAL INFORMATION:
; APPLICANT: Goodman, Murray
; APPLICANT: Oesapay, George
; TITLE OF INVENTION: Lanthionin Bridged Proteins
; FILE REFERENCE: LKR 9122-D
; CURRENT APPLICATION NUMBER: US/09/852,870A
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/384,601
; PRIOR FILING DATE: 1999-08-26
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cys-Ser lanthionine bridge
US-09-852-870A-15
Query Match 46.6%; Score 27; DB 4; Length 9;
Best Local Similarity 83.3%; Pred. No. 3e+05; 1; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GNSPKG 7
DB 4 GNSPLG 9

Search completed: July 29, 2004, 09:15:31
Job time : 18 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:27 ; Search time 23.6945 Seconds
(without alignments)
982.436 Million cell updates/sec

Title: US-09-661-992B-82

Perfect score: 1299

Sequence: 1 EVKLVSGLPKXPGTIVKI.....QQDYGSPPTFGGTTKLEIKR 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Pir1.*
- 2: Pir2.*
- 3: Pir3.*
- 4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	665	51.2	268	2 A56446	Ig heavy chain V r
2	639.5	49.2	249	2 S41374	single chain Fv antibody - mouse
3	613.5	47.2	233	2 J05322	p3 specific singl
4	543.5	41.8	120	2 B42848	L6 mAb heavy chain
5	543.5	41.8	146	4 A33905	Ig heavy chain pre
6	535	41.2	119	2 A53285	Ig heavy chain V a
7	533	41.0	118	2 S19967	Ig heavy chain V r
8	529	40.7	117	2 S32120	Ig heavy chain V r
9	525.5	40.5	118	2 S37284	Ig heavy chain V r
10	523.5	40.3	109	2 S26325	Ig heavy chain V r
11	522	40.2	136	2 S35759	BHD9D10 protein -
12	518	39.9	225	2 S37484	Ig kappa chain - m
13	514	39.6	113	2 B36259	Ig heavy chain V r
14	511	39.3	117	2 S32187	Ig heavy chain V r
15	508.5	39.1	115	2 S19968	Ig heavy chain V r
16	508	39.1	124	2 P1404	Ig heavy chain V r
17	504.5	38.8	115	2 S19965	Ig heavy chain V r
18	504.5	38.8	139	2 P11225	Ig heavy chain pre
19	504	38.8	119	2 H45722	anti-glycoprotein
20	500.5	38.5	120	2 S19963	Ig heavy chain V r
21	494.5	38.1	127	2 S04577	Ig kappa chain pre
22	492.5	37.9	114	2 D32957	Ig heavy chain V r
23	492.5	37.9	118	2 A32530	Ig heavy chain V r
24	487.5	37.5	114	2 C32957	Ig heavy chain V r
25	484	37.3	105	2 S24765	Ig heavy chain V r
26	481	37.0	119	2 B32530	Ig heavy chain V r
27	480.5	37.0	115	2 B25924	Ig kappa chain pre
28	479	36.9	107	2 S09264	Ig kappa chain V-J
29	472	36.3	105	2 S24764	Ig heavy chain V r

```

30 469.5 36.1 101 2 D24672      Ig heavy chain V r
31 468 36.0 149 1 KVM511      Ig kappa chain pre
32 466 35.9 114 2 PLO256      Ig heavy chain V r
33 459 35.3 105 2 S24766      Ig heavy chain V r
34 457 35.2 119 2 PQ0265      Ig kappa chain V a
35 456 35.1 107 2 D53285      Ig heavy chain V r
36 452 34.8 99 2 S26326      Ig kappa chain V r
37 450 34.6 107 2 S32192      Ig heavy chain V r
38 446.5 34.4 120 2 S26789      Ig heavy chain V r
39 445.5 34.3 93 2 C24672      Ig heavy chain V r
40 445 34.3 107 2 S32191      Ig kappa chain V r
41 441.5 34.0 115 2 A25924      Ig kappa chain pre
42 439 33.8 105 2 S24763      Ig heavy chain V r
43 435 33.5 131 2 S26792      Ig heavy chain V r
44 433 33.3 142 2 S19245      Ig heavy chain pre
45 432.5 33.3 108 2 PLO083      Ig kappa chain V r

```

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C;Accession: A56446
R;Yang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical to the native protein
A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-268 <TAN>
A;Cross-references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin

Query Match 51.2%; Score 665; DB 2; Length 268;

Best Local Similarity 54.1%; Pred. No. 6.8e-42;

Matches 131; Conservative 40; Mismatches 69; Indels 2; Gaps 2;

```

QY 1 EVKLVSGLPKXPGTIVKI SCASGYIFTNYGMWVKQAPGKGLKMGWINTYTGPTY 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 QVQLQESGELVKPGASVKLSCTTSGFNFKDTYMWVKQRPQGLEWIGRIAPANGITKY 62
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADDPKGRPAFSLTASTAYLQINNLKNEDTATYFCALYGNSPKGFAYWGQGLTVTSAG 120
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 DPKFQGGKATIAADTSSNTAYLQLSSILTSDETAIVYCASY-YLTRYENYWGQGLTVTSAG 121
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 GGSGGRASGGGSDIQMTQSPKFLVLSAGDVTITCKASQSVNDVAVYQKPGQSPK 180
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 GGSGGGGSDGGGGSDIELTQSPAIMSASLGEKVTWSCRASSSV-NFIYVYQKSDASPKL 180
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 LMVYASNRITGVDPDRFTSGYGTDFTTISTVYQAEGLAVYFCQDYGSPPTFGGTTKLEI 240
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 WYITSHLPVGPVAPFSGSGSGNSYSLTISSEGEADAITYCQFTSSPFTFGGTTKLEI 240
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 KR 242
    ||
Db 241 KR 242

```

RESULT 2

S41374
single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C;Accession: S41374
R;Artezenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization of a single chain Fv antibody
A;Reference number: S41374

C;Accession: A53285
R;Sawada, J.; Mizusawa, S.; Terao, T.; Naito, M.; Kurosawa, Y.
Mol. Immunol. 28, 1063-1072, 1991
A;Title: Molecular characterization of monoclonal anti-steroid antibodies: primary structure and their pH-reactivity profiles.
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
A;Accession: A53285
A;Status: preliminary
A;Molecule type: DNA; protein
A;Residues: 1-119 <SAW>
A;Cross-references: GB:D12736; NID:9220595; PIDN:BAA02228.1; PID:9220596
A;Note: sequence extracted from NCBI backbone (NCBIN:63271, NCBI:P:63299)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Query Match 41.2%; Score 535; DB 2; Length 119;
Best Local Similarity 83.2%; Pred. No. 1e-32;
Matches 99; Conservative 7; Mismatches 13; Indels 0; Gaps 0;
QY 1 EVKLVSQPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKWMGINTYTGPTY 60
Db 1 QIQLVQSGPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKWMGINTYTGPTY 60
QY 61 ADDFKGRFAPSLETSASTAYLQINLNKEDTATYFCALYGNSPKGFAYWGQGLTVTSA 119
Db 61 ADDFKGRFAPSLETSASTAYLQINLNKEDTATYFCALYGNSPKGFAYWGQGLTVTSS 119
RESULT 7
S19967
Ig heavy chain V region (M-7406) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S19967
R;Weissenhorn, W.; Riettmueller, G.; Weiss, E.M.; Rieber, E.P.
Submitted to the EMBL Data Library, March 1992
A;Description: Structural characterization of CD4 mAb.
A;Reference number: S19963
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <WEI>
A;Cross-references: EMBL:X65090
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;12-95/Domain: immunoglobulin homology <IMM>
Query Match 41.0%; Score 533; DB 2; Length 118;
Best Local Similarity 84.7%; Pred. No. 1.4e-32;
Matches 100; Conservative 4; Mismatches 12; Indels 2; Gaps 1;
QY 4 LVESGPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKWMGINTYTGPTYADD 63
Db 1 LVQSGPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKWMGINTYTGPTYADD 60
QY 64 FKGRFAPSLETSASTAYLQINLNKEDTATYFC--ALYGNSPKGFAYWGQGLTVTSA 119
Db 61 FKGRFAPSLETSASAFLINLNKEDTATYFCTRAPYDYGAWFPYWGQGLTVTSA 118
RESULT 8
S32190
Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C;Accession: S32190
R;Izui, S.
Submitted to the EMBL Data Library, February 1993
A;Reference number: S32195
A;Accession: S32190
A;Status: preliminary
A;Molecule type: mRNA

A;Residues: 1-117 <IZU>
A;Cross-references: EMBL:X70098; NID:9288258; PIDN:CAA49702.1; PID:9288259
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
Query Match 40.7%; Score 529; DB 2; Length 117;
Best Local Similarity 81.5%; Pred. No. 2.8e-32;
Matches 97; Conservative 11; Mismatches 9; Indels 2; Gaps 1;
QY 1 EVKLVSQPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKWMGINTYTGPTY 60
Db 1 QIQLVQSGPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKWMGINTYSGPTY 60
QY 61 ADDFKGRFAPSLETSASTAYLQINLNKEDTATYFCALYGNSPKGFAYWGQGLTVTSA 119
Db 61 ADDFKGRFAPSLETSASTAYLQINLNKEDTATYFCARWITT--AFDYWGQGLTVTSS 117
RESULT 9
S37204
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Jun-2000
C;Accession: S37204
R;Fischer, R.; Voss, A.; Runziker, W.; Stierhof, Y.D.; Kreuzaler, F.
Submitted to the EMBL Data Library, August 1993
A;Description: Production and cloning of TMV-specific monoclonal antibodies.
A;Reference number: S37200
A;Accession: S37204
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-118 <FIS>
A;Cross-references: EMBL:X74589; NID:9402599; PIDN:CAAS2666.1; PID:91333981
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;15-98/Domain: immunoglobulin homology <IMM>
Query Match 40.5%; Score 525.5; DB 2; Length 118;
Best Local Similarity 83.2%; Pred. No. 5.1e-32;
Matches 99; Conservative 7; Mismatches 12; Indels 1; Gaps 1;
QY 1 EVKLVSQPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKWMGINTYTGPTY 60
Db 1 QIQLVQSGPELKKPGETVKISKASGYIFTIDYSMHWKQVPGKGLKWMGINTETGEAKY 60
QY 61 ADDFKGRFAPSLETSASTAYLQINLNKEDTATYFCALYGNSPKGFAYWGQGLTVTSA 119
Db 61 ADDFKGRFAPSLETSASTAYLQINLNKEDTATYFCARWYS-AMFPYWGQGLTVTSA 118
RESULT 10
S26325
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C;Accession: S26325
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein
A;Reference number: S26309; MUID:91341421; PMID:1908510
A;Accession: S26325
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-109 <STA>
A;Cross-references: EMBL:X59210; NID:952080; PID:91334043
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;5-88/Domain: immunoglobulin homology <IMM>
Query Match 40.3%; Score 523.5; DB 2; Length 109;
Best Local Similarity 88.5%; Pred. No. 6.5e-32;
Matches 100; Conservative 0; Mismatches 4; Indels 9; Gaps 2;

QY 11 LKPGETVKISKASGYFTNYGNWVKQAPGKGLKMWGINTYTGPTTADDFKGRFAP 70
Db 1 LKPGETVKISKASGYFTNYGNWVKQAPGKGLKMWGINTYTGPTTADDFKGRFAP 60
QY 71 SLETSASTAYLQINLNKNEPATYFCALYGNP-----KGFAYWGQGLTVTVS 118
Db 61 SLETSASTAYLQINLNKNEPATYFCALYGNP-----RPAFYRYDGFAYWGQGLTVTVS 109

RESULT 11
S35759
BHD9D10 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C:Accession: S35759
R:Proyen, G.F.V.
submitted to the EMBL Data Library, May 1993
A:Reference number: S35759
A:Accession: S35759
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-136 <FRC>
A:Cross-references: EMBL:X72796; NID:g312496; PIDN:CAA51316.1; PID:g312497
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 40.2%; Score 522; DB 2; Length 136;
Best Local Similarity 80.3%; Pred. No. 1.1e-31;
Matches 98; Conservative 8; Mismatches 8; Indels 8; Gaps 2;

QY 1 EVKLVSPELKKPGETVKISKASGYFTNYGNWVKQAPGKGLKMWGINTYTGPTT 60
Db 20 QIQLVQSGPELKKPGETVKISKASGYFTNYGNWVKQAPGKGLKMWGINTYTGPTT 79
QY 61 ADDFKGRFAFSLTSASTAYLQINLNKNEPATYFCALYGNP-----AYWGQGLTVTV 117
Db 80 VDDFKGRFVFLTSASTAYLQINLNKNEPATYFCALYGNP-----RRGFYAMYWGQGLTVTV 134

QY 118 SA 119
Db 135 SS 136

RESULT 12
S37484
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37484
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 39.9%; Score 518; DB 2; Length 225;
Best Local Similarity 90.4%; Pred. No. 3.6e-31;
Matches 103; Conservative 4; Mismatches .5; Indels 2; Gaps 2;

QY 129 SGGGSDIQMTQSPKFLVLSAGDRVTICKASQSVNDVAVYQKQSPKLLMYASNR 198
Db 8 SGAHGS-IVMTQTPEKLLLSAGDRVTICKASQSVNDVAVYQKQSPKLLIYASSR 66
QY 189 YTGVPDRFTGSGYGTDFTFTISTVQAEADLAVYFCQQYGSPTFGGQTKLEIKR 242
Db 67 YTGVPDRFTGSGYGTDFTFTISTVQAEADLAVYFCQQYSS-YTGGGQTKLEIKR 119

RESULT 13
S36259
Ig heavy chain V region TE34 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 18-Jan-1991 #sequence_revision 13-Jan-1993 #text_change 21-Jan-2000
C:Accession: S36259
R:Zilber, B.; Scherf, T.; Levitt, M.; Anglister, J.
Biochemistry 29, 10032-10041, 1990
A:Title: NMR-derived model for a peptide-antibody complex.
A:Reference number: A36259; MUID:91104915; PMID:2271636
A:Accession: S36259
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <ZIL>
A:Cross-references: GB:M30459; GB:M30480; GB:M30481; GB:M30482; GB:M30483
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.6%; Score 514; DB 2; Length 113;
Best Local Similarity 78.2%; Pred. No. 3.4e-31;
Matches 93; Conservative 11; Mismatches 9; Indels 6; Gaps 1;

QY 1 EVKLVSPELKKPGETVKISKASGYFTNYGNWVKQAPGKGLKMWGINTYTGPTT 60
Db 1 QIQLVQSGPELKKPGETVKISKASGYFTNYGNWVKQAPGKGLKMWGINTYTGPTT 60
QY 61 ADDFKGRFAFSLTSASTAYLQINLNKNEPATYFCALYGNP-----RPFDSWGQGLTVTVSS 119
Db 61 VDDFKGRFAFSLTSASTAYLQINLNKNEPATYFCALYGNP-----RPFDSWGQGLTVTVSS 113

RESULT 14
S32187
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32187
R:Izui, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32187
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <IZU>
A:Cross-references: EMBL:X70091; NID:g288251; PIDN:CAA49696.1; PID:g288252
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 511; DB 2; Length 117;
Best Local Similarity 79.8%; Pred. No. 5.8e-31;
Matches 95; Conservative 10; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVKLVSPELKKPGETVKISKASGYFTNYGNWVKQAPGKGLKMWGINTYTGPTT 60
Db 1 QIQLVQSGPELKKPGETVKISKASGYFTNYGNWVKQAPGKGLKMWGINTYTGPTT 60
QY 61 ADDFKGRFAFSLTSASTAYLQINLNKNEPATYFCALYGNP-----RPFDSWGQGLTVTVSS 119
Db 61 ADDFKGRFAFSLTSASTAYLQINLNKNEPATYFCALYGNP-----RPFDSWGQGLTVTVSS 117

RESULT 15
S19968
Ig heavy chain V region (M-T408) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S19968
R:Weissenhorn, W.; Rietmueller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963

A/Accession: S19968
A/Status: Preliminary
A/Molecule type: mRNA
A/Residues: 1-115 <WEI>
A/Cross-references: EMBL:X65089
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/10-93/Domain: immunoglobulin homology <IMM>

Query Match 39.1%; Score 508.5; DB 2; Length 115;
Best Local Similarity 80.5%; Pred. No. 8.7e-31;
Matches 95; Conservative 6; Mismatches 10; Indels 7; Gaps 2;
QY 6 ESQPELKKPGETVTKISKASGYFTNYGMNVVKQAPGKGLKWMGWINTYTGEPYADDFK 65
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 QSGPELKTPTGETVTKISKASGYFTNYGMNVVKQAPGKGLKWMGWINTYTGEPYADDFK 60
QY 66 GRFAPSLETSASTAYLQINNLKNEDEATYFCALYGNSPK----GFAYWGQGLVTVA 119
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GRFAPSLETSASTAYLQINNLKNEDEATYFCALYGNSPK----RGPPYRFSFDYWGQGLTVA 115

Search completed: July 29, 2004, 08:51:47
Job time : 24.6945 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 16.1123 Seconds
(without alignments)
782.073 Million cell updates/sec

Title: US-09-661-992B-82

Perfect score: 1299

Sequence: 1 EVKLVEGPELKKPGETVKI.....QQDYGSPPTGGGKTLEIKR 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	468	36.0	149	1 KV5A_MOUSE	P01633 mus musculus
2	404	31.1	136	1 KV5B_MOUSE	P01634 mus musculus
3	394.5	30.4	133	1 KV4B_HUMAN	P06313 homo sapien
4	391	30.1	114	1 KV4A_HUMAN	P01625 homo sapien
5	390	30.0	134	1 KV4C_HUMAN	P06314 homo sapien
6	386	29.7	108	1 KV1M_HUMAN	P01605 homo sapien
7	378	29.1	108	1 KV1Y_HUMAN	P80362 homo sapien
8	376	28.9	108	1 KV1H_HUMAN	P01600 homo sapien
9	376	28.9	108	1 KV1N_HUMAN	P01606 homo sapien
10	373	28.7	129	1 KV1W_HUMAN	P04431 homo sapien
11	372	28.6	114	1 KV1A_MOUSE	P01632 mus musculus
12	370.5	28.5	109	1 KV3D_HUMAN	P01622 homo sapien
13	368	28.3	108	1 KV1A_HUMAN	P01593 homo sapien
14	367.5	28.3	129	1 KV3H_HUMAN	P04207 homo sapien
15	367	28.3	108	1 KV1P_HUMAN	P01608 homo sapien
16	366	28.2	108	1 KV1S_HUMAN	P01611 homo sapien
17	365	28.1	108	1 KV1K_HUMAN	P01603 homo sapien
18	365	28.1	108	1 KV5M_MOUSE	P01646 mus musculus
19	363.5	28.0	109	1 KV3B_HUMAN	P01620 homo sapien
20	363	27.9	108	1 KV1G_HUMAN	P01599 homo sapien
21	362.5	27.9	129	1 KV3L_HUMAN	P18135 homo sapien
22	361	27.8	108	1 KV1B_HUMAN	P01594 homo sapien
23	361	27.8	108	1 KV1O_HUMAN	P01607 homo sapien
24	360	27.7	108	1 KV1C_HUMAN	P01595 homo sapien
25	359	27.6	108	1 KV1V_HUMAN	P04430 homo sapien
26	358.5	27.6	109	1 KV3F_HUMAN	P01624 homo sapien
27	358	27.6	108	1 KV5P_MOUSE	P01649 mus musculus
28	357.5	27.5	129	1 KV3M_HUMAN	P18136 homo sapien
29	356.5	27.4	113	1 KV2G_MOUSE	P01631 mus musculus
30	356	27.4	108	1 KV5K_MOUSE	P01644 mus musculus
31	354	27.3	108	1 KV1F_HUMAN	P01598 homo sapien
32	354	27.3	108	1 KV1R_HUMAN	P01610 homo sapien
33	354	27.3	108	1 KV5O_MOUSE	P01648 mus musculus

ALIGNMENTS

RESULT 1

KV5A_MOUSE
ID KV5A_MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region MPC11 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=83001944; PubMed=6288267;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RT 5'-terminal regions of immunoglobulin variable-region genes.";
RL Cell 29:681-689(1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Matthysens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes.";
RL Can. J. Biochem. 59:176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11.";
RL Biochem. J. 171:337-347(1978).
CC -!- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00561; AAA38776.1; -;
CC PIR; A90823; KVMG11.
CC HSP; P80362; 1WTL.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Igv; 1.
CC PROSITE; PS0835; IG LIKE; 1.
CC Immunoglobulin V region; Signal; Repeat.
FT SIGNAL 1 29

P01645 mus musculus
P01647 mus musculus
P01597 homo sapien
P01652 mus musculus
P04432 homo sapien
P01623 homo sapien
P01504 homo sapien
P01746 mus musculus
P06312 homo sapien
P01596 homo sapien
P01643 mus musculus
P83593 homo sapien

1 KV5L_MOUSE
1 KV5N_MOUSE
1 KV5E_HUMAN
1 KV5S_MOUSE
1 KV1X_HUMAN
1 KV3E_HUMAN
1 KV1L_HUMAN
1 HV02_MOUSE
1 KV40_HUMAN
1 KV1D_HUMAN
1 KV5J_MOUSE
1 KV4D_HUMAN

353 27.2 108
351 27.0 108
350 26.9 108
350 26.9 108
350 26.9 108
348.5 26.8 109
348 26.8 108
348 26.8 108
348 26.8 108
347 26.7 121
346.5 26.7 107
345 26.6 108
345 26.6 109

SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 30.4%; Score 394.5; DB 1; Length 133;
Best Local Similarity 66.9%; Pred. No. 7.6e-25;
Matches 79; Conservative 13; Mismatches 19; Indels 7; Gaps 2;

QY 131 GGGSDIQNTQSPKFLVLSAGDRVTITCKASQSV-----SNDVAVYQKPGQSPKLLIYY 184
Db 17 GAYGDIVMTQSPDLSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPKLLIYW 76

QY 185 ASNRYTGVDPDRFTSGYGTDTFTTISTVQAEADLAVYFCQDYGSPTFGGKLEIKR 242
Db 77 ASTRESGVDRFSGSGGTDTFTLTISLQAEADVAVYCCQ-YDTPTFGGKTVKLEIKR 133

RESULT 4

ID KV4A HUMAN STANDARD; PRT; 114 AA.

AC P01625;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig kappa chain V-IV region Len.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RA MEDLINE=76004342; PubMed=50995;

RA Schneider M., Hilschmann N.;

RT "The primary structure of a monoclonic immunoglobulin-L-chain of
subgroup IV of the kappa type (Bence-Jones protein len).";
Hoppe-Sejler's Z. Physiol. Chem. 356:507-557(1975).
[2]

RN REVISION TO 9.

RA Salomon A.;

RA Submitted (AUG-1996) to Swiss-Prot.

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- MISCELLANEOUS: This is a Bence-Jones protein.

DR PDB; 1EEQ; 01-FEB-01.

DR PDB; 1EEU; 03-FEB-01.

DR PDB; 1EFQ; 09-FEB-01.

DR PDB; 1EK3; 06-MAR-01.

DR PDB; 1LVE; 21-JAN-98.

DR PDB; 3LVE; 18-MAY-99.

DR PDB; 5LVE; 28-MAR-01.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS00835; IG LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.

FT DOMAIN 1 23 FRAMEWORK-1.

FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 41 55 FRAMEWORK-2.

FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 63 94 FRAMEWORK-3.

FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 102 113 FRAMEWORK-4.

FT DISULFID 23 94 BY SIMILARITY.

FT NON TER 114 114

SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;

Query Match 30.1%; Score 391; DB 1; Length 114;
Best Local Similarity 67.5%; Pred. No. 1.2e-24;
Matches 77; Conservative 13; Mismatches 18; Indels 6; Gaps 1;

QY 135 DIQWTSQPKFLVLSAGDRVTITCKASQSV-----SNDVAVYQKPGQSPKLLIYYASNR 188

Db 17 GAYGDIVMTQSPDLSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPKLLIYW 76

QY 185 ASNRYTGVDPDRFTSGYGTDTFTTISTVQAEADLAVYFCQDYGSPTFGGKLEIKR 242

Db 77 ASTRESGVDRFSGSGGTDTFTLTISLQAEADVAVYCCQ-YDTPTFGGKTVKLEIKR 133

RESULT 5

ID KV4C HUMAN STANDARD; PRT; 134 AA.

AC P06314;

DT 01-JAN-1988 (Rel. 06, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-IV region B17 precursor.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=60411954; PubMed=29977113;

RA Marsh P., Mills F., Gould H.;

RT "Detection of a unique human V kappa IV germline gene by a cloned
cDNA probe.";

RL Nucleic Acids Res. 13:6531-6544(1985).

RN [2]

RP REVISION TO 76.

RA Marsh P.;

RA Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.

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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).

CC EMBL; X02990; CAA26733.1; -.

DR HSSP; P80362; 1WTL.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS00835; IG LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 20

FT CHAIN 21 134 IG KAPPA CHAIN V-IV REGION B17.

FT DOMAIN 21 43 FRAMEWORK-1.

FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 61 75 FRAMEWORK-2.

FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 83 114 FRAMEWORK-3.

FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 122 133 FRAMEWORK-4.

FT DISULFID 43 114 BY SIMILARITY.

FT NON TER 134 134

SQ SEQUENCE 134 AA; 14966 MW; 6413A22FD0738832 CRC64;

Query Match 30.0%; Score 390; DB 1; Length 134;
Best Local Similarity 65.3%; Pred. No. 1.7e-24;
Matches 77; Conservative 13; Mismatches 22; Indels 6; Gaps 1;

QY 131 GGGSDIQNTQSPKFLVLSAGDRVTITCKASQSV-----SNDVAVYQKPGQSPKLLIYY 184
Db 17 GAYGDIVMTQSPDLSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPKLLIYW 76

QY 185 ASNRYTGVDPDRFTSGYGTDTFTTISTVQAEADLAVYFCQDYGSPTFGGKLEIKR 242

Db 77 ASTRESGVDRFSGSGGTDTFTLTISLQAEADVAVYCCQ-YDTPTFGGKTVKLEIKR 133

Db 77 ASTRESGVDRFSGSGSDFTLTISLQAEADVAVYCCQYNLPLWTFGGTKVEIKR 134

RESULT 6

KV1M HUMAN

ID KV1M_HUMAN STANDARD; PRT; 108 AA.

AC P01605;

DT 21-JUL-1996 (Rel. 01, Created)

DT 21-JUL-1996 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Lay.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE.

RA MEDLINE=77038198; PubMed=824717;

RA Capra J.D., Klapper D.G.;

RT "Complete amino acid sequence of the variable domains of two human

RT IgM anti-gamma globulins (Iay/Pom) with shared idiotypic

RT specificities.";

RL Scand. J. Immunol. 5:677-684(1976).

CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS

CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,

CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.

CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA

CC GLOBULIN ACTIVITY.

DR PIR; A01871; KIHULY.

DR HSSP; P01607; IREI.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS0835; IG LIKE; 1.

KW Immunoglobulin V region.

FT DOMAIN 1 23

FT STRAND 10 13

FT TURN 15 16

FT STRAND 19 25

FT TURN 30 31

FT STRAND 33 38

FT TURN 40 41

FT STRAND 45 49

FT TURN 50 52

FT STRAND 53 54

FT TURN 56 57

FT TURN 60 61

FT STRAND 62 67

FT TURN 68 69

FT STRAND 70 75

FT TURN 80 82

FT STRAND 84 90

FT TURN 98 98

FT STRAND 102 106

FT NON_TER 108

SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 29.7%; Score 386; DB 1; Length 108;

Best Local Similarity 68.5%; Pred. No. 2.8e-24;

Matches 74; Conservative 13; Mismatches 21; Indels 0; Gaps 0;

QY 135 DIQMTQSPKFLVSGAGRVTTTCASQSVNDVAVYCCQSPKLLMYASNRVTGVPD 194

Db 1 DIQMTQSPSSLSVSGDVRVTTTCASQSNVAYLWYQOKPGAPKLLIYGASTREAGVPS 60

QY 195 RFTSGSGYGTDTFTTISTVQAEDLAVYFCQDYGSPTFGGKLEIKR 242

Db 61 RPSGSGSGTDTFTTISLQPEDIAITYCCQYNNWPTFGGTKVEIKR 108

RESULT 7

KV1Y HUMAN

ID KV1Y_HUMAN STANDARD; PRT; 108 AA.

AC P80362;

DT 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ig kappa chain V-I region WAT.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).

RX MEDLINE=95086080; PubMed=7993911;

RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,

RA Solomon A., Stevens F.J., Schiffer M.;

RT "Comparison of crystal structures of two homologous proteins:

RT structural origin of altered domain interactions in immunoglobulin

RT light-chain dimers.";

RL Biochemistry 33:14848-14857(1994).

RN [2]

RP SEQUENCE OF 1-35.

RX MEDLINE=81267384; PubMed=6167731;

RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,

RA Popp R.A., Solomon A.;

RT "Characterization and preliminary crystallographic data on the VL-

RT related fragment of the human XI Bence Jones protein Wat.";

RL J. Mol. Biol. 147:185-193(1981).

CC -!- MISCELLANEOUS: This is a Bence-Jones protein.

DR PDB; 1WTL; 01-NOV-94.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS0835; IG LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.

FT DOMAIN 1 23

FT STRAND 10 13

FT TURN 15 16

FT STRAND 19 25

FT TURN 30 31

FT STRAND 33 38

FT TURN 40 41

FT STRAND 45 49

FT TURN 50 52

FT STRAND 53 54

FT TURN 56 57

FT TURN 60 61

FT STRAND 62 67

FT TURN 68 69

FT STRAND 70 75

FT TURN 80 82

FT STRAND 84 90

FT TURN 98 98

FT STRAND 102 106

FT NON_TER 108

SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 29.1%; Score 378; DB 1; Length 108;

Best Local Similarity 66.7%; Pred. No. 1.2e-23;

Matches 72; Conservative 15; Mismatches 21; Indels 0; Gaps 0;

QY 135 DIQMTQSPKFLVSGAGRVTTTCASQSVNDVAVYCCQSPKLLMYASNRVTGVPD 194

Db 1 DIQMTQSPSSLSVSGDVRVTTTCASQSDITVYNNWFOQRPGAPKLLIYGASILETGVS 60

QY 195 RFTSGSGYGTDTFTTISTVQAEDLAVYFCQDYGSPTFGGKLEIKR 242

Db 61 RPSGSGSGTDTFTTISLQPEDIAITYCCQYNNWPTFGGTKVEIKR 108

RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RT Science 169:56-59(1970) .
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01872; KIHUOU.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105827E CRC64;

Query Match 28.9%; Score 376; DB 1; Length 108;
Best Local Similarity 56.5%; Pred. No. 1.8e-23;
Matches 61; Conservative 28; Mismatches 19; Indels 0; Gaps 0;

QY 135 DIQMTQSPKFLVLSAGDRVTITCKASQSVNDVAVYQOKPGQSPKILMYASNRYTGVPD 194
Db 1 DIQMTZSPSSLSASVGBRVITICRASZTISVLYBZZKPKAPBLIYAASBLHSGVPS 60

QY 195 RTGSGYGTDFTTISTVQAEADLAVYFCQDYGSPTFGGKLEIKR 242
Db 61 RFGSGSGTDFTTISLQPEDPATYCCQNYITPTSGGQTRVEIKR 108

RESULT 10
KV1W_HUMAN
ID KV1W_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobeck H.G.; Combrato G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RT lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00965; CAA25477.1; ALT_TERM.
DR PIR; A01883; KIHUWK.
DR HSSP; P01607; IREI.

RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains.";
RT Science 169:56-59(1970) .
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC MACROGLOBULIN.
DR PIR; A01872; KIHUOU.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

Query Match 28.9%; Score 376; DB 1; Length 108;
Best Local Similarity 63.9%; Pred. No. 1.8e-23;
Matches 69; Conservative 21; Mismatches 18; Indels 0; Gaps 0;

QY 135 DIQMTQSPKFLVLSAGDRVTITCKASQSVNDVAVYQOKPGQSPKILMYASNRYTGVPD 194
Db 1 DIQMTZSPSSLSASVGBRVITICRASZTISVLYBZZKPKAPQVLIYAASLPSGVPS 60

QY 195 RTGSGYGTDFTTISTVQAEADLAVYFCQDYGSPTFGGKLEIKR 242
Db 61 RFGSGSGTDFTTISLQPEDPATYCCQNYITPTSGGQTRVEIKR 108

RESULT 9
KV1N_HUMAN
ID KV1N_HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;

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DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129  
FT DOMAIN 23 45 IG KAPPA CHAIN V-I REGION WALKER.  
FT DOMAIN 23 45  
FT DOMAIN 23 45  
FT DOMAIN 23 45  
FT DOMAIN 46 56  
FT DOMAIN 57 71  
FT DOMAIN 72 78  
FT DOMAIN 79 110  
FT DOMAIN 111 129  
FT DOMAIN 120 129  
FT DISULFID 45 110  
FT NON_TER 129 129  
SQ SEQUENCE 129 AA; 14069 MW; P941FA07D4AFC2P9 CRC64;  
  
Query Match 28.7%; Score 373; DB 1; Length 129;  
Best Local Similarity 64.9%; Pred. No. 3.7e-23;  
Matches 72; Conservative 14; Mismatches 25; Indels 0; Gaps 0;  
  
QY 131 GGSGDIQMTQSPKFLVSGAGDRVTITCKASQSVNDVAVYQKPGQSPKLLMYASNYR 190  
Db 19 GARCIDIQMTQSPSLASVGRVTITCKASQSVNLYNWYQKPGKAPKLLIYAASLQS 78  
  
QY 191 GVPDRFTGSGYGTDTFTTISTVQAEADLAVYFCQDYGSPTFGGKLEIK 241  
Db 79 GVTFRFGSGSGTDTFTLTISLQPEDSATYCCQSYSLTIFGQGTLEIK 129  
  
RESULT 11  
KVIA_MOUSE STANDARD; PRT; 114 AA.  
ID KVIA_MOUSE  
AC P01632;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region S107A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=81241357; PubMed=6788890;  
RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;  
RT "Nucleic acid and protein sequences of phosphocholine-binding light  
chains.";  
RL J. Exp. Med. 153:1366-1370 (1981).  
CC -----  
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CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; U29423; ABC00033.1; -  
DR PIR; A01945; KMS7A.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 23 45  
FT DOMAIN 46 56  
FT DOMAIN 57 71  
FT DOMAIN 72 78  
FT DOMAIN 79 110  
FT DOMAIN 111 129  
FT DOMAIN 120 129  
FT DISULFID 45 110  
FT NON_TER 129 129  
SQ SEQUENCE 129 AA; 14069 MW; P941FA07D4AFC2P9 CRC64;  
  
Query Match 28.7%; Score 373; DB 1; Length 129;  
Best Local Similarity 64.9%; Pred. No. 3.7e-23;  
Matches 72; Conservative 14; Mismatches 25; Indels 0; Gaps 0;  
  
QY 131 GGSGDIQMTQSPKFLVSGAGDRVTITCKASQSVNDVAVYQKPGQSPKLLMYASNYR 190  
Db 19 GARCIDIQMTQSPSLASVGRVTITCKASQSVNLYNWYQKPGKAPKLLIYAASLQS 78  
  
QY 191 GVPDRFTGSGYGTDTFTTISTVQAEADLAVYFCQDYGSPTFGGKLEIK 241  
Db 79 GVTFRFGSGSGTDTFTLTISLQPEDSATYCCQSYSLTIFGQGTLEIK 129  
  
RESULT 12  
KV3D_HUMAN STANDARD; PRT; 109 AA.  
ID KV3D_HUMAN  
AC P01622;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region Ti.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72188439; PubMed=5027703;  
RA Suter L., Barnikol H.U., Watanabe S., Hilschmann M.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein  
Ti). IV. The complete amino acid sequence and its significance for  
RT the mechanism of antibody production.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208 (1972).  
CC -!- MISCELLANEOUS; THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- MISCELLANEOUS; This is a Bence-Jones protein.  
DR PIR; A01895; K3HUT1.  
DR HSSP; P80362; 1WTL.  
DR GO; GO:0005576; C:extracellular; NAS.  
DR GO; GO:0003823; P:antigen binding; NAS.  
DR GO; GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Igv; 1.  
DR SMART; SM00406; Igv; 1.  
DR PROSITE; PS50835; IG LIKE; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DISULFID 23 89  
FT NON_TER 109 109  
SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;  
  
Query Match 28.5%; Score 370.5; DB 1; Length 109;  
Best Local Similarity 64.2%; Pred. No. 4.9e-23;  
Matches 70; Conservative 19; Mismatches 19; Indels 1; Gaps 1;  
  
QY 135 DIQMTQSPKFLVSGAGDRVTITCKASQSVNDVAVYQKPGQSPKLLMYASNYR 193  
Db 1 EIVLTQSPGTSLSPGERATLSCRASQSVNLFVAVYQKPGAPRLLIYVASSPATGIP 60  
  
QY 194 DRFTGSGYGTDTFTTISTVQAEADLAVYFCQDYGSPTFGGKLEIK 242  
Db 61 DRFGSGSGTDTFTLTISRLEPEDFAVYVYCCQYVGSPTFGGKLEIK 109  
  
Query Match 28.5%; Score 370.5; DB 1; Length 109;  
Best Local Similarity 64.2%; Pred. No. 4.9e-23;  
Matches 70; Conservative 19; Mismatches 19; Indels 1; Gaps 1;
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RESULT 13
KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence and the location of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A01861; KIHUAG.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Hance-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 FRAMEWORK-2.
FT DOMAIN 35 49 FRAMEWORK-3.
FT DOMAIN 50 56 FRAMEWORK-4.
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 FRAMEWORK-4.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 28.3%; Score 368; DB 1; Length 108;
Best Local Similarity 65.7%; Pred. No. 7.6e-23;
Matches 71; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

Qy 135 DIQMTQSPKFLVSGDRVTITCKASQSVNDVAVYQKQSGPKLLMYASNRVTGVPD 194
Db 1 DIQMTQSPSSLASVGRVTITCKASQSDINHLNLYQKQPKKPKILYDASNLETVGPS 60

Qy 195 RFTSGYGTDTFTTISTVQAEADLAVYFCQDYGSPTFGGTKLEIKR 242
Db 61 RFGSGGFGTDTFTTISGLQPEDATYCYQQYDTLPRTFGGQTKLEIKR 108

RESULT 14
KV3H_HUMAN STANDARD; PRT; 129 AA.
AC P04207;
DT 20-MAR-1987 (Rel. 04, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region CIL precursor (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86177570; PubMed=3083417;
RA Jirik F.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,

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RA Goldfien R., Carson D.A.;
RT "Cloning and sequence determination of a human rheumatoid factor
RT light-chain gene.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL; M12740; AAA58992.1; -.
DR HSSP; P80362; LWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 69 FRAMEWORK-2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 77 108 FRAMEWORK-3.
FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 108 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14275 MW; 5C13B411B560CC14 CRC64;

Query Match 28.3%; Score 367.5; DB 1; Length 129;
Best Local Similarity 65.1%; Pred. No. 1e-22;
Matches 71; Conservative 17; Mismatches 20; Indels 1; Gaps 1;

Qy 135 DIQMTQSPKFLVSGDRVTITCKASQSVNDVAVYQKQSGPKLLMYASNRVTGVPD 194
Db 21 EVWTSQSPATLSVSGERATLSCRASQSVSNLAWYQKQGPQPRLLYGASTRATGIPA 80

Qy 195 RFTSGYGTDTFTTISTVQAEADLAVYFCQDYGSPP-TFGGTKLEIKR 242
Db 81 RFGSGSGGTEFTLTISRLQSDFAVYCYQQYNNWPPFTFGQGRVEIKR 129

RESULT 15
KV1P_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RX Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;

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(In) Franek F., Shugar D. (eds.);
Gamma globulins: structure and function, pp.57-74, Academic Press,
New York (1969).
-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDESA313DF3A CRC64;

Query Match 28.3%; Score 367; DB 1; Length 108;
Best Local Similarity 64.8%; Pred.No.9.2e-23;
Matches 70; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 135 DIQMTQSPKFLVSGDRVTITCKASQSVSNDAVWYQQKPKQSPKLLMYASNRYTGVDP 194
DB 1 DIQMTQSPSSLASVGDRTITTCASQDISIFLNWYQQKPKAPKLLIYDASKLEAGVPS 60

QY 195 RFTSGYGTDTFTTISTVQAEEDLAVYFCQDYGSPPTFGGGTKLEIKR 242
DB 61 RFSCTGSGTDTFTTISLIQPEDIATYCCQFDNLPLTFGGGTRVDKFR 108

Search completed: July 29, 2004, 08:47:34
Job time : 16.1123 secs

Result No.	Score	Query %		Length	DB	ID	Description
		Match					
1	906	69.7	241	11	Q921A6		Q921a6 mus musculus
2	755.5	58.2	218	11	Q92S51		Q92S51 mus musculus
3	716	55.1	243	11	Q7TQM2		Q7Tqm2 mus musculus
4	694.5	53.0	298	11	Q9QYF0		Q9qyf0 mus musculus
5	507	33.0	99	11	Q9JL74		Q9jl74 mus musculus
6	500.5	38.5	484	11	Q991A6		Q991a6 mus musculus
7	461	35.5	102	11	Q9JL79		Q9jl79 mus musculus
8	399	30.7	108	11	Q8VJF0		Q8vjf0 mus musculus
9	395	30.4	120	11	Q92O88		Q92o88 mus musculus
10	383.5	29.5	170	11	Q92S52		Q92S52 mus musculus
11	382.5	29.4	107	4	Q36S29		Q36sa9 homo sapien
12	377	29.0	108	4	Q3UL79		Q3ul79 homo sapien
13	377	29.0	119	4	Q9UL94		Q9ul94 homo sapien
14	376.5	29.0	124	4	Q9UL92		Q9ul92 homo sapien
15	376	28.9	108	4	Q3UL70		Q3ul70 homo sapien
16	376	28.9	108	4	Q9UL77		Q9ul77 homo sapien

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QY 61 ADDKGRFAFSLTSASTAYLQIINNKNEDTATYFCALYGNPKGFAYWQOGLTVTSAG 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 ADDKGRFAFSLTSASTAYLQIINNKNEDTATYFCA-RKDLRYFDYWGQGITVTVSSG 119
QY 121 GGGSGGRASGGGSDIQMTQSPKFLVSGDRVTITCKASQSVNDVAVYQQKPGPK- 179
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 GGGSGGGGGGGSDIELTQSPSLASLGGKVTITCKASQDINKYIATYCHKPGKPRS 179
QY 180 ---LLMYASNRVTGVPDRFTGSGVGTDTFTTISTVQAEADLAVYFCQDYGSPPTFGCGT 236
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
180 AHTLHIYI----QPGIPRFSGSGSGRDYSPSISNLPEDIATYICLH-YDNLHTFGCGT 234
QY 237 KLEIKR 242
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
235 KLEIKR 240

RESULT 2
Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRPS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_C
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGV.1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 218
SQ SEQUENCE 218 AA; 23013 MW; 527E4FA8F7982817 CRC64;

Query Match 58.2%; Score 755.5; DB 11; Length 218;
Best Local Similarity 68.1%; Pred. No. 7.7e-54;
Matches 145; Conservative 24; Mismatches 39; Indels 5; Gaps 2;

QY 1 EVKLVSPELKKPGETVKISCKASGYIFTNYGNMVKQAPGKGLKMWGINTVYTGPEPT 60
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
3 QVQLQQSGPELKKPGETVKISCKASGYFTTFTAGQWVQKMPGKGLKRWIGINTSHSGVPKY 62
QY 61 ADDKGRFAFSLTSASTAYLQIINNKNEDTATYFCALYGNPKGFAYWQOGLTVTSAG 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
63 ABEFKGRFAFSLTSASTAYLQIINNKNEDTATYFCMRW-DYDGGFAYWQGITVTVSSG 121
QY 121 GGGSGGRASGGGSDIQMTQSPKFLVSGDRVTITCKASQSVN---DVAVYQQKPGQ 176
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 GGGSGGGGGGGSDIVLTQSPASLAVSLGORATISCRASESDVNIIGISPMNWFQKPGQ 181
QY 177 SPKLIMYASNRVTGVPDRFTGSGVGTDTFTTISTVQAEADLAVYFCQDYGSPPTFGCGT 209
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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DB 182 PPKLLIYAASKQSGVPAGLLASGSGTDFSLNI 214

RESULT 3
Q77QM2 PRELIMINARY; PRT; 243 AA.
AC Q77QM2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SCFv 6H8 protein (Fragment).
GN SCFv 6H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_C
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RA Peter J.C., Eitekhari P., Billiald P., Wallukat G.;
RT "scfv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ574851; CAE00495.1; -.
FT NON_TER 1
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DCFAF76 CRC64;

Query Match 55.1%; Score 716; DB 11; Length 243;
Best Local Similarity 56.8%; Pred. No. 1.5e-50;
Matches 137; Conservative 43; Mismatches 57; Indels 4; Gaps 2;

QY 1 EVKLVSPELKKPGETVKISCKASGYIFTNYGNMVKQAPGKGLKMWGINTVYTGPEPT 60
DB 1 QVQLQQSGSELVRPGASVKLSCKASGYFTTYWMMHWVKQRHGQGLEWIGNYPGSGITNY 60
QY 61 ADDKGRFAFSLTSASTAYLQIINNKNEDTATYFCALYGNPKGFAYWQOGLTVTSAG 120
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 DEKFNKGLITVDTSSTAYVHLSLASEDSAVVYCARGG--RGLDVWGAGTTLTVSSG 117
QY 121 GGGSGGRASGGGSDIQMTQSPKFLVSGDRVTITCKASQSVNDVAVYQQKPGQSPKL 180
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
118 GGGSGGGGGGGGSDIQMTQSSFSVSLGDRVTITCKASEDIYNRLAWYQOKPGNAPRL 177
QY 181 LMVYASNRVTGVPDRFTGSGVGTDTFTTISTVQAEADLAVYFCQDYGSPPTFGGKLEI 240
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
178 LISGATSLVETGVPFRFSGSGSKDYTLSTLSQIEDVATYICQQ-YWSTRFTGGGKLEI 236
QY 241 K 241
DB 237 K 237

RESULT 4
Q9QVF0 PRELIMINARY; PRT; 298 AA.
AC Q9QVF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CN 8 scfv.
GN CN 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_C
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
RT recognizing a cell polarity by using a phage display subtraction
RT method.";
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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A.CA;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206027; AAF69325.1; -.
DR HSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 102 102
SQ SEQUENCE 102 AA; 11543 MW; E590C292093F6711 CRC64;

Query Match 35.5%; Score 461; DB 11; Length 102;
Best Local Similarity 85.6%; Pred. No. 3.1e-30;
Matches 89; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

QY 16 ETVKISKASGYFTNYGMNVKQAPGKGLKMGWINTYGTGEPTVADDFKGRFAFSLETS 75
Db 1 ETVKISKASGYFTFDYSHWVQAPGKGLKMGWINTETGEPTVADDFKGRFAFSLETS 60

QY 76 ASTAYLQINLNKEDTATYFCALYGNSPKGFAYWGQGLTVTVA 119
Db 61 ASTAYLQINLNKEDTATYFCVGRWAS--WFAWGQGLTVTVA 102

RESULT 8
QSVIJO
ID QSVIJO PRELIMINARY; PRT; 108 AA.
AC QSVIJO;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Anti-DNA light chain (Fragment).
GN VK19
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ-lpr/lpr;
RX MEDLINE=96409289; PubMed=8814271;
RA Wloch M.K., Alexander A.L., Phippen A.M., Pisetsky D.S., Gilkeson G.S.;
RT "Differences in V kappa gene utilization and VH CDR3 sequence among
RT anti-DNA from C3H-lpr mice and lupus mice with nephritis.";
RL Eur. J. Immunol. 26:2225-2233(1996).
DR EMBL; U59155; AAB02917.1; -.
DR PIR; A33933; A33933.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11859 MW; 68506D75613DBFBE CRC64;

Query Match 30.7%; Score 399; DB 11; Length 108;
Best Local Similarity 72.2%; Pred. No. 3.8e-25;
Matches 78; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

QY 135 DIQTTQSPKFLVSGDVTITTCASQSVNDVAWYQCKPGSKLAMYVASHRYTGVPD 194
Db 1 DIVTQSTQFMSTVGDRSVTRCKASQNVGTNVAWYQCKPGSKALIYASPYSGVPH 60

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QY 195 RFTGSGYGTDFTTTSTVQAEADLAYFCOODYGSPTFGGGTKLEIKR 242
Db 61 RFTGSGSGDTLTITISNVQSEDLAYFCQOYNSPYTFTGGGTKLEIKR 108

RESULT 9
Q920E8
ID Q920E8 PRELIMINARY; PRT; 120 AA.
AC Q920E8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF307936; AAL09420.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1 1
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;

Query Match 30.4%; Score 395; DB 11; Length 120;
Best Local Similarity 60.8%; Pred. No. 9.1e-25;
Matches 73; Conservative 21; Mismatches 24; Indels 2; Gaps 1;

QY 1 EVKLVSQPELKKPGETVKISKASGYFTNYGMNVKQAPGKGLKMGWINTYGTGEPT 60
Db 1 EVQLQSGPELEKPGASVKISKASGYFTNYGMNVKQSNKSLQEWICNIDPYVGTSY 60

QY 61 ADDFKGRFAFSLETSASTAYLQINLNKEDTATYFCAL--YGNSPKGFAYWGQGLTVTVA 118
Db 61 NQKFGKATLVYDKSSSTAYVQLKSLTSEDSAVYCAVYIYGNSPAFAWGQGLTVTVA 120

RESULT 10
Q925S2
ID Q925S2 PRELIMINARY; PRT; 170 AA.
AC Q925S2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE MRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium

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RT of the irradiated mice by treatment with the intestinal RNA of mice of
RL the same strain."
DR Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240167; AAX43732.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
SQ SEQUENCE 170 AA; 17578 MW; 5042823CC6C10F38 CRC64;

Query Match 29.5%; Score 383.5; DB 11; Length 170;
Best Local Similarity 50.7%; Pred. No. 1.2e-23;
Matches 73; Conservative 27; Mismatches 39; Indels 5; Gaps 2;

QY 1 EVKLVEGPELKKGETVKISKASGYIFTNYGNWVKQAPGKLGKWMGINTVTGPTY 60
DB 3 QVKLQSGPEVVRGVSVKISKSGSYFTDYSNHWLKNHQAQSLWIGIISYDGNWY 62
QY 61 ADPKFAPAFSLTSASTAYLQINNKNEDATYFCA--LYGNSPKGFAYWGQTLVTVS 118
DB 63 NQKFKGATMTVDKSSITAYMELARLTSDDSAIYCARGAYGYSFYFDYWGQTLVTVS 122
QY 119 AGGGSGGGRASGGGSDIQWTQSP 142
DB 123 SGGGGSGGGGGGGSE---SSSP 143

RESULT 11
Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DR 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DR 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375693; PubMed=9712075;
RA Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 29.4%; Score 382.5; DB 4; Length 107;
Best Local Similarity 68.5%; Pred. No. 8.3e-24;
Matches 74; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

QY 135 DIQWTQSPKFLVLSAGDRVTITCKASQSVNDVAWYQKQPKQLMYASNRYTGVPD 194
DB 1 DIQWTQSPSLASVGRVITTCRASQSSISYLNWYQKQKAPKLLIYAASLQSGVPS 60
QY 195 RFTGSGYGTDTFTTISTVQAEADLVYFCQDYGSPPTFGGKLEIKR 242
DB 61 RFSGSGSGTDTFTLTISLQSEDFATYCCQSY-STLTFGGGKVEIKR 107

RESULT 12
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79;
AC Q9UL79;
DR 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DR 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR FIR; S23638; S23638.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 29.0%; Score 377; DB 4; Length 108;
Best Local Similarity 64.8%; Pred. No. 2.3e-23;
Matches 70; Conservative 15; Mismatches 23; Indels 0; Gaps 0;

QY 135 DIQWTQSPKFLVLSAGDRVTITCKASQSVNDVAWYQKQPKQLMYASNRYTGVPD 194
DB 1 DIVMTQSPSLASVGRVITTCRASQSSISYLNWYQKQKAPKLLIYAASLQSGVPS 60
QY 195 RFTGSGYGTDTFTTISTVQAEADLVYFCQDYGSPPTFGGKLEIKR 242
DB 61 RFSGSGSGTDTFTLTISLQSEDFATYCCQSYSTLTFGGGKVEIKR 108

RESULT 13
Q9UL94 PRELIMINARY; PRT; 119 AA.
ID Q9UL94;
AC Q9UL94;
DR 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DR 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035020; AAD56256.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 74.5587 Seconds
(without alignments)
917.082 Million cell updates/sec

Title: US-09-661-992B-82
Perfect score: 1299
Sequence: 1 EVKLIVSGPELKPGETVKI.....QQDYGSPPTFGGKLEIKR 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04:*
- 1: Geneseqp1980s:*
 - 2: Geneseqp1980s:*
 - 3: Geneseqp2000s:*
 - 4: Geneseqp2001s:*
 - 5: Geneseqp2002s:*
 - 6: Geneseqp2003as:*
 - 7: Geneseqp2003bs:*
 - 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1299	100.0	242	4	AAB20433 Anti-FIX/
2	1013	78.0	461	2	AAR85508 Leader-sc
3	1008	77.6	530	2	AAR95053 scFv(FRP5
4	1008	77.6	615	2	AAR95056 GAL4-DT-s
5	1008	77.6	617	2	AAR95057 GAL4-DT-s
6	1008	77.6	651	2	AAR95057 scFv(FRP5
7	1008	77.6	699	2	AAR95136 scFv(FRP5
8	1008	77.6	711	2	AAR28980 scFv(FRP5)
9	1008	77.6	892	2	AAR28980 FV(FRP5)-
10	1008	77.6	892	2	AAR28980 scFv2(225
11	1008	77.6	892	2	AAR28980 scFv2(FRP
12	1008	77.6	892	2	AAR28980 scFv2(FRP
13	1008	77.6	892	2	AAR28980 scFv2(FRP
14	1008	77.6	892	2	AAR28980 scFv2(FRP
15	1005	77.4	637	2	AAR28982 (FRP5)-ET
16	1003	77.2	240	2	AAR85494 ErtB-2-sp
17	1003	77.2	240	2	AAR85494 Single ch
18	1000.5	77.0	250	2	AAR22278 Anti-c-er
19	1000.5	77.0	250	2	AAR22278 Anti-c-er
20	1000.5	77.0	250	2	AAR22400 Single ch
21	1000.5	77.0	250	2	AAR22400 Single ch
22	1000.5	77.0	250	2	AAR22400 Single ch
23	1000.5	77.0	250	2	AAR22400 Single ch
24	1000.5	77.0	250	2	AAR22400 Single ch
25	994	76.5	241	2	AAR26979 Fv heavy

26	965.5	74.3	667	2	AAR39573	Aar39573 Sequence
27	961.5	74.0	505	5	AAU72875	Aau72875 Human NKG
28	918	70.7	365	2	AAW35131	Aaw35131 R. pipien
29	918	70.7	366	2	AAW35132	Aaw35132 R. pipien
30	911.5	70.2	259	3	AA309779	Aab09779 Antiviral
31	894.5	68.9	284	2	AAV06130	Aay06130 Monoclonal
32	894.5	68.9	284	4	AAW50155	Aaw50155 Type II c
33	894.5	68.9	503	5	AAU72874	Aau72874 3B10xP5-2
34	893.5	68.8	554	2	AAR70827	Aar70827 Anti-cata
35	892	68.7	267	4	AAU04944	Aau04944 Humanised
36	876.5	67.5	534	2	AAR39571	Aar39571 Sequence
37	875.5	67.4	503	5	AAU72873	Aau72873 3B10xP5-2
38	873	67.2	409	4	AAU04945	Aau04945 Humanised
39	868.5	66.9	243	2	AAW86002	Aaw86002 Murine an
40	868.5	66.9	243	2	AAV42294	Aay42294 Anti-5T4
41	868.5	66.9	243	2	AAV42294	Aay42294 Anti-5T4
42	868.5	66.9	243	4	AAW83835	Aaw83835 Amino aci
43	868.5	66.9	592	4	AAW83838	Aaw83838 Amino aci
44	868.5	66.9	595	2	AAW86003	Aaw86003 Anti-5T4
45	866.5	66.7	267	2	AAW85688	Aaw85688 Humanised

ALIGNMENTS

RESULT 1
AAB20433
ID AAB20433 standard; protein; 242 AA.
XX AAB20433;
XX AC
XX XX
XX 21-JUN-2001 (first entry)
XX XX
XX Anti-FIX/FIXa antibody 193/AD3 scFv.

XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
XX Factor VIII cofactor; blood coagulation disorder; haemophilia A;
XX haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
XX Mus musculus.
XX Synthetic.
XX Chimeric.

XX Key Location/Qualifiers
XX FT Protein 1..119
XX FT Region 98..108
XX FT Peptide 120..134
XX FT Protein 135..242
XX FT Region 223..231
XX WO200119992-A2.
XX 22-MAR-2001.
XX 13-SEP-2000; 2000WO-EP008936.
XX 14-SEP-1999; 99AT-00001576.
XX (BAXT) BAXTER AG.
XX Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX WPI: 2001-290358/30.
XX N-PSDB; AAR30723.

XX New factor IX/factor IXa antibodies and their derivatives useful for
XX increasing amidolytic activity of factor IXa, and for treating blood
XX coagulation disorders such as hemophilia A and hemorrhagic diathesis.

Claim 8; Fig 14; 138pp; English.

The present sequence is that of a single chain Fv (scFv) derivative of antibody 193/AD3, comprising the heavy (VH) and light (VL) chain variable regions of 193/AD3 joined by an artificial, flexible linker peptide. The scFv was obtained by PCR amplification of cDNAs for 193/AD3 VH and VL regions and cloning in vector pDA2. 193/AD3 is an example of anti-human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention. Anti-FIX/FIXa and their derivatives, including scFv and CDR3 fragments, have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity. Administration leads to an increase in the procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis.

XX SQ Sequence 242 AA;

Query Match 100.0%; Score 1299; DB 4; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.3e-86;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKLVESGPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKMWGINTVTGSPTY 60
Db 1 EVKLVESGPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKMWGINTVTGSPTY 60

QY 61 ADDFKGRFAFSLSTSASTAYLQINLNKEDTATYFCALYGNSPKGFAYWGQGLTLVTSAG 120
Db 61 ADDFKGRFAFSLSTSASTAYLQINLNKEDTATYFCALYGNSPKGFAYWGQGLTLVTSAG 120

QY 121 GGGSGGRASGGGSDIQMTQSPKFLVNSAGDRVTITCKASQSVSNDAVAYQKQKPGPKL 180
Db 121 GGGSGGRASGGGSDIQMTQSPKFLVNSAGDRVTITCKASQSVSNDAVAYQKQKPGPKL 180

QY 181 LMYIASNRITGVDPDRFTGSGYGTDTFTISTVQAEADLAVYFCQDYGSPPTFGGQTKLEI 240
Db 181 LMYIASNRITGVDPDRFTGSGYGTDTFTISTVQAEADLAVYFCQDYGSPPTFGGQTKLEI 240

QY 241 KR 242
Db 241 KR 242

RESULT 2
AAR85508
ID AAR85508 standard; protein; 461 AA.
AC AAR85508;
XX
DT 16-MAR-1996 (first entry)
DE Leader-scFv(FRP5):lyt-2 hinge:zeta.

XX
XX Single chain antibody; scFv; antibody engineering; antitumour;
KW tumour antigen binding; T-cell receptor; cytotoxic T-lymphocyte;
KW monoclonal antibody; erbB-2; cancer; cell targeting;
KW adoptive immunotherapy.
OS Synthetic.

XX
XX Key Location/Qualifiers
FH Peptide 40..93
FT /label= IGH_chain_leader
FT Domain 94..819
FT /label= scFv(FRP5)
FT Peptide 261..322
FT /label= Lys-2_hinge
FT Domain 323..461
FT /label= Zeta_chain
XX

OS Saccharomyces cerevisiae.
OS Chimeric.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..8 /label= FLAG_epitope
FT Peptide 9..17 /label= Spacer
FT Domain 18..257 /label= ScFv(FRP5)
FT Peptide 258..260 /label= Spacer
FT Domain 261..375 /label= ETA
FT Peptide /note= "amino acids 252-366 of exotoxin-A"
FT Peptide 376 /label= Spacer
FT Domain 377..522 /label= GAL4
FT Peptide /note= "amino acids 2-147 of yeast GAL4"
FT Peptide 523..530 /label= Spacer
FT Peptide /note= "endoplasmic reticulum retention peptide"
XX WO9613599-A1.
XX 09-MAY-1996.
XX 31-OCT-1995; 95WO-EP004270.
XX 01-NOV-1994; 94EP-00810627.
XX (WELS/) WELS W.
XX Wels W, Fominaya J;
XX WPI; 1996-239505/24.
XX N-PSDB; AAT29409.
XX Nucleic acid transfer system for gene therapy, e.g. against cancer - includes toxin translocation domain to target nucleic acid to specific cell.
XX Claim 7; Page 59-61; 106pp; English.
XX A multidomain protein (AAR95053) has a FLAG epitope, a single chain antibody, scFv, of monoclonal antibody FRP5 (raised against human tumour cell HER2 antigen) that acts as a ligand domain, a non-cytotoxic portion of Pseudomonas aeruginosa exotoxin A acting as a translocation domain and the DNA binding domain of yeast GAL4. It is the product of a fusion gene (AAT29409) and can be expressed in E. coli (resulting in removal of ompA signal peptide). It is used with an effector nucleic acid that comprises e.g. a gene to be delivered to a cell and a cognate structure for the GAL4 DNA binding domain. This provides a novel means of nucleic acid transfer, suitable for gene therapy. (Updated on 16-OCT-2003 to standardise OS field)
XX Sequence 530 AA;
Query Match 77.6%; Score 1008; DB 2; Length 530;
Best Local Similarity 79.2%; Pred. No. 3.9e-65;
Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
QY 1 EVKLVSQPELKKFGETVKISCKASGYIFTNYGNWYKQAPGKGLKMGWINTYTGEPY 60
DB 18 QVQLQQSGPELKKFGETVKISCKASGYFTNYGNWYKQAPGQGLKRWGINTSTGESTF 77
QY 61 ADDEKGFASFLETSASTAYLQINLNKNEDTATVFCF- ---LYGNSPKGFAYWGQGLT 116
DB 78 ADDEKGFDFLETSANTAYLQINLNKSEMDATVFCARWEVYHGYP- ---YWGQGLT 133
QY 117 VSAGGGSGGRASGGGSDIQMTOSPKFLVLSAGDRVTITCKASQSVSNDVAVYQKPGQ 176

DB 134 VSSGGGGGGGGGGSDIQLTQSHKFLSTVSGRVSITCKASQDVYNAVAYQKPGQ 193
QY 177 SPKLLMYASNRYTGVPDRFTGSGYGTDTFTTISTVQABDLAVYFCQDYGSPPFTFGGT 236
DB 194 SPKLLIYASRRYTGVPDRFTGSGGPDFTFTISSVQABDLAVYFCQCHFTFTFGSGT 253
QY 237 KLEIK 241
DB 254 KLEIK 258
RESULT 4
AAR95056
ID AAR95056 standard; protein; 615 AA.
XX AAR95056;
AC AAR95056;
XX 16-OCT-2003 (revised)
DT 19-AUG-1996 (first entry)
XX GAL4-DT-scFv(FRP5) multidomain protein.
XX Nucleic acid transfer system; gene transfer; gene therapy; cell targeting; multidomain protein; vector; cancer; GAL4; diphtheria toxin; single chain antibody; scFv; FRP5.
XX Saccharomyces; cerevisiae.
OS Clostridium; diphtheriae.
OS Mus sp.
OS Chimeric.
OS Synthetic.
XX Key Location/Qualifiers
FT Peptide 1..8 /label= FLAG_epitope
FT Peptide 9..15 /label= Spacer
FT Domain 16..161 /label= GAL4
FT Peptide /note= "amino acids 2-147 of yeast GAL4"
FT Peptide 162..165 /label= Spacer
FT Domain 166..354 /label= DT
FT Peptide /note= "amino acids 196-384 of diphtheria toxin"
FT Peptide 355..361 /label= Spacer
FT Domain 362..601 /label= scFv(FRP5)
FT Peptide 602..615 /label= Spacer
XX WO9613599-A1.
XX 09-MAY-1996.
XX 31-OCT-1995; 95WO-EP004270.
XX 01-NOV-1994; 94EP-00810627.
XX (WELS/) WELS W.
XX Wels W, Fominaya J;
XX WPI; 1996-239505/24.
XX N-PSDB; AAT29412.
XX Nucleic acid transfer system for gene therapy, e.g. against cancer - includes toxin translocation domain to target nucleic acid to specific cell.
XX Claim 7; Page 81-83; 106pp; English.

XX DE scFv(FRP5)-ETA fusion protein.
XX KW Single chain antibody; scFv; monoclonal antibody; MAb; EGF; erbB-2;
KW epidermal growth factor; receptor; plasmid pSW202-5; cancer; therapy;
XX KW antitumour; exotoxin A; ETA.
XX OS Mus; sp.
OS Pseudomonas; aeruginosa.
OS Synthetic.
OS Chimeric.
XX FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Sig_peptide
FT /note= "ompA signal peptide"
FT Peptide 22..38
FT /label= Spacer
FT Protein 39..278
FT /label= scFv(FRP5)
FT Peptide 279..289
FT /label= Spacer
FT Protein 290..651
FT /label= ETA
FT /note= "exotoxin A amino acids 252-613"
XX EP739984-A1.
XX 30-OCT-1996.
XX 26-APR-1995; 95EP-00106275.
XX 26-APR-1995; 95EP-00106275.
XX (SANT-) SAN TUMORFORSCHUNGS GMBH.
XX Wels W, Schmidt M, Groner B;
XX WPI; 1996-478748/48.
XX N-PSDB; AAT42036.
XX Bivalent fusion proteins that bind epidermal growth factor receptor or
PT analogues - and comprise at least two different cell surface binding
PT domain(s), useful for tumour therapy.
XX Example 7; Page 21-22; 52pp; English.
XX scFv(FRP5)-ETA (AAW05136) comprises the single-chain binding region (see
CC also AAW05134) of murine monoclonal antibody rap05, which is specific for
CC human epidermal growth factor receptor erbB-2, joined to exotoxin A
CC (ETA). It is encoded by plasmid pSW202-5 (see also AAT42036) obt'd. by
CC ligating an scFv(FRP5) gene (AAT42034) into plasmid pSW200 contg. the
CC Pseudomonas aeruginosa PAK ETA gene. The construct can be used to produce
CC novel bivalent fusion proteins (see also AAW05135-44) in bacterial host
CC cells, for use as antitumour agents
XX SQ Sequence 651 AA;
Query Match 77.6%; Score 1008; DB 2; Length 651;
Best Local Similarity 79.2%; Pred. No. 4.8e-65;
Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
QY 1 EVKLVESEPELKKPGETVKISKASGYIFTNYGNWVKQAPGKGLKMWGINTVYGEPTY 60
DB 39 QVQLQQSGPELKKPGETVKISKASGYFTFNYGNWVKQAPGKGLKMWGINTVYGEPT 98
QY 61 ADPFKGRFAFSLTASATAYLQINLNKLNEDTATYFCA----LYGNSPKGFAYWQGGTLVT 116
DB 99 ADPFKGRFDFSLTASATAYLQINLNKLNEDMATYFCARWEVYHGYVP----YWGQGTVT 154
QY 117 VSAGGGSGGRASGGGSDIQWTPKELLVSAGDRVITTCCKASQSYNDVAVWYQKPGQ 176
DB 155 VSSGGGGSGGGGGGGSDIQLTQSHKFLSTVSGDRVSIITCKASQDYNAVAVYQKPGQ 214

QY 177 SPKLLMYASNEYTGVPDRFTGSGYGTDFTTISTVQAEADLAVYFCQDYGSPPTFGSGT 236
DB 215 SPKLLIYSSSRITGVPSRFTGSGGPDFTFTISSVQAEADLAVYFCQHFRTFTFGSGT 274
QY 237 KLEIK 241
DB 275 KLEIK 279
RESULT 7
AAW05138
ID AAW05138 standard; protein; 699 AA.
XX AC AAW05138;
XX DT 29-JAN-1997 (first entry)
XX DE scFv(FRP5)/TGF alpha-ETA.
XX KW Single chain antibody; scFv; monoclonal antibody; MAb; EGF; erbB-2;
KW epidermal growth factor; receptor; plasmid pMS238-5-TGF; cancer;
KW exotoxin A; ETA; transforming growth factor alpha; TGF; antitumour.
XX OS Homo; sapiens.
OS Mus; sp.
OS Pseudomonas; aeruginosa.
OS Synthetic.
OS Chimeric.
XX FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Sig_peptide
FT /note= "ompA signal peptide"
FT Peptide 22..38
FT /label= Spacer
FT Region 39..278
FT /label= scFv(FRP5)
FT Peptide 279..289
FT /label= Spacer
FT Region 290..404
FT /label= ETA
FT /note= "exotoxin A amino acids 252-366"
FT Peptide 405..410
FT /label= Spacer
FT Region 411..460
FT /label= TGF-alpha
FT Peptide 461..465
FT /label= Spacer
FT Region 466..699
FT /label= ETA
FT /note= "endotoxin-A amino acids 380-613"
XX EP739984-A1.
XX 30-OCT-1996.
XX 26-APR-1995; 95EP-00106275.
XX 26-APR-1995; 95EP-00106275.
XX (SANT-) SAN TUMORFORSCHUNGS GMBH.
XX Wels W, Schmidt M, Groner B;
XX WPI; 1996-478748/48.
XX N-PSDB; AAT42038.
XX Bivalent fusion proteins that bind epidermal growth factor receptor or
PT analogues - and comprise at least two different cell surface binding
PT domain(s), useful for tumour therapy.
XX Example 10; Page 25-27; 52pp; English.

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XX scFv(FRP5)/TGF alpha-ETA (AAW05138) comprises the single-chain binding
CC region of murine monoclonal antibody FRP5 (specific for human epidermal
CC growth factor receptor erbB-2, see also AAW05134) joined to portions of
CC exotoxin A from Pseudomonas aeruginosa and to human transforming growth
CC factor (TGF) alpha (see also AAW05137). It is encoded by plasmid pMS238-5
CC -TGF (AAT42038). This plasmid can be utilised in the prodn. of the
CC bispecific fusion protein in bacterial (esp. E. coli) host cells. Such
CC fusion proteins (see also AAW05139-44) are useful as antitumour agents
XX
XX Sequence 699 AA;
XX
XX Query Match 77.6%; Score 1008; DB 2; Length 699;
XX Best Local Similarity 79.2%; Pred. No. 5.1e-65;
XX Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
XX
QY 1 EVKLVSPELKKPGETVKISKASGYFTNYGMWVKQAPGKGLKMWGINTYTGEPTY 60
DB 39 QVQLQQSGPELKKPGETVKISKASGYFTNYGMWVKQAPGQGLKMWGINTSTGE 98
QY 61 ADDFKGRFAFSLSTSASTAYLIQINLNKEDTATVFCA----LYGNSPKGFAYWGQGLVT 116
DB 99 ADDFKGRFDFSLSTSANTAYLIQINLNKSEDMATVFCARWEVYHGVP----YWGQGT 154
QY 117 VSAGGGSGGRASGGGSDIQMTQSPKLLVSAGDRVITTCASQSVSNVAVYQKPGQ 176
DB 155 VSSGGGGSGGGSGGGSDIQLTQSHKFLSTSVGDRVSITTCASQSDVYNVAVYQKPGQ 214
QY 177 SPKLIMYASNRVYTCVPRDFTGSGVGTDTFTTISTVQAEADLVVFCOODYGSPTFGGT 236
DB 215 SPKLLIYASRRYTCVPSRFTGSGSGGPDFTFTISSVQAEADLVVFCQHPRTPTFGSGT 274
QY 237 KLEIK 241
DB 275 KLEIK 279
XX
XX RESULT 8
XX ID AAR26980 standard; protein; 711 AA.
XX AC AAR26980;
XX
XX 25-MAR-2003 (revised)
XX 11-FEB-1993 (first entry)
XX
XX Fv(FRP5)-phoA recombinant antibody.
XX Monoclonal antibody; light chain; heavy chain; tumour; phoA;
XX variable region; alkaline phosphatase; c-erbB-2; ss.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX Domain 23..141
XX /label= ompA_signal_peptide
XX /label= FRP5_heavy_chain_variable_domain
XX Peptide 142..156
XX /label= Linker
XX Domain 157..264
XX /label= FRP5_light_chain_variable_domain
XX Protein 265..711
XX /label= phoA
XX
XX EP502812-A1.
XX
XX 09-SEP-1992.
XX
XX 27-JAN-1992; 92EP-00810056.
XX
XX 05-FEB-1991; 91EP-00810079.
XX

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PA (CIBA ) CIBA GEIGY AG.
XX
XX Wells WS, Hynes NE, Harwerth I, Groner B, Hardman N, Zwickl M;
XX
XX WPI; 1992-302096/37.
XX N-PSDB; AAQ28257.
XX
XX Recombinant antibodies directed to growth factor receptor C-ERBB-2 - for
XX diagnosing and treating tumours expressing C-ERBB-2 e.g. breast or
XX ovarian tumours.
XX
XX Disclosure; Page 34-40; 67pp; English.
XX
XX The sequence given is the single chain recombinant antibody designated
XX Fv(FRP5)-phoA. The alkaline phosphatase gene (phoA) was used as a marker
XX gene so that E. coli transformed with the fusion gene could be
XX identified. The fusion gene was expressed in E. coli and the antibody was
XX extracted. This recombinant antibody can be used for the qualitative and
XX quantitative determination of c-erbB-2. This can be used for monitoring
XX or in-vivo localisation of tumours overexpressing c-erbB-2. (Updated on
XX 25-MAR-2003 to correct PN field.)
XX
XX Sequence 711 AA;
XX
XX Query Match 77.6%; Score 1008; DB 2; Length 711;
XX Best Local Similarity 79.2%; Pred. No. 5.2e-65;
XX Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
XX
QY 1 EVKLVSPELKKPGETVKISKASGYFTNYGMWVKQAPGKGLKMWGINTYTGEPTY 60
DB 23 QVQLQQSGPELKKPGETVKISKASGYFTNYGMWVKQAPGQGLKMWGINTSTGE 82
QY 61 ADDFKGRFAFSLSTSASTAYLIQINLNKEDTATVFCA----LYGNSPKGFAYWGQGLVT 116
DB 83 ADDFKGRFDFSLSTSANTAYLIQINLNKSEDMATVFCARWEVYHGVP----YWGQGT 138
QY 117 VSAGGGSGGRASGGGSDIQMTQSPKLLVSAGDRVITTCASQSVSNVAVYQKPGQ 176
DB 139 VSSGGGGSGGGSGGGSDIQLTQSHKFLSTSVGDRVSITTCASQSDVYNVAVYQKPGQ 198
QY 177 SPKLIMYASNRVYTCVPRDFTGSGVGTDTFTTISTVQAEADLVVFCOODYGSPTFGGT 236
DB 199 SPKLLIYASRRYTCVPSRFTGSGSGGPDFTFTISSVQAEADLVVFCQHPRTPTFGSGT 258
QY 237 KLEIK 241
DB 259 KLEIK 263
XX
XX RESULT 9
XX ID AAW05140 standard; protein; 892 AA.
XX AC AAW05140;
XX
XX 29-JAN-1997 (first entry)
XX
XX scFv2(225/FRP5)-ETA.
XX
XX Single chain antibody; scFv; monoclonal antibody; MAb; EGF; erbB-2;
XX epidermal growth factor; receptor; plasmid pMS238-225-5; cancer;
XX exotoxin A; ETA; antitumour.
XX
XX Mus; sp.
XX Pseudomonas; aeruginosa.
XX Synthetic.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX /label= sig_peptide
XX /note= "ompA signal peptide"
XX Peptide 22..38

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FT      Region      /label= Spacer
FT      Peptide     39..278
FT      Peptide     /label= scFv(225)
FT      Region      279..289
FT      Region      /label= Spacer
FT      Region      290..404
FT      Region      /label= ETA
FT      Peptide     /note= "exotoxin A amino acids 252-366"
FT      Region      405..407
FT      Region      /label= Spacer
FT      Peptide     408..647
FT      Region      /label= scFv(FRP5)
FT      Peptide     648..658
FT      Region      /label= Spacer
FT      Region      659..892
FT      Region      /label= ETA
FT      Region      /note= "endotoxin-A amino acids 380-613"
PN      EP739984-A1.
XX
XX      30-OCT-1996.
XX
XX      26-APR-1995; 95EP-00106275.
XX
XX      26-APR-1995; 95EP-00106275.
XX
XX      (SANT-) SAN TUMORFORSCHUNGS GMBH.
XX
XX      Wels W, Schmidt M, Groner B;
XX      WPI; 1996-478748/48.
XX      N-PSDB; AAT42040.
XX
XX      Bivalent fusion proteins that bind epidermal growth factor receptor or
XX      analogues - and comprise at least two different cell surface binding
XX      domain(s), useful for tumour therapy.
XX
XX      Example 11; Page 31-33; 52pp; English.
XX
XX      scFv2(225/FRP5)-ETA (AAW05140) comprises the single-chain binding region
XX      of murine monoclonal antibody 225 (specific for human epidermal growth
XX      factor receptor, see also AAW05133) joined to portions of exotoxin A from
XX      Pseudomonas aeruginosa and to the single-chain binding region of murine
XX      monoclonal antibody FRP5 (specific for human epidermal growth factor
XX      receptor erbB-2, see also AAW05134). It is encoded by plasmid pMS238-225-
XX      5 (AAT42040). This plasmid can be utilised in the prodn. of the bivalent
XX      fusion protein in bacterial (esp. E. coli) host cells. Such fusion
XX      proteins (see also AAW05138-44) are useful as antitumour agents
XX
XX      Sequence 892 AA;
XX
XX      Query Match      77.6%; Score 1008; DB 2; Length 892;
XX      Best Local Similarity 79.2%; Pred. No. 6.6e-65;
XX      Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
XX
QY      1 EVKLVSQPELKKGGTIVKISCKASGYIFTYGNWVKQAPGKGLKMGWINTVGTPT 60
DB      408 QVQLQQSGPELKKGGTIVKISCKASGYIFTYGNWVKQAPGKGLKMGWINTVGTPT 467
QY      61 ADDFKGRFAPLSASTAYLIQINLNKEDTATYFCA----LYGNSPKGFAYWQGLVT 116
DB      468 ADDFKGRFDFLSASTAYLIQINLNKEDTATYFCAREWYHGVV-----YWGQGTIVT 523
QY      117 VSAGGGSGGRASGGGSDIQMTQSPKFLVLSAGDRVITCKASQSVSNVDVAVYQKPGQ 176
DB      524 VSSGGGGSGGGSGGGSDIQLTQSHKFLSTSVGDRVSIITCKASQDVYNAVAVYQKPGQ 583
QY      177 SPKLIMYASNRVYGVPRFTGSGVGTDTFTTISTVQAEIDLAVFCQDVGSPPTFGGT 236
DB      584 SPKLIIYASNRVYGVPRFTGSGGSDPTFTTISVQAEIDLAVFCQHFRTPTFGGT 643
QY      237 KLEIK 241

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DB      644 KLEIK 648
XX
XX      RESULT 10
XX      AAW05143
XX      ID      AAW05143 standard; protein; 892 AA.
XX
XX      AC      AAW05143;
XX
XX      DT      29-JAN-1997 (first entry)
XX
XX      DE      scFv2(FRP5/FRP5)-ETA (version 2).
XX
XX      KW      Single chain antibody; scFv; monoclonal antibody; Mab; EGF; erbB-2;
XX      epidermal growth factor; receptor; plasmid pMS238-5-5; cancer;
XX      exotoxin A; ETA; antitumour.
XX
XX      OS      Mus; sp.
XX      OS      Pseudomonas; aeruginosa.
XX      OS      Synthetic.
XX      OS      Chimeric.
XX
XX      Key      Location/Qualifiers
XX      Peptide 1..21
XX      /label= Sig_peptide
XX      /note= "ompA signal peptide"
XX      Peptide 22..38
XX      /label= Spacer
XX      Region 39..278
XX      /label= scFv(FRP5)
XX      Peptide 279..289
XX      /label= Spacer
XX      Region 290..404
XX      /label= ETA
XX      /note= "exotoxin A amino acids 252-366"
XX      Peptide 405..407
XX      /label= Spacer
XX      Region 408..647
XX      /label= scFv(FRP5)
XX      Peptide 648..658
XX      /label= Spacer
XX      Region 659..892
XX      /label= ETA
XX      /note= "exotoxin A amino acids 380-613"
XX
XX      EP739984-A1.
XX
XX      30-OCT-1996.
XX
XX      26-APR-1995; 95EP-00106275.
XX
XX      26-APR-1995; 95EP-00106275.
XX
XX      (SANT-) SAN TUMORFORSCHUNGS GMBH.
XX
XX      Wels W, Schmidt M, Groner B;
XX      WPI; 1996-478748/48.
XX      N-PSDB; AAT42043.
XX
XX      Bivalent fusion proteins that bind epidermal growth factor receptor or
XX      analogues - and comprise at least two different cell surface binding
XX      domain(s), useful for tumour therapy.
XX
XX      Example 12; Page 40-42; 52pp; English.
XX
XX      scFv2(FRP5/FRP5)-ETA version 2 (AAW05143) includes 2 copies of the single
XX      -chain binding region of murine monoclonal antibody FRP5 (specific for
XX      human epidermal growth factor receptor erbB-2, see also AAW05134) joined
XX      to portions of exotoxin A from Pseudomonas aeruginosa. It is encoded by
XX      plasmid pMS238-5-5 (AAT42043). This plasmid can be utilised in the prodn.
XX      of the bivalent fusion protein in bacterial (esp. E. coli) host cells.
XX      Such fusion proteins (see also AAW05138-44) are useful as antitumour

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OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Sig peptide
FT /note= "ompA signal peptide"
FT Peptide 22..44
FT /label= Spacer
FT Region 45..139
FT /label= ETA
FT Peptide 160..162
FT /label= Spacer
FT Region 163..402
FT /label= scFv(FRP5)
FT Peptide 403..413
FT /label= Spacer
FT Region 414..644
FT /label= ETA
FT Peptide 645..646
FT /label= Spacer
FT Region 647..886
FT /label= scFv(FRP5)
FT Peptide 887..895
FT /label= Spacer
XX EP739984-A1.
PN
XX
XX 30-OCT-1996.
XX
XX 26-APR-1995; 95EP-00106275.
XX
XX 26-APR-1995; 95EP-00106275.
XX (SANT-) SAN TUMORFORSCHUNGS GMBH.
XX
XX Wels W, Schmidt M, Groner B;
XX WPI; 1996-478748/48.
XX N-PSDB; AAT42042.
XX
XX Bivalent fusion proteins that bind epidermal growth factor receptor or
XX analogues - and comprise at least two different cell surface binding
XX domain(s), useful for tumour therapy.
XX
XX Example 12; Page 37-39; 52pp; English.
XX
XX scFv2(FRP5/FRP5)-ETA version 1 (AAW05144) includes 2 copies of the single
XX -chain binding region of murine monoclonal antibody FRP5 (specific for
XX human epidermal growth factor receptor erbB-2, see also AAW05134) joined
XX to portions of exotoxin A from Pseudomonas aeruginosa. It is encoded by
XX plasmid pMS242-5-5 (AAT42042). This plasmid can be utilised in the prodn.
XX of the bivalent fusion protein in bacterial (esp. E. coli) host cells.
XX Such fusion proteins (see also AAW05138-44) are useful as antitumour
XX agents
XX
XX Sequence 895 AA;
XX
XX Query Match 77.6%; Score 1008; DB 2; Length 895;
XX Best Local Similarity 79.2%; Pres. No. 6.6e-65;
XX Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
XX
Qy 1 EVKLVEGPELKKPGETVKISKASGYIFITNYGNMVKQAPGKGLKWMGINTYTGEPTY 60
Db 163 QVQLQSGPELKKPGETVKISKASGYIFITNYGNMVKQAPGQGLKWMGINTSTGE 222
Qy 61 ADDEKGFASLETSASTAYLIQNNLNKEDTATYFCA----LYGNSPKGFAYWGQGLTVT 116
Db 223 ADDEKGFASLETSASTAYLIQNNLNKEDTATYFCA---YWGQGLTVT 278
Qy 117 VSAGGGSGGRASGGGGSDIQMOSQPKFLVLSAGDRVITITCKASQSVNSDVAVYQKPGQ 176

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Db 279 VSSGGGGSGGGGGGGSDIQLTQSHKFLSTSVGRVSIITCKASQDVNNAVYQKPGQ 338
Qy 177 SPKLLMYASNRYTGVPRFTGSGYGTDTFTTISTVQAEADLAVYFCQDYGSPTFGGQT 236
Db 339 SPKLLIYSASSRYTGVPSKFTGSGGSDPFTFTISSVQAEADLAVYFCQGHFRPTFGSOT 398
Qy 237 KLEIK 241
Db 399 KLEIK 403

RESULT 13
AAW05144
ID AAW05144 standard; protein; 899 AA.
XX
AC AAW05144;
XX
DT 29-JAN-1997 (first entry)
XX
DE scFv2(FRP5/FRP5)-ETA (version 3).
XX
XX Single chain antibody; scFv; monoclonal antibody; MAb; erbB-2;
XX epidermal growth factor; receptor; plasmid pMS246-5-5; cancer;
XX exotoxin A; ETA; antitumour.
XX
OS Mus; sp.
OS Pseudomonas; aeruginosa.
OS Synthetic.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /label= Sig peptide
FT /note= "ompA signal peptide"
FT Peptide 22..38
FT /label= Spacer
FT Region 39..278
FT /label= scFv(FRP5)
FT Peptide 279..289
FT /label= Spacer
FT Region 290..648
FT /label= ETA
FT Peptide 649..650
FT /label= Spacer
FT Region 651..890
FT /label= scFv(FRP5)
FT Peptide 891..899
FT /label= Spacer
FT
FT EP739984-A1.
XX
XX 30-OCT-1996.
XX
XX 26-APR-1995; 95EP-00106275.
XX
XX 26-APR-1995; 95EP-00106275.
XX (SANT-) SAN TUMORFORSCHUNGS GMBH.
XX
XX Wels W, Schmidt M, Groner B;
XX WPI; 1996-478748/48.
XX N-PSDB; AAT42044.
XX
XX Bivalent fusion proteins that bind epidermal growth factor receptor or
XX analogues - and comprise at least two different cell surface binding
XX domain(s), useful for tumour therapy.
XX
XX Example 12; Page 43-45; 52pp; English.
XX
XX scFv2(FRP5/FRP5)-ETA version 3 (AAW05144) includes 2 copies of the single
XX -chain binding region of murine monoclonal antibody FRP5 (specific for

```

CC human epidermal growth factor receptor erbB-2, see also AAW05134) joined
 CC to portions of exotoxin A from Pseudomonas aeruginosa. It is encoded by
 CC plasmid pMS246-5-5 (AA42044). This plasmid can be utilised in the prodn.
 CC of the bivalent fusion protein in bacterial (esp. E. coli) host cells.
 CC Such fusion proteins (see also AAW05138-43) are useful as antitumour
 CC agents
 XX
 XX Sequence 899 AA;

Query Match 77.6%; Score 1008; DB 2; Length 899;
 Best Local Similarity 79.2%; Pred. No. 6.7e-65;
 Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
 QY 1 EVKLVSPELKKPGETVKISKASGYIFTNYGNWVKQAPGKGLKMGWINITYGPTY 60
 DB 39 QVQLQQSGPELKKPGETVKISKASGYIFTNYGNWVKQAPGQGLKMGWINITSGSTF 98
 QY 61 ADDFKGRFAFSLSTSASTAYLIQINLNKEDTATYFCA---LYGNSPKGFAYWGQTLVT 116
 DB 99 ADDFKGRFDFSLSTSANTAYLIQINLNKSEDMATYFCARWEVYHGVP---YWGQTTVT 154
 QY 117 VSAGGGGGGRASGGGGSDIQMTQSPKLLVSAGDRVITTCASQSVSNDAVYQQKPGQ 176
 DB 155 VSSGGGGGGGGGGGGSDIQLTQSHKFLSTSVGDRVSIITCKASQDVYNAVAYQQKPGQ 214
 QY 177 SPKLLMYASNRVYGVPRFTGSGVGTDFTTISTVQAEADLVAVFCQDYGSPPTFGGT 236
 DB 215 SPKLLIYASNRVYGVPRFTGSGVGTDFTTISTVQAEADLVAVFCQDHFPTFTFGSGT 274
 QY 237 KLEIK 241
 DB 275 KLEIK 279

RESULT 14
 AAW05141
 ID AAW05141 standard; protein; 1020 AA.
 XX
 AC AAW05141;
 XX
 DT 29-JAN-1997 (first entry)
 XX
 DE scFv2 (FRP5/225)-ETA (version 2).
 XX
 KW Single chain antibody; scFv; monoclonal antibody; MAB; EGF; erbB-2;
 KW epidermal growth factor; receptor; plasmid pMS240-5-225; cancer;
 KW exotoxin A; ETA; antitumour.
 XX
 OS Mus; sp.
 OS Pseudomonas; aeruginosa.
 OS Synthetic.
 OS Chimeric.

Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Sig_peptide
 FT /note= "ompA signal peptide"
 FT 22..38
 FT /label= Spacer
 FT 39..278
 FT /label= scFv(FRP5)
 FT 279..289
 FT /label= Spacer
 FT 290..404
 FT /label= ETA
 FT /note= "exotoxin A amino acids 252-366"
 FT 405..407
 FT /label= Spacer
 FT 408..647
 FT /label= scFv(225)
 FT 648..658
 FT /label= Spacer
 FT 659..1020
 FT Region

/label= ETA
 /note= "endotoxin-A amino acids 252-613"
 FT
 XX
 PN EP739984-A1.
 XX
 PD 30-OCT-1996.
 XX
 PF 26-APR-1995; 95EP-00106275.
 XX
 PR 26-APR-1995; 95EP-00106275.
 XX
 PA (SANT-) SAN TUMORFORSCHUNGS GMBH.
 XX
 PI Wels W, Schmidt M, Groner B;
 XX
 DR WPI; 1996-478748/48.
 DR N-PSDB; AAT42041.

Bivalent fusion proteins that bind epidermal growth factor receptor or
 PT analogues - and comprise at least two different cell surface binding
 PT domain(s), useful for tumour therapy.
 XX
 XX Example 11; Page 34-36; 52pp; English.
 XX scFv2 (FRP5/225)-ETA version 2 (AAW05141) comprises the single-chain
 CC binding region of murine monoclonal antibody FRP5 (specific for human
 CC epidermal growth factor receptor erbB-2, see also AAW05134) joined to
 CC portions of exotoxin A from Pseudomonas aeruginosa and to the single-
 CC chain binding region of murine monoclonal antibody 225 (specific for
 CC human epidermal growth factor receptor, see also AAW05133). It is encoded
 CC by plasmid pMS240-5-225 (AAT42041). This plasmid can be utilised in the
 CC prodn. of the bivalent fusion protein in bacterial (esp. E. coli) host
 CC cells. Such fusion proteins (see also AAW05138-44) are useful as
 CC antitumour agents
 XX
 XX Sequence 1020 AA;

Query Match 77.6%; Score 1008; DB 2; Length 1020;
 Best Local Similarity 79.2%; Pred. No. 7.6e-65;
 Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
 QY 1 EVKLVSPELKKPGETVKISKASGYIFTNYGNWVKQAPGKGLKMGWINITYGPTY 60
 DB 39 QVQLQQSGPELKKPGETVKISKASGYIFTNYGNWVKQAPGQGLKMGWINITSGSTF 98
 QY 61 ADDFKGRFAFSLSTSASTAYLIQINLNKEDTATYFCA---LYGNSPKGFAYWGQTLVT 116
 DB 99 ADDFKGRFDFSLSTSANTAYLIQINLNKSEDMATYFCARWEVYHGVP---YWGQTTVT 154
 QY 117 VSAGGGGGGRASGGGGSDIQMTQSPKLLVSAGDRVITTCASQSVSNDAVYQQKPGQ 176
 DB 155 VSSGGGGGGGGGGGGSDIQLTQSHKFLSTSVGDRVSIITCKASQDVYNAVAYQQKPGQ 214
 QY 177 SPKLLMYASNRVYGVPRFTGSGVGTDFTTISTVQAEADLVAVFCQDYGSPPTFGGT 236
 DB 215 SPKLLIYASNRVYGVPRFTGSGVGTDFTTISTVQAEADLVAVFCQDHFPTFTFGSGT 274
 QY 237 KLEIK 241
 DB 275 KLEIK 279

RESULT 15
 AAR26982
 ID AAR26982 standard; protein; 637 AA.
 XX
 AC AAR26982;
 XX
 DT 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 11-FEB-1993 (first entry)
 XX
 DE (FRP5)-ETA fusion protein.

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XX KW Monoclonal antibody; light chain; heavy chain; tumour; c-erbB-2;
XX KW variable region; ETA.
XX OS Pseudomonas aeruginosa; PAX.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT Peptide /label= ompA_signal_peptide
XX FT Peptide 22..29
XX FT Peptide /label= FLAG_peptide_and_enterokinase_cleavage_site
XX FT Domain 33..151
XX FT Peptide /label= FRP5_heavy_chain_variable_domain
XX FT Peptide 152..166
XX FT Peptide /label= Linker
XX FT Domain 167..274
XX FT Peptide /label= FRP5_light_chain_variable_domain
XX FT Protein 276..397
XX FT /label= ETA_252-613
XX EP502812-A1;
XX FN
XX PD
XX PF
XX PR
XX PA (CIBA ) CIBA GEIGY AG.
XX PI Wels WS, Hynes NE, Harwerth I, Groner B, Hardman N, Zwickl M;
XX DR WPI; 1992-302096/37.
XX DR N-PSDB; AAQ28262.
XX PT Recombinant antibodies directed to growth factor receptor C-ERBB-2 - for
XX PT diagnosing and treating tumours expressing C-ERBB-2 e.g. breast or
XX PT ovarian tumours.
XX PS Disclosure; Page 47-52; 67pp; English.
XX CC The sequences given in AAR26992-3 contain part of the exotoxin A (ETA)
XX CC sequence corresponding to positions 252-613 of the full exotoxin A
XX CC sequence. These sequences are encoded by Fv(FRP5)-ETA fusion genes. The
XX CC ETA sequence was used as a marker gene so that E. coli transformed with
XX CC the fusion gene could be identified. The fusion genes were expressed in
XX CC E. coli and the antibodies were extracted. These recombinant antibodies
XX CC can be used for the qualitative and quantitative determination of c-erbB-
XX CC 2. This can be used for monitoring or in-vivo localisation of tumours
XX CC overexpressing c-erbB-2. (Updated on 25-MAR-2003 to correct PN field.)
XX CC (Updated on 24-OCT-2003 to standardise OS field)
XX SQ Sequence 637 AA;
Query Match 77.4%; Score 1005; DB 2; Length 637;
Best Local Similarity 78.8%; Pred. No. 7.7e-65;
Matches 193; Conservative 17; Mismatches 27; Indels 8; Gaps 2;
Qy 1 EVKLVSQPELKPGETVKISCKASGYIFNTYGNMVKQAPGKGLKMGWINTYGTGPTY 60
Db 33 QVQLQQSGPELKPGETVKISCKASGYFTNYGNMVKQAPGQGLKMGWINTSTGESTF 92
Qy 61 ADDPKGRFAFSLTASATYLIQINNKNEDTATYFCA---LYGNSPKGFAYWQQTTLVT 116
Db 93 ADDPKGRFDFSLTASATYLIQNMNLSKEDMATYFCARWEVYHGYVP---YWGQGTITVT 148
Qy 117 VSAGGGSGGSRASGGGSDIQMTQSPKELLVSAGDRVTITCKASQSVSNDVAVYQQKPGQ 176
Db 149 VSSGGGSGGSGGGGGSDIQLTQSHKFLSTSVGDRVSIITCKASQDYINAVAVYQQKPGQ 208
Qy 177 SPKLLIMYASNRYTGVPDRFTGSGGYDTFTFTITVQAEIDLAVYFCQDYGSPPTFGGTT 236
Db 209 SPKLLIYASASRYTGVPDRFTGSGGSDPTFTITSSVQAEIDLAVYFCQDHFPTFTFGSGT 268
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QY 237 KLEIK 241
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DB 269 KLEIK 273

Search completed: July 29, 2004, 08:46:35
Job time : 77.5587 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 08:50:28 ; Search time 59.3943 Seconds
(without alignments)
1278.091 Million cell updates/sec

Title: US-09-661-992B-82

Perfect score: 1299

Sequence: 1 EVLVESGPELKPGETVKI.....QDYGSPPTFGGKLEIKR 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313692936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA: *

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3:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4:	/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1000.5	77.0	250	9	US-09-887-853-2
2	961.5	74.0	505	12	US-10-293-418-1921
3	894.5	68.9	503	12	US-10-239-656-79
4	892	68.7	267	9	US-09-766-543-10
5	880	67.7	276	9	US-09-766-543-12
6	875.5	67.4	503	12	US-10-239-656-75
7	859.5	66.9	240	14	US-10-127-890-148
8	868.5	66.9	243	16	US-10-334-235-37
9	868.5	66.9	600	16	US-10-334-235-38
10	866.5	66.7	267	14	US-10-071-485-2
11	866.5	66.7	541	14	US-10-071-485-85
12	866.5	66.7	711	14	US-10-071-485-90
13	863.5	66.5	488	16	US-10-334-235-39
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16	856.5	65.9	251	10	US-09-880-748-1921
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19	845	65.1	248	12	US-10-293-418-1446
20	844.5	65.0	499	12	US-10-239-656-73
21	840.5	64.7	243	9	US-09-887-853-6
22	840	64.7	240	14	US-10-071-485-91
23	825.5	63.5	331	14	US-10-059-261-169
24	814.5	62.7	249	10	US-09-880-748-1635
25	814.5	62.7	249	12	US-10-293-418-1635
26	814	62.7	248	10	US-09-880-748-1778
27	814	62.7	248	12	US-10-293-418-1778
28	812.5	62.5	235	14	US-10-071-485-93
29	811	62.4	250	10	US-09-880-748-932
30	811	62.4	250	12	US-10-293-418-932
31	810	62.4	240	14	US-10-096-246-35
32	807	62.1	248	10	US-09-880-748-1700
33	807	62.1	248	12	US-10-293-418-1700
34	805.5	62.0	247	14	US-10-322-673-56
35	803.5	61.9	243	10	US-09-880-748-2063
36	803.5	61.9	243	12	US-10-293-418-2063
37	801.5	61.7	258	12	US-10-239-656-59
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39	800.5	61.6	241	12	US-10-293-418-1948
40	800	61.6	240	14	US-10-096-246-36
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42	799	61.5	242	10	US-09-880-748-1915
43	799	61.5	242	12	US-10-293-418-1915
44	798.5	61.5	247	12	US-10-293-418-3240
45	797.5	61.4	249	9	US-09-984-186-18

ALIGNMENTS

RESULT 1

US-09-887-853-2

; Sequence 2, Application US/09887853

; Patent No. US20020168375A1

; GENERAL INFORMATION:

; APPLICANT: Huston, James S.

; Oppermann, Hermann

; Houston, L. L.

; Ring, David B.

; TITLE OF INVENTION: Biosynthetic Binding Proteins For

; Imaging

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESS:

; ADDRESSER: Testa, Hurwitz & Thibault/Patent Department

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/887,853

; FILING DATE: 21-Jun-2001

; CLASSIFICATION: <Unknown>

; PRIORITY INFORMATION:

; APPLICATION NUMBER: US/08/133,804

; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:

; NAME: Kelley, Robin D.

; REGISTRATION NUMBER: 34,637

; REFERENCE/DOCKET NUMBER: 2054/22

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-248-7477

; TELEFAX: 617-248-7100

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; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 250 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-887-853-2

Query Match      77.0%; Score 1000.5; DB 9; Length 250;
Best Local Similarity 78.0%; Pred. No. 2.4e-71;
Matches 192; Conservative 17; Mismatches 28; Indels 9; Gaps 3;

QY 1 EVKLVSPELKKPGETVKISKASGYFTNYGNMVKQAPGKGLKMGWINTYTGPTY 60
DB 3 EIQLVQSGPELKKPGETVKISKASGYFTNYGNMVKQAPGKGLKMGWINTYTGPTY 62
QY 61 ADDFKGRFAFSLSTASTAYLIQINNKNEDTATYFCARF---LYGNSPKGFAYMGQGT 116
DB 63 AEEFKGRFAFSLSTASTAYLIQINNKNEDTATYFCGRQPTYG---GFANMGQGT 118
QY 117 VSAGGGSGGRASGGGSDIOMTQSPKFLVVSAGDRVTITCKASQSVNDVANYQQXPGQ 176
DB 119 VSA-SSSSGSSSSGSSSDIOMTQSPKFLVVSAGDRVTITCKASQSVNDVANYQQXPGQ 177
QY 177 SPKLLMYASNRYTGVDPDRFTGSGVGTFTTISTVQAEADLAVYFCQDYGSPPTFGGT 236
DB 178 SPKLLIYWTSTRTGVPDRFTGSGVGTFTTISTVQAEADLAVYFCQDYGSPPTFGGT 237
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RESULT 2
US-10-239-656-79
; Sequence 79, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 79
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 3B10xP5-
; OTHER INFORMATION: 23 bispecific single chain Fv
US-10-239-656-79

Query Match      74.0%; Score 961.5; DB 12; Length 505;
Best Local Similarity 53.0%; Pred. No. 6.1e-68;
Matches 195; Conservative 19; Mismatches 27; Indels 127; Gaps 4;

QY 1 EVKLVSPELKKPGETVKISKASGYFTNYGNMVKQAPGKGLKMGWINTYTGPTY 60
DB 128 QVQLQQSGPELKKPGETVKISKASGYFTNYGNMVKQAPGKGLKMGWINTYTGPTY 187

; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 250 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-887-853-2

Query Match      77.0%; Score 1000.5; DB 9; Length 250;
Best Local Similarity 78.0%; Pred. No. 2.4e-71;
Matches 192; Conservative 17; Mismatches 28; Indels 9; Gaps 3;

QY 1 EVKLVSPELKKPGETVKISKASGYFTNYGNMVKQAPGKGLKMGWINTYTGPTY 60
DB 3 EIQLVQSGPELKKPGETVKISKASGYFTNYGNMVKQAPGKGLKMGWINTYTGPTY 62
QY 61 ADDFKGRFAFSLSTASTAYLIQINNKNEDTATYFCARF---LYGNSPKGFAYMGQGT 116
DB 63 AEEFKGRFAFSLSTASTAYLIQINNKNEDTATYFCGRQPTYG---GFANMGQGT 118
QY 117 VSAGGGSGGRASGGGSDIOMTQSPKFLVVSAGDRVTITCKASQSVNDVANYQQXPGQ 176
DB 119 VSA-SSSSGSSSSGSSSDIOMTQSPKFLVVSAGDRVTITCKASQSVNDVANYQQXPGQ 177
QY 177 SPKLLMYASNRYTGVDPDRFTGSGVGTFTTISTVQAEADLAVYFCQDYGSPPTFGGT 236
DB 178 SPKLLIYWTSTRTGVPDRFTGSGVGTFTTISTVQAEADLAVYFCQDYGSPPTFGGT 237
QY 237 KLEIKR 242
DB 238 KLEIKR 243

RESULT 2
US-10-239-656-79
; Sequence 79, Application US/10239656
; Publication No. US20040038339A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RIETHMULLER, GERT
; APPLICANT: LUTTERBUSE, RALF
; APPLICANT: BORSCHERT, KATRIN
; APPLICANT: KISCHEL, ROMAN
; APPLICANT: MAYER, MONIKA
; APPLICANT: HOFMEISTER, ROBERT
; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
; FILE REFERENCE: 029976/0106
; CURRENT APPLICATION NUMBER: US/10/239,656
; PRIOR FILING DATE: 2003-03-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03414
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: EP 00106467.4
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 79
; LENGTH: 505
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic 3B10xP5-
; OTHER INFORMATION: 23 bispecific single chain Fv
US-10-239-656-79

Query Match      68.9%; Score 894.5; DB 12; Length 503;
Best Local Similarity 49.9%; Pred. No. 1.2e-62;
Matches 182; Conservative 23; Mismatches 37; Indels 123; Gaps 4;

QY 1 EVKLVSPELKKPGETVKISKASGYFTNYGNMVKQAPGKGLKMGWINTYTGPTY 60
DB 128 QVQLQQSGPELKKPGETVKISKASGYFTNYGNMVKQAPGKGLKMGWINTYTGPTY 187
QY 61 ADDFKGRFAFSLSTASTAYLIQINNKNEDTATYFCALY----- 99
DB 188 GDDFKGRFAFSLSTASTAYLIQINNKNEDTATYFCARFTSPDYWGQGT 247
QY 100 -----GNS----- 102
DB 248 EVQLLEESGGGLVQPGGSKLSVAGSFTFGNYMNVWVRSQSPKGLWVAIRLKSNNYA 307
```


QY 103 -----PKGPA--YWGQGLTVTVS 118
Db 308 THVAESVKGRFTISRDDSKSVLYOMNLRADRTGIYCTELPVGFMADYWGQGLTVTVS 367
QY 119 AGGSGSGRASGGGSGDIQMTQSPKLLVSGADRVTITCKASQSV-SNDVAVYQQKPGQS 177
Db 368 SGGSGSGGGGGGSLVLTQSPTTMAASPGEXITITCSASSISSNLYLHWYQKPGFS 427
QY 178 PKLWYASNRYTGVPDRFTSGVGTDTFTTISTVQAEADLVYFCQDYGSPPFTFGGKTK 237
Db 428 PKLLIYTSNLASGVAPRFGSGSGTSYSLTIGTNEADVATYCCQGGSSIPLTFGAGTK 487
QY 238 LEIKR 242
Db 488 LEIKR 492

RESULT 4

US-09-766-543-10

; Sequence 10, Application US/09766543

; Patent No. US20020041865A1

; GENERAL INFORMATION:

; APPLICANT: Austin, Richard

; APPLICANT: Kwok, Cheuk S.

; TITLE OF INVENTION: METHODS FOR TREATING TUMORS

; FILE REFERENCE: PP01679.002

; CURRENT APPLICATION NUMBER: US/09/766,543

; PRIOR FILING DATE: 2000-01-19

; PRIOR APPLICATION NUMBER: 60/177,258

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 267

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: 520C9

; OTHER INFORMATION: humanized single-chain antibody used in the

; OTHER INFORMATION: IL-2-antibody fusions

US-09-766-543-10

Query Match

Best Local Similarity 68.7%; Score 892; DB 9; Length 267;

Matches 163; Conservative 33; Mismatches 41; Indels 4; Gaps 1;

QY 1 EVKLVEGPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKMWGWINTYTGEPY 60
Db 23 EMQLVESGPEVKKPGASVKYKSKASGYFTNYGMNVKQAPGQGLEWGMWINTYTGQSTY 82
QY 61 ADDPKGRFAFSLETSASTAYLQINLNKEDTATYFCALYGNSPKGFAYWGQGLTVTVSAG 120
Db 83 ADDPKERVTTTDTSTSTAYMDLRSRSDDTAVYICA----RRFGFAYWGQGLTVTVSSG 138
QY 121 GGGSGGRASGGGSDIQMTQSPKLLVSGADRVTITCKASQSVNDVAVYQQKPGQSPKL 180
Db 139 GGGSGGGGGGGSDIQMTQSPSLSASVGDRTVITCRASQDIGNSLTWLQKPGKTIKR 198
QY 181 LMVYASNRYTGVPDRFTSGVGTDTFTTISTVQAEADLVYFCQDYGSPPFTFGGKTKLEI 240
Db 199 LIYATSSLDGVPFRSGSGSDTFTTISLQPEDVYVYCYLQYAIFFYTFGGTKRLEI 258
QY 241 K 241
Db 259 K 259

RESULT 5

US-09-766-543-12

; Sequence 12, Application US/09766543

; Patent No. US20020041865A1

GENERAL INFORMATION:

; APPLICANT: Austin, Richard

; APPLICANT: Kwok, Cheuk S.

; APPLICANT: Ring, David B.

; TITLE OF INVENTION: METHODS FOR TREATING TUMORS

; FILE REFERENCE: PP01679.002

; CURRENT APPLICATION NUMBER: US/09/766,543

; CURRENT FILING DATE: 2000-01-19

; PRIOR APPLICATION NUMBER: 60/177,258

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 12

; LENGTH: 276

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: H520C9sfv plus

; OTHER INFORMATION: linker

US-09-766-543-12

Query Match

Best Local Similarity 67.7%; Score 880; DB 9; Length 276;

Matches 164; Conservative 31; Mismatches 42; Indels 4; Gaps 1;

QY 1 EVKLVEGPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKMWGWINTYTGEPY 60
Db 23 EIQLVQSGPEVKKPGASVKYKSKASGYFTNYGMNVKQAPGQGLEWGMWINTYTGQSTY 82
QY 61 ADDPKGRFAFSLETSASTAYLQINLNKEDTATYFCALYGNSPKGFAYWGQGLTVTVSAG 120
Db 83 ADDPKERVTTTDTSTSTAHLEISRSDDTAVYICA----RRFGFAYWGQGLTVTVSSG 138
QY 121 GGGSGGRASGGGSDIQMTQSPKLLVSGADRVTITCKASQSVNDVAVYQQKPGQSPKL 180
Db 139 GGGSGGGGGGGSDIQMTQSPSLSASVGDRTVITCRASQDIGNSLTWLQKPGKTIKR 198
QY 181 LMVYASNRYTGVPDRFTSGVGTDTFTTISTVQAEADLVYFCQDYGSPPFTFGGKTKLEI 240
Db 199 LIYATSSLDGVPFRSGSGSDTFTTISLQPEDVYVYCYLQYAIFFYTFGGTKRLEI 258
QY 241 K 241
Db 259 K 259

RESULT 6

US-10-239-656-75

; Sequence 75, Application US/10239656

; Publication No. US20040038339A1

; GENERAL INFORMATION:

; APPLICANT: KUFER, PETER

; APPLICANT: RIETHMULLER, GERT

; APPLICANT: LUTTEREUSE, RALF

; APPLICANT: BORSCHERT, KATRIN

; APPLICANT: KISCHEL, ROMAN

; APPLICANT: MAYER, MONIKA

; APPLICANT: HOFWEISTER, ROBERT

; TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE

; FILE REFERENCE: TO AN EPIOTOPE OF THE NKGD2 RECEPTOR COMPLEX

; FILE REFERENCE: 029976/0106

; CURRENT APPLICATION NUMBER: US/10/239,656

; CURRENT FILING DATE: 2003-03-06

; PRIOR APPLICATION NUMBER: PCT/EP01/03414

; PRIOR FILING DATE: 2001-03-26

; PRIOR APPLICATION NUMBER: EP 00106467.4

; NUMBER OF SEQ ID NOS: 92

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 75

; LENGTH: 503

; TYPE: PRT

; ORGANISM: Artificial Sequence


```
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mature secreted protein of 5T4 scFv, designated
US-10-334-235-37

Query Match      66.9%; Score 868.5; DB 16; Length 243;
Best Local Similarity 68.2%; Pred. No. 6.4e-61;
Matches 167; Conservative 28; Mismatches 45; Indels 5; Gaps 2;

QY 1 EVKLVESGPELKKPGETVKISKASGYIFTNMGNNVKKQAPGKGLKMWGINTYTGPTY 60
Db 1 EVQLQSGGPDLVKPGASVKISKASGYFTGYHWWKQSHGKSLGWIGRINPNNGVTLY 60

QY 61 ADDFKGRFAFSLETSASTAYLQINLNKEDTATYFCA---LYGNSPKGFAYWGQGTLTVT 117
Db 61 NQKFKDKAILTVDKSSTAYMELRSLTSEDSAVVYCARSTMITNYV--MDYWGQVTSVT 118

QY 118 SAGGGSGGRASGGGSDIQMTQSPKFLVLSAGDRVTITCKASQSVNDVAVYQKPGQS 177
Db 118 SAGGGSGGRASGGGSDIQMTQSPKFLVLSAGDRVTITCKASQSVNDVAVYQKPGQS 177

QY 178 PKLLMYASNRYTGVPRFTGSGYGTDTFTTISTVQAE DLAVYFCQDYGSPTFGGQTK 237
Db 178 PKLLMYASNRYTGVPRFTGSGYGTDTFTTISTVQAE DLAVYFCQDYGSPTFGGQTK 237

QY 238 LEIKR 242
Db 238 LEIKR 242

QY 239 LEIKR 243
Db 239 LEIKR 243

RESULT 9
US-10-334-235-38
; Sequence 38, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikanda, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 53268200920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of 5T4sabl
US-10-334-235-38

Query Match      66.9%; Score 868.5; DB 16; Length 600;
Best Local Similarity 68.2%; Pred. No. 1.6e-60;
Matches 167; Conservative 28; Mismatches 45; Indels 5; Gaps 2;

QY 1 EVKLVESGPELKKPGETVKISKASGYIFTNMGNNVKKQAPGKGLKMWGINTYTGPTY 60
Db 23 EVQLQSGGPDLVKPGASVKISKASGYFTGYHWWKQSHGKSLGWIGRINPNNGVTLY 82

; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: mature secreted protein of 5T4 scFv, designated
US-10-334-235-37

Query Match      66.7%; Score 866.5; DB 14; Length 267;
Best Local Similarity 67.8%; Pred. No. 1e-60;
Matches 166; Conservative 26; Mismatches 44; Indels 9; Gaps 3;

QY 1 EVKLVESGPELKKPGETVKISKASGYIFTNMGNNVKKQAPGKGLKMWGINTYTGPTY 60
Db 23 QVQLVQSGSELKPKGASVKISKASGYFTFDYGMNWKVQAPGQGLKMWGINTYTGESTY 82

QY 61 ADDFKGRFAFSLETSASTAYLQINLNKEDTATYFCA---AYWGQGTLTVT 117
Db 61 VDDFKGRFVPSLDTSVSAAYLQISSLKAEADTATYFCA-----RRGFYADYWGQGT 137

QY 118 SAGGGSGGRASGGGSDIQMTQSPKFLVLSAGDRVTITCKASQSVNDVAVYQKPGQS 177
Db 118 SAGGGSGGRASGGGSDIQMTQSPKFLVLSAGDRVTITCKASQSVNDVAVYQKPGQS 177

QY 178 PKLLMYASNRYTGVPRFTGSGYGTDTFTTISTVQAE DLAVYFCQDYGSPTFGGQTK 237
Db 178 PKLLMYASNRYTGVPRFTGSGYGTDTFTTISTVQAE DLAVYFCQDYGSPTFGGQTK 237

QY 238 LEIKR 242
Db 238 LEIKR 242

QY 257 LEIKR 261
Db 257 LEIKR 261

RESULT 10
US-10-071-485-2
; Sequence 2, Application US/10071485
; Publication No. US2003009848A1
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-071-485-2

Query Match      66.7%; Score 866.5; DB 14; Length 267;
Best Local Similarity 67.8%; Pred. No. 1e-60;
Matches 166; Conservative 26; Mismatches 44; Indels 9; Gaps 3;

QY 1 EVKLVESGPELKKPGETVKISKASGYIFTNMGNNVKKQAPGKGLKMWGINTYTGPTY 60
Db 23 QVQLVQSGSELKPKGASVKISKASGYFTFDYGMNWKVQAPGQGLKMWGINTYTGESTY 82

QY 61 ADDFKGRFAFSLETSASTAYLQINLNKEDTATYFCA---AYWGQGTLTVT 117
Db 61 VDDFKGRFVPSLDTSVSAAYLQISSLKAEADTATYFCA-----RRGFYADYWGQGT 137

QY 118 SAGGGSGGRASGGGSDIQMTQSPKFLVLSAGDRVTITCKASQSVNDVAVYQKPGQS 177
Db 118 SAGGGSGGRASGGGSDIQMTQSPKFLVLSAGDRVTITCKASQSVNDVAVYQKPGQS 177

QY 178 PKLLMYASNRYTGVPRFTGSGYGTDTFTTISTVQAE DLAVYFCQDYGSPTFGGQTK 237
Db 178 PKLLMYASNRYTGVPRFTGSGYGTDTFTTISTVQAE DLAVYFCQDYGSPTFGGQTK 237

QY 238 LEIKR 242
Db 238 LEIKR 242

QY 257 LEIKR 261
Db 257 LEIKR 261
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RESULT 11
US-10-071-485-85
; Sequence 85, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85
; LENGTH: 541
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-85

Query Match 66.7%; Score 866.5; DB 14; Length 541;
Best Local Similarity 67.8%; Pred. No. 2.1e-60;
Matches 166; Conservative 26; Mismatches 44; Indels 9; Gaps 3;

QY 1 EVKLVSPELKKPGETVKISKASGYFTFYGNMVKQAPGKGLKMWGWINTYTGEPTY 60
DB 1 QVQLVQSGSELKPKGASVKISKASGYFTFYGNMVKQAPGQGLKMWGWINTYTGEPTY 60
QY 61 ADDFKGRFAFSLTSASTAYLIQINLNKEDTATYFCALYGNSPKGF---AYWGQGLTVTV 117
DB 61 VDDFKGRFVFLSDTSVAAYLIQISLKAEDTATYFCA-----RRGFYAMDYWGQGLTVTV 115
QY 118 SAGGGSGGRASGGGSDIOMTQSPKFLVLSAGDRVTITCKASQSVNDVAVYQOKPGQS 177
DB 116 SSGGGSGGGSGGGSDIVLTQSPATMSASPGERVILTCSASSISY-MFWYHQRPGQS 174
QY 178 PKLLMYASNRYTGVDPDRFTGSGYGTDTFTTISTVQAEADLAVYFCQDDYGSPPFTFGGQTK 237
DB 175 PRLLYDTSNLASGVAPRFGSGGSGTSLTISRMEPEDPATYFCHQSSSYPTFTFGGQTK 234
QY 238 LEIKR 242
DB 235 LEIKR 239

RESULT 12
US-10-071-485-90
; Sequence 90, Application US/10071485
; Publication No. US20030099648A1
; GENERAL INFORMATION:
; APPLICANT: Buysse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165

```

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; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

Query Match 66.7%; Score 866.5; DB 14; Length 711;
Best Local Similarity 67.8%; Pred. No. 2.8e-60;
Matches 166; Conservative 26; Mismatches 44; Indels 9; Gaps 3;

QY 1 EVKLVSPELKKPGETVKISKASGYFTFYGNMVKQAPGKGLKMWGWINTYTGEPTY 60
DB 473 QVQLVQSGSELKPKGASVKISKASGYFTFYGNMVKQAPGQGLKMWGWINTYTGEPTY 532
QY 61 ADDFKGRFAFSLTSASTAYLIQINLNKEDTATYFCALYGNSPKGF---AYWGQGLTVTV 117
DB 533 VDDFKGRFVFLSDTSVAAYLIQISLKAEDTATYFCA-----RRGFYAMDYWGQGLTVTV 587
QY 118 SAGGGSGGRASGGGSDIOMTQSPKFLVLSAGDRVTITCKASQSVNDVAVYQOKPGQS 177
DB 588 SSGGGSGGGSGGGSDIVLTQSPATMSASPGERVILTCSASSISY-MFWYHQRPGQS 646
QY 178 PKLLMYASNRYTGVDPDRFTGSGYGTDTFTTISTVQAEADLAVYFCQDDYGSPPFTFGGQTK 237
DB 647 PRLLYDTSNLASGVAPRFGSGGSGTSLTISRMEPEDPATYFCHQSSSYPTFTFGGQTK 706
QY 238 LEIKR 242
DB 707 LEIKR 711

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```

RESULT 13
US-10-334-235-39
; Sequence 39, Application US/10334235
; Publication No. US20040131591A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Ltd.
; APPLICANT: Kingsman, Alan
; APPLICANT: Bebbington, Christopher
; APPLICANT: Carroll, Miles
; APPLICANT: Ellard, Fiona
; APPLICANT: Kingsman, Susan
; APPLICANT: Myers, Kevin
; APPLICANT: Lamikandra, Abigail
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 532682000920
; CURRENT APPLICATION NUMBER: US/10/334,235
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 10/060,585
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 09/445,375
; PRIOR FILING DATE: 1998-06-04
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 488
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide of B7-1.574.1
US-10-334-235-39

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Query Match      66.5%; Score 863.5; DB 16; Length 488;
Best Local Similarity 66.0%; Pred. No. 3.3e-60;
Matches 166; Conservative 28; Mismatches 45; Indels 5; Gaps 2;

Qy 1 EVKLVEGPELKKPGETVKISKASGYIFTNYGNWVKQAPGKGLKWMGMINITYTGEPTY 60
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
247 EVQLVQSGPDVLRFGASVKISKASGYFTGYNHWVKQSHGKSLGWGRINPNNGVTLY 306
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
61 ADDPKGRFAFSLTSASTAYLQINNKNEDTATYFCA---LYGNSPKGFAYWGQGLTVTV 117
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
307 NQKFKRAILLTVDKSSITAYMELASLTSEDSAVYICARSTMTINVV--MDYWGQVTSVTV 364
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
118 SAGGGSGGRASGGGGSDIQWTSKPKLLVSAGDRVITCKASQSVNDVAVTQKPGQS 177
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
365 SSGGGSGGGGTGGGGSSIVMTQTFLLVSAGDRVITCKASQSVNDVAVTQKPGQS 424
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
178 PKLLMYASNRYTVGPDRFTGSGYGTDTFTISTVQAEADLAVYFCQDYGSPPTFGGTX 237
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
425 PTLIISYTSRYAGVDRFVGGSGYGTDTFTISTVQAEADLAVYFCQDYGSPPTFGGTX 484
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
238 LEIK 241
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
485 LEIK 488

RESULT 14
US-09-880-748-1104
; Sequence 1104, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/275,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1104.
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1104

Query Match      66.1%; Score 859; DB 10; Length 248;
Best Local Similarity 62.9%; Pred. No. 3.7e-60;
Matches 156; Conservative 39; Mismatches 47; Indels 6; Gaps 1;

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Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
1 EVQLVQSGAEVKKPGASVKISKASGYFTSYGISWVRQAPGQGLEWMGWSAYNGNTNY 60
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
61 ADDPKGRFAFSLTSASTAYLQINNKNEDTATYFCA-----LYGNSPKGFAYWGQGLT 114
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
61 AQKFGQGRVTTTADSTSTAYMELSLRSEDATVYICARMEYDILTGYGGYFDYWGQGT 120
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
115 VTWSAGGGSGGRASGGGSDIQWTSKPKLLVSAGDRVITCKASQSVNDVAVYQKXP 174
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
121 VTWSGGGGSGGGSGGSDVMTQSPSSLSASLGDRVITCRASQDITNDLAWYQKXP 180
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175 GQSPKLLMYASNRYTVGPDRFTGSGYGTDTFTISTVQAEADLAVYFCQDYGSPPTFGG 234
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Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|

Search completed: July 29, 2004, 09:12:25
Job time : 59.3943 secs
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Best Local Similarity 66.0%; Pred. No. 3.3e-60;
Matches 166; Conservative 28; Mismatches 45; Indels 5; Gaps 2;

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307 NQKFKRAILLTVDKSSITAYMELASLTSEDSAVYICARSTMTINVV--MDYWGQVTSVTV 364
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118 SAGGGSGGRASGGGGSDIQWTSKPKLLVSAGDRVITCKASQSVNDVAVTQKPGQS 177
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Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
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Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
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238 LEIK 241
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485 LEIK 488

RESULT 14
US-09-880-748-1104
; Sequence 1104, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1104.
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1104

Query Match      66.1%; Score 859; DB 10; Length 248;
Best Local Similarity 62.9%; Pred. No. 3.7e-60;
Matches 156; Conservative 39; Mismatches 47; Indels 6; Gaps 1;

Qy 1 EVKLVEGPELKKPGETVKISKASGYIFTNYGNWVKQAPGKGLKWMGMINITYTGEPTY 60
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1 EVQLVQSGAEVKKPGASVKISKASGYFTSYGISWVRQAPGQGLEWMGWSAYNGNTNY 60
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
61 ADDPKGRFAFSLTSASTAYLQINNKNEDTATYFCA-----LYGNSPKGFAYWGQGLT 114
Qy |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
61 AQKFGQGRVTTTADSTSTAYMELSLRSEDATVYICARMEYDILTGYGGYFDYWGQGT 120
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115 VTWSAGGGSGGRASGGGSDIQWTSKPKLLVSAGDRVITCKASQSVNDVAVYQKXP 174
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121 VTWSGGGGSGGGSGGSDVMTQSPSSLSASLGDRVITCRASQDITNDLAWYQKXP 180
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Search completed: July 29, 2004, 09:12:25
Job time : 59.3943 secs
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3	1008	77.6	617	4	US-08-840-713-37	Sequence 37, Appli
4	1008	77.6	637	1	US-08-835-838-14	Sequence 14, Appli
5	1008	77.6	637	2	US-08-465-473B-14	Sequence 14, Appli
6	1008	77.6	711	1	US-08-235-838-7	Sequence 7, Appli
7	1008	77.6	711	2	US-08-465-473B-7	Sequence 7, Appli
8	1003	77.2	241	1	US-08-235-838-5	Sequence 5, Appli
9	1003	77.2	241	2	US-08-465-473B-5	Sequence 5, Appli
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11	1000.5	77.0	250	1	US-08-461-184-8	Sequence 8, Appli
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15	1000.5	77.0	250	2	US-08-461-386-2	Sequence 2, Appli
16	977.5	75.3	622	2	US-08-356-786-16	Sequence 16, Appli
17	918	70.7	365	3	US-08-875-811-53	Sequence 53, Appli
18	918	70.7	366	3	US-08-875-811-55	Sequence 55, Appli
19	894.5	68.9	284	3	US-09-184-658-40	Sequence 40, Appli
20	894.5	68.9	284	4	US-09-504-262D-40	Sequence 40, Appli
21	878.5	67.6	534	2	US-08-356-786-10	Sequence 10, Appli
22	869.5	66.9	240	1	US-08-488-113B-148	Sequence 148, Appli
23	869.5	66.9	240	1	US-08-477-484B-148	Sequence 148, Appli
24	869.5	66.9	240	2	US-08-646-360-148	Sequence 148, Appli
25	869.5	66.9	240	3	US-08-839-765-148	Sequence 148, Appli
26	869.5	66.9	240	3	US-09-136-389-148	Sequence 148, Appli
27	869.5	66.9	240	4	US-09-610-838-148	Sequence 148, Appli

US-08-235-838-14
; Sequence 14, Application US/08235838
; Patent No. 5571894
; GENERAL INFORMATION:
; APPLICANT: Wels, Winfried S.
; APPLICANT: Hynes, Nancy E.
; APPLICANT: Harwerth, Ina-Maria
; APPLICANT: Groer, Bernd
; APPLICANT: Hardman, No. 5571894man
; APPLICANT: Zwickl, Markus
; TITLE OF INVENTION: Recombinant Antibodies Specific for a
; TITLE OF INVENTION: Growth Factor Receptor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,838
; FILING DATE: TBA
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/828,832
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 91-810079.3
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 637 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-235-838-14

Query Match 77.6%; Score 1008; DB 1; Length 637;
Best Local Similarity 79.2%; Pred. No. 1.3e-84;
Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
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Db 33 QVQLQSGPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKMWGINTSTGESTF 92
QY 61 ADPKGRFAFSLTSASTAYLQINNKNEDTATYFCA----LYGNSPKGFAYWQQTLYT 116
Db 93 ADPKGRFDFSLTSANTAYLQINNKNEDMATYFCARWEVYHGYP----YWGQGTITV 148
QY 117 VSAGGGSGGRASGGGSDIOMTSKPKLLVSAGRVITTCASQSVNDVAVYQKPKQ 176
Db 149 VSSGGGGSGGGGGSDIQLTQSHKFLSTSVGDRVSIITCKASQDVYNAVAYQKPKQ 208
QY 177 SPKLLMYASNRYTGVPDRFTGSGYGTDFTTISTVQAEADLVAVFCQDYGSPPFTFGGT 236
Db 209 SPKLLIYASSRITGVPSRFTGSGGPDFTFTISSVQAEADLVAVFCQHFRTFTFGSGT 268
QY 237 KLEIK 241
Db 269 KLEIK 273

RESULT 5
US-08-465-473B-14
; Sequence 14, Application US/08465473B
; Patent No. 5939531
; GENERAL INFORMATION:
; APPLICANT: Wels, Winfried S.
; APPLICANT: Hynes, Nancy E.
; APPLICANT: Harwerth, Ina-Maria
; APPLICANT: Groer, Bernd
; APPLICANT: Hardman, No. 5939531man
; APPLICANT: Zwickl, Markus
; TITLE OF INVENTION: Recombinant Antibodies Specific for a
; TITLE OF INVENTION: Growth Factor Receptor
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NOVARTIS Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901-6940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,473B
; FILING DATE: 5 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/828,832
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 91-810079.3
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pfeiffer, Hesna J.
; REGISTRATION NUMBER: 22,640
; REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)522 6940
; TELEFAX: (908)522 6955
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 637 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-465-473B-14

Query Match 77.6%; Score 1008; DB 2; Length 637;
Best Local Similarity 79.2%; Pred. No. 1.3e-84;
Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
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Db 33 QVQLQSGPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKMWGINTSTGESTF 92
QY 61 ADPKGRFAFSLTSASTAYLQINNKNEDTATYFCA----LYGNSPKGFAYWQQTLYT 116
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US-08-235-838-7			
; Sequence 7, Application US/08235838			
; Patent No. 5571894			
; GENERAL INFORMATION:			
; APPLICANT: Wels, Winfried S.			
; APPLICANT: Hynes, Nancy E.			
; APPLICANT: Harwerth, Ina-Maria			
; APPLICANT: Groner, Bernd			
; APPLICANT: Hardman, No. 5571894man			
; APPLICANT: Zwickl, Markus			
; TITLE OF INVENTION: Recombinant Antibodies Specific for a			
; TITLE OF INVENTION: Growth Factor Receptor			
; NUMBER OF SEQUENCES: 16			
; CORRESPONDENCE ADDRESS:			
; ADDRESSEE: CIBA-GEIGY Corporation			
; STREET: 7 Skyline Drive			
; CITY: Hawthorne			
; STATE: New York			
; COUNTRY: USA			
; ZIP: 10532			
; COMPUTER READABLE FORM:			
; MEDIUM TYPE: Floppy disk			
; OPERATING SYSTEM: PC-DOS/MS-DOS			
; SOFTWARE: Patent In Release #1.0, Version #1.25			
; CURRENT APPLICATION DATA:			
; APPLICATION NUMBER: US/08/235,838			
; FILING DATE: TEA			
; CLASSIFICATION: 435			
; PRIOR APPLICATION NUMBER: US 07/828,832			
; FILING DATE: 31-JAN-1992			
; PRIOR APPLICATION DATA:			
; APPLICATION NUMBER: GB 91-810079.3			
; FILING DATE: 05-FEB-1991			
; ATTORNEY/AGENT INFORMATION:			
; NAME: Elmer, James Scott			
; REGISTRATION NUMBER: 36,129			
; REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT			
; TELECOMMUNICATION INFORMATION:			
; TELEPHONE: (919)541-8614			
; TELEFAX: (919)541-8689			
; INFORMATION FOR SEQ ID NO: 7:			
; SEQUENCE CHARACTERISTICS:			
; LENGTH: 711 amino acids			
; TYPE: amino acid			
; TOPOLOGY: linear			
; MOLECULE TYPE: protein			
US-08-235-838-7			
Query Match 77.6%; Score 1008; DB 1; Length 711;			
Best Local Similarity 79.2%; Pred. No. 1.4e-84;			
Matches 194; Conservative 16; Mismatches 27; Indels 8; Gaps 2;			
QY	1	EVKLVSGPELKKPGTETVTKISKASGYIFPTNGMNVKQAPGKLKMWGWINTYTGETTY 60	
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Db	83	ADDFKGRFPDLSLETSAATAYLQINLNKEDMATYFCARWEVTHGVYP-----YWGGTIVT 138	
QY	117	VSAAGGGSGGRASGGGSDIQMTQSPKFLVLSAGDRVTITCKASVSNDVNVAWYQQKPGQ 176	
Db	139	VSSGGGGSGGGSGGGSDIQMTQSHKFLSVSGDRVTSITCKASQDVNVAWYQQKPGQ 198	
QY	177	SPKLMIYASNRYTGVPFRFTTGTGGSGDPDTFTISTVQAEDLAIVFCQOHFRPFFFGSGT 236	

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Qy 177 SPKLLMYASNRYTGVDRFTGSGYGTDFTTTISTVQAEADLAVYFCQDDYGSPTFGGTT 236
Db 199 SPKLLIYASASRYTGVPSRFTGSGGPDFTFTTSSVQAEADLAVYFCQDHRTFTFGSGT 258
Qy 237 KLEIK 241
Db 259 KLEIK 263

RESULT 8
US-08-235-838-5
; Sequence 5, Application US/08235838
; Patent No. 5571894
; GENERAL INFORMATION:
; APPLICANT: Wels, Winfried S.
; APPLICANT: Hynes, Nancy E.
; APPLICANT: Harwerth, Ina-Maria
; APPLICANT: Groner, Bernd
; APPLICANT: Hardman, No. 5571894man
; APPLICANT: Zwickl, Markus
; TITLE OF INVENTION: Recombinant Antibodies Specific for a
; TITLE OF INVENTION: Growth Factor Receptor
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/235,838
; FILING DATE: TBA
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/828,832
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 91-810079.3
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8614
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-235-838-5

Query Match 77.2%; Score 1003; DB 1; Length 241;
Best Local Similarity 79.1%; Pred. No. 1.1e-84;
Matches 193; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
Qy 1 EVKLVSQPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKWMGINTYTGPTY 60
Db 2 QVQLQQSGPELKKPGETVKISKASGYIFTNYGMNVKQAPGQGLKWMGINTSTGSETF 61
Qy 61 ADDEPKGFATSLFSTASTAYLIQINLNKNDATYFCA-----LYGNSPKGFAYVQGTLYT 116
Db 62 ADDEPKGRFDFSLFSTASTAYLIQINLNKSDMATYFCARWEYHYGVF-----YWGQGTIVT 117

Qy 117 VSAGGGGGGRASGGGGDIQMTQSPKFLLYSAGDRVITCKASQSVNDVAVYQKPGQ 176
Db 118 VSSGGGGGGGGGGGGGGGGGGDIQTOHKLSTSVGDRVSIITCKASQDVYNAVAVYQKPGQ 177
Qy 177 SPKLLMYASNRYTGVDRFTGSGYGTDFTTTISTVQAEADLAVYFCQDDYGSPTFGGTT 236
Db 178 SPKLLIYASASRYTGVPSRFTGSGGPDFTFTTSSVQAEADLAVYFCQDHRTFTFGSGT 237
Qy 237 KLEI 240
Db 238 KLEI 241

RESULT 9
US-08-465-473B-5
; Sequence 5, Application US/08465473B
; Patent No. 5939531
; GENERAL INFORMATION:
; APPLICANT: Wels, Winfried S.
; APPLICANT: Hynes, Nancy E.
; APPLICANT: Harwerth, Ina-Maria
; APPLICANT: Groner, Bernd
; APPLICANT: Hardman, No. 5939531man
; APPLICANT: Zwickl, Markus
; TITLE OF INVENTION: Recombinant Antibodies Specific for a
; TITLE OF INVENTION: Growth Factor Receptor
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NOVARTIS Corporation
; STREET: 564 Morris Avenue
; CITY: Summit
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07901-6940
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,473B
; FILING DATE: 5 June 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/828,832
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 91-810079.3
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pfeiffer, Hesna J.
; REGISTRATION NUMBER: 22,640
; REFERENCE/DOCKET NUMBER: 4-18518/A/CIP/CONT2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)522 6940
; TELEFAX: (908)522 6955
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-465-473B-5

Query Match 77.2%; Score 1003; DB 2; Length 241;
Best Local Similarity 79.1%; Pred. No. 1.1e-84;
Matches 193; Conservative 16; Mismatches 27; Indels 8; Gaps 2;
Qy 1 EVKLVSQPELKKPGETVKISKASGYIFTNYGMNVKQAPGKGLKWMGINTYTGPTY 60
Db 2 QVQLQQSGPELKKPGETVKISKASGYIFTNYGMNVKQAPGQGLKWMGINTSTGSETF 61


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Db 178 SPKLLIYWTSTRHTGVPDRFTGSGGTDYTLTSSVQAEADLALHYCQOHRYVPTFGGTT 237
QY 237 KLEIKR 242
Db 238 KLEIKR 243

RESULT 12
US-08-463-675-8
; Sequence 8, Application US/08463675
; Patent No. 5658763
; GENERAL INFORMATION:
; APPLICANT: DORAI, HAIMANTI
; APPLICANT: OPPERMAN, HERMANN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,675
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/143,498
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 230 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-463-675-8

Query Match 77.0%; Score 1000.5; DB 1; Length 250;
Best Local Similarity 78.0%; Pred. No. 1.9e-84;
Matches 192; Conservative 17; Mismatches 28; Indels 9; Gaps 3;

QY 1 EVKLVEGPELKKPGETVKISKASGYFTNYGNWVKQAPGKGLKWMGWINNTGPTY 60
Db 3 EIQLVQSGPELKKPGETVKISKASGYFTNYGNWVKQAPGKGLKWMGWINNTGPTY 62
QY 61 ADDPKGRFAFSLTASATAYLQINNKNEDTATYFCA---LYGNSPKGFAYWGQGLVT 116
Db 63 ABEFKGRFAFSLTASATAYLQINNKNEDTATYFCGRQFTYG---GFANWGQGLVT 118
QY 117 VSAGGGGGGASGGGSDIOMTQSPKFLVLSAGDRVITTCASQSVSNDVAVYQOKPG 176
Db 119 VSA-SSSSSSSSSSSDIVMTQSPKFMSTSVGDRVSISSCKASQDVSTAVAVYQOKPG 177
QY 177 SPKLLMYASNRYTGVPDRFTGSGGTDFTFTISVQAEADLAVYFCQDYGSPPTFGGTT 236
Db 178 SPKLLIYWTSTRHTGVPDRFTGSGGTDYTLTSSVQAEADLALHYCQOHRYVPTFGGTT 237
QY 237 KLEIKR 242
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```
Db 238 KLEIKR 243

RESULT 13
US-08-464-589-8
; Sequence 8, Application US/08464589
; Patent No. 5733782
; GENERAL INFORMATION:
; APPLICANT: DORAI, HAIMANTI
; APPLICANT: OPPERMAN, HERMANN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR HIGH PROTEIN
; TITLE OF INVENTION: PRODUCTION FROM NON-NATIVE DNA
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES, INC
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 07148
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,589
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,498
; FILING DATE: 25-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KELLEY, ROBIN D
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: CRP093
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/248-7000
; TELEFAX: 617/248-7100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-464-589-8

Query Match 77.0%; Score 1000.5; DB 1; Length 250;
Best Local Similarity 78.0%; Pred. No. 1.9e-84;
Matches 192; Conservative 17; Mismatches 28; Indels 9; Gaps 3;

QY 1 EVKLVEGPELKKPGETVKISKASGYFTNYGNWVKQAPGKGLKWMGWINNTGPTY 60
Db 3 EIQLVQSGPELKKPGETVKISKASGYFTNYGNWVKQAPGKGLKWMGWINNTGPTY 62
QY 61 ADDPKGRFAFSLTASATAYLQINNKNEDTATYFCA---LYGNSPKGFAYWGQGLVT 116
Db 63 ABEFKGRFAFSLTASATAYLQINNKNEDTATYFCGRQFTYG---GFANWGQGLVT 118
QY 117 VSAGGGGGGASGGGSDIOMTQSPKFLVLSAGDRVITTCASQSVSNDVAVYQOKPG 176
Db 119 VSA-SSSSSSSSSSSDIVMTQSPKFMSTSVGDRVSISSCKASQDVSTAVAVYQOKPG 177
QY 177 SPKLLMYASNRYTGVPDRFTGSGGTDFTFTISVQAEADLAVYFCQDYGSPPTFGGTT 236
Db 178 SPKLLIYWTSTRHTGVPDRFTGSGGTDYTLTSSVQAEADLALHYCQOHRYVPTFGGTT 237
QY 237 KLEIKR 242
Db 238 KLEIKR 243
```

RESULT 14

US-08-461-838-2
; Sequence 2, Application US/08461838
; Patent No. 5753204
; GENERAL INFORMATION:
; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; APPLICANT: Houston, L. L.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461.838
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-838-2

Query Match 77.0%; Score 1000.5; DB 1; Length 250;
Best Local Similarity 78.0%; Pred. No. 1.9e-84;
Matches 192; Conservative 17; Mismatches 28; Indels 9; Gaps 3;
QY 1 EVKLVSQPELKKPGETVKISCKASGYFTNYGMNWKQAPGKGLKMWGINTYTGPTY 60
DB 3 EQLVQSGPELKKPGETVKISCKASGYFTNYGMNWKQAPGKGLKMWGINTYTGPTY 62
QY 61 ADDEKGRFAFSLSTSASTAYLQINLNKEDTATYFCA-----LYGNSPKGFAYWQGTLYT 116
DB 63 AEEFKGRFAFSLSTSASTAYLQINLNKEDTATYFCA-----LYGNSPKGFAYWQGTLYT 118
QY 117 VSAGGGSGGRASGGGSDIOMTOSPKFLVLSAGDRVTITCKASQSVNDVAVYQKPGQ 176
DB 119 VSA-SSSSGSSSSGSSSDIVMTQSPKFMSTSVGDRVSIKASQSDVSTAVAVYQKPGQ 177
QY 177 SPKLLMYANRYTGVPDRFTGSGYGHDTFTTISTVQAEADLAVYFCQDYGSPPTFGGTT 236
DB 178 SPKLLIYWTSTRHTGVDPDRFTGSGGSDTYLTITSSVQAEADLALHYCQOHYRVPYTFGGT 237
QY 237 KLEIKR 242
DB 238 KLEIKR 243

RESULT 15

US-08-461-386-2
; Sequence 2, Application US/08461386
; Patent No. 5837846
; GENERAL INFORMATION:

; APPLICANT: Huston, James S.
; APPLICANT: Oppermann, Hermann
; APPLICANT: Houston, L. L.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: Biosynthetic Binding Proteins For
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault/Patent Department
; STREET: Exchange Place, 53 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461.386
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Kelley, Robin D.
; REGISTRATION NUMBER: 34,637
; REFERENCE/DOCKET NUMBER: 2054/22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-248-7477
; TELEFAX: 617-248-7100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 250 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-461-386-2

Query Match 77.0%; Score 1000.5; DB 2; Length 250;
Best Local Similarity 78.0%; Pred. No. 1.9e-84;
Matches 192; Conservative 17; Mismatches 28; Indels 9; Gaps 3;
QY 1 EVKLVSQPELKKPGETVKISCKASGYFTNYGMNWKQAPGKGLKMWGINTYTGPTY 60
DB 3 EQLVQSGPELKKPGETVKISCKASGYFTNYGMNWKQAPGKGLKMWGINTYTGPTY 62
QY 61 ADDEKGRFAFSLSTSASTAYLQINLNKEDTATYFCA-----LYGNSPKGFAYWQGTLYT 116
DB 63 AEEFKGRFAFSLSTSASTAYLQINLNKEDTATYFCA-----LYGNSPKGFAYWQGTLYT 118
QY 117 VSAGGGSGGRASGGGSDIOMTOSPKFLVLSAGDRVTITCKASQSVNDVAVYQKPGQ 176
DB 119 VSA-SSSSGSSSSGSSSDIVMTQSPKFMSTSVGDRVSIKASQSDVSTAVAVYQKPGQ 177
QY 177 SPKLLMYANRYTGVPDRFTGSGYGHDTFTTISTVQAEADLAVYFCQDYGSPPTFGGTT 236
DB 178 SPKLLIYWTSTRHTGVDPDRFTGSGGSDTYLTITSSVQAEADLALHYCQOHYRVPYTFGGT 237
QY 237 KLEIKR 242
DB 238 KLEIKR 243

Search completed: July 29, 2004, 08:53:07
Job time : 22.799 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:27 ; Search time 24.3799 Seconds
(without alignments)
982.436 Million cell updates/sec

Title: US-09-661-992B-84
Perfect score: 1317
Sequence: 1 EVQLVESGGGLVPGGSLKL.....FQGSHPVWTFGGGTTKLEIKR 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 23366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	763	57.9	249	2	S41374	single chain Fv an
2	661	50.2	233	2	JC5322	p53 specific singl
3	654.5	49.7	268	2	A56446	Ig heavy chain v r
4	566	43.0	113	2	PJ0203	anti-DNA autoantib
5	562	42.7	219	2	S52028	Ig kappa chain - m
6	560	42.5	131	2	B39276	Ig light chain pre
7	559	42.4	219	2	P04203	Ig kappa chain (mo
8	557	42.3	122	2	E27888	Ig heavy chain v r
9	555	42.1	118	2	P70359	Ig kappa chain v r
10	554	42.1	112	2	A18077	Ig kappa chain v r
11	553	42.0	110	2	S26335	Ig kappa chain v r
12	550	41.8	131	2	B34904	Ig kappa chain pre
13	548	41.6	112	2	S38719	Ig light chain v r
14	547	41.5	114	2	A32967	Ig kappa chain v r
15	546.5	41.5	119	2	E27888	Ig heavy chain v r
16	546	41.5	131	2	C34904	Ig kappa chain pre
17	543	41.2	112	2	B1485	Ig kappa chain v r
18	542	41.2	112	2	F27887	Ig kappa chain v r
19	542	41.2	152	2	B26471	Ig heavy chain v r
20	541	41.1	219	2	S16112	Ig kappa chain v r
21	540	41.0	112	2	A27887	Ig kappa chain v r
22	539	40.9	112	2	A49715	Ig kappa chain v r
23	539	40.9	225	2	JL0029	Ig kappa chain pre
24	538	40.9	114	2	B32967	Ig kappa chain v r
25	537	40.8	112	2	E27887	Ig kappa chain v r
26	537	40.8	112	2	C27887	Ig kappa chain v r
27	535.5	40.7	118	2	PH0097	Ig heavy chain v r
28	534	40.5	131	2	D29380	Ig kappa chain pre
29	532	40.4	112	2	S53750	antibody Fab Jcl 1

30	532	40.4	131	2	B32513	Ig kappa chain pre
31	532	40.4	131	2	B30577	Ig kappa chain pre
32	532	40.4	131	2	S09259	Ig kappa chain pre
33	531	40.3	112	2	S32189	Ig kappa chain v r
34	531	40.3	114	2	A34353	anti-peptide Fab'
35	531	40.3	120	2	S35536	Ig heavy chain v r
36	531	40.3	131	2	D34904	Ig kappa chain pre
37	530.5	40.3	121	2	H27888	Ig heavy chain v r
38	530	40.2	113	2	B41940	Ig light chain v r
39	529.5	40.2	118	2	PH0096	Ig heavy chain v r
40	529	40.2	132	2	PH0106	anti-digoxin trans
41	528.5	40.1	121	2	I27887	Ig heavy chain v r
42	528	40.1	103	2	PH1043	Ig light chain v r
43	528	40.1	112	2	D27887	Ig kappa chain v r
44	527	40.0	112	2	D27887	Ig kappa chain v r
45	527	40.0	115	2	S60066	Ig kappa chain v r

ALIGNMENTS

RESULT 1

S41374
single chain Fv antibody - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995
C:Accession: S41374
R:Artsenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.
A:Description: Construction and functional characterization of a single chain Fv antibody submitted to the EMBL Data Library, January 1994
A:Reference number: S41374
A:Accession: S41374
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-249 <ART>
A:Cross-references: EMBL: Z29480

Query Match 57.9%; Score 763; DB 2; Length 249;
Best Local Similarity 59.8%; Pred. No. 2.5e-47;
Matches 149; Conservative 35; Mismatches 63; Indels 2; Gaps 1;

QY	1	EVQLVESGGGLVPGGSLKLSCAASGFTPTSTMTVMWVROTPKRLWVATISGGGSYTY	60
DB	1	QVQLQQSGAELVPGASVKLSCTASGTFNPKDDYIHVKQRPKGLWFIAPASGNVY	60
QY	61	PDSVRGRTISRDNKNTLYLQMSLSKSDTAMVYCTRDGGHGVGSSPDYWGQTTLTVS	120
DB	61	VRFQDKATITADTSNTAYLLSLTSDTAVVYCAR--RDTLYTSLGVWQGSYTVTS	118
QY	121	SGGGSGGGRASGGGSGQIVLTQSLPLSPVSLGDAQSISCRSSQSIHVSNGNTYLEWYLOK	180
DB	119	SRGGSGGGGGGGGGSDIELTQSPFVVVPGESVSVISCRSSKSLLYSDGDSYLFWFLQR	178
QY	181	PGQSPKLLIYKYNRPSGYPDKFSGSGSTDTLTLSRVEADLGYYVYCFQGSHPVWTFG	240
DB	179	PGQSPQLLIYRNSNLASGVPDRFSGSGSGTSTLTLSRVEADVGYYVYCMQHREYPLTFG	238
QY	241	GGTKLEIKR	249
DB	239	AGTKLEIKR	247

RESULT 2

JC5322
p53 specific single-chain antibody Fab421 - human
C:Species: Homo sapiens (man)
C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: JC5322
R:Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: JC5322; MUID:97168950; PMID:9016757
A:Accession: JC5322

A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hydrioloma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 50.2%; Score 661; DB 2; Length 233;
Best Local Similarity 56.6%; Pred. No. 4.2e-40;
Matches 138; Conservative 26; Mismatches 66; Indels 14; Gaps 4;

QY 6 EGGGLVPGGSLKLSCAASGFTFTSTYMSVRQTPKRLFWATISSGGSYTYPPDSVR 65
DB 2 EGAELVSGASVKLSCTTSFNINDYMHVKKRPEQGLEWIGRIDPENGADMTSSG 61

QY 66 GRFTISRDNAKTYLQWSSLSKSDTAMYYCTRDGGHGYGSSFPYWGQGTTLTVSSGGG 125
DB 62 VKATMTADTSNTAYLQLSLSTSDTAVYYC-----NAGMDYWGQGTTVTVSSGGG 113

QY 126 SGGASGGGGQIVLTQSPSLPVSIGDQASISCRSSQSIHVSNGNTYLEWYLPKQPS 185
DB 114 SGGASGGGGSDIELTQSPASLAVSLGQATISCRASKS-VSTSGYSYMHWNQKPGQPP 172

QY 186 KLLIYKVNRSQVDPKPSGGSGGTDFTLKISRVEADLGVYFCQSHVPP--WTFGGT 243
DB 173 RLLIYLVNLSGVPARFSGSGGTDFTLNIHPVEEDAAITYC---QHIRELTRSEGT 229

QY 244 KLEI 247
DB 230 KLEI 233

RESULT 3
A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C:Species: Mus musculus (house mouse)
C:Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C:Accession: A56446
R:Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A:Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical to the heavy chain of anti-digoxin antibody
A:Reference number: A56446; MUID:95229583; PMID:7713873
A:Accession: A56446
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-268 <TAN>
A:Cross-references: GB:U20617
C:Keywords: heterotetramer; immunoglobulin

Query Match 49.7%; Score 654.5; DB 2; Length 268;
Best Local Similarity 51.4%; Pred. No. 1.4e-39;
Matches 131; Conservative 34; Mismatches 69; Indels 21; Gaps 3;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFTSTYMSVRQTPKRLFWATISSGGSYTY 60
DB 3 QVQLQESGAELVKFGASVKLSCTTSFNINDYMHVKKRPEQGLEWIGRIANGITKY 62

QY 61 PDSVRCGFTISRDNAKTYLQWSSLSKSDTAMYYCTRDGGHGYGSSFPYWGQGTTLTVSSGGG 114
DB 63 DPKFQGRATIAADTSNTAYLQLSLSTSDTAVYYC-----ASYLTRYENTWGQ 113

QY 115 TTLTVSSGGGGSGRAGSGGGSQIVLTQSPSLPVSIGDQASISCRSSQSIHVSNGNTYL 174
DB 114 TTLTVSSGGGGSGGSDGGGSDIELTQSPASLAVSLGQATISCRASKS-VSTSGYSYMHWNQKPGQPP 172

QY 175 EWLQKPGQSPKLLIYKVNRSQVDPKPSGGSGGTDFTLKISRVEADLGVYFCQSHVPP--WTFGGT 243
DB 168 YWYQKQSDASPKLVVYTTSHLPQVPARFSGSGGSGNSYSLTSSMEGEDAATYTCQFTS 227

QY 235 VPWTFGGGTKLEIKR 249
DB 228 SPFTFGSGTKLEIKR 242

RESULT 4

PL0203
anti-DNA autoantibody BV17-31, kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: PL0203
R:Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N. murina
A:Reference number: PL0198; MUID:90309768; PMID:2114528
A:Accession: PL0203
A:Molecule type: mRNA
A:Residues: 1-113 <SMI>
A:Cross-references: GB:X53643; NID:950196; PIDN:CAA37694.1; PID:930142
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-95/Domain: immunoglobulin homology <IMM>
F:24-39/Region: complementarity-determining 1
F:55-61/Region: complementarity-determining 2
F:94-102/Region: complementarity-determining 3
F:101-113/Region: D region

Query Match 43.0%; Score 566; DB 2; Length 113;
Best Local Similarity 95.5%; Pred. No. 1.1e-33;
Matches 107; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 138 IVLTQSPSLPVSIGDQASISCRSSQSIHVSNGNTYLEWYLPKQPSKLLIYKVNRS 197
DB 2 VVMTQTPSLPVSIGDQASISCRSSQSIHVSNGNTYLEWYLPKQPSKLLIYKVNRS 61

QY 198 GVPDKFSGSGGTFTLKISRVEADLGVYFCQSHVPPWTFGGTKLEIKR 249
DB 62 GVPDKFSGSGGTFTLKISRVEADLGVYFCQSHVPPWTFGGTKLEIKR 113

RESULT 5
S52028
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52028
R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994
A:Description: Coordinate expression of antibody subunit genes yields high levels of fun
A:Reference number: S52028
A:Accession: S52028
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <VAN>
A:Cross-references: EMBL:L35138; NID:9522336; PIDN:AAA67525.1; PID:9522337
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 42.7%; Score 562; DB 2; Length 219;
Best Local Similarity 95.5%; Pred. No. 4.3e-33;
Matches 107; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 138 IVLTQSPSLPVSIGDQASISCRSSQSIHVSNGNTYLEWYLPKQPSKLLIYKVNRS 197
DB 2 VVMTQTPSLPVSIGDQASISCRSSQSIHVSNGNTYLEWYLPKQPSKLLIYKVNRS 61

QY 198 GVPDKFSGSGGTFTLKISRVEADLGVYFCQSHVPPWTFGGTKLEIKR 249
DB 62 GVPDKFSGSGGTFTLKISRVEADLGVYFCQSHVPPWTFGGTKLEIKR 113

RESULT 6
B39276
Ig light chain precursor V-D-J region (6-19) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: B39276
R:Reininger, L.; Berney, T.; Shibata, T.; Spertini, F.; Merino, R.; Izui, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 10038-10042, 1990

A;Title: Cryoglobulinemia induced by a murine IgG3 rheumatoid factor: skin vasculitis and
A;Reference number: A39276; MUID:91089540; PMID:2263605
A;Accession: B39276
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-131 <REI>
A;Cross-references: GB:M55313; NID:g198095; PIDN:AAA63385.1; PID:g198096
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;35-114/Domain: immunoglobulin homology <IMM>

Query Match 42.5%; Score 560; DB 2; Length 131;
Best Local Similarity 92.9%; Pred. No. 3.3e-33;
Matches 105; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 136 SOIVLTQSLPLSVSLGDAQSISCRSSQSIHVHSGNTYLEWYLOKPGQSPKLLIYKVSNR 195
Db 19 SDVMTQTPLSLPLSVSLGDAQSISCRSSQSIHVHSGNTYLEWYLOKPGQSPKLLIYKVSNR 78

Qy 196 FSGVPDRFSGSGGTFTLKISRVEAEDLGVYFCQGSHPVPTFGGTTKLEIK 248
Db 79 FSGVPDRFSGSGGTFTLKISRVEAEDLGVYFCQGSHPVPTFGGTTKLEIK 131

RESULT 7
PC4203
Ig kappa chain (monoclonal antibody MAbA34) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C;Accession: PC4203
R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
A;Reference number: PC4202; MUID:97082978; PMID:8964510
A;Accession: PC4203
A;Molecule type: mRNA
A;Residues: 1-219 <KWA>
A;Cross-references: GB:U99147; NID:g1594225; PIDN:AACT52821.1; PID:g1594226
C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>

Query Match 42.4%; Score 559; DB 2; Length 219;
Best Local Similarity 93.8%; Pred. No. 7e-33;
Matches 105; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 138 IVLTQSLPLSVSLGDAQSISCRSSQSIHVHSGNTYLEWYLOKPGQSPKLLIYKVSNRFS 197
Db 2 VMTQTPLSLPLSVSLGDAQSISCRSSQSIHVHSGNTYLEWYLOKPGQSPKLLIYKVSNRFS 61

Qy 198 GVPDRFSGSGGTFTLKISRVEAEDLGVYFCQGSHPVPTFGGTTKLEIKR 249
Db 62 GVPDRFSGSGGTFTLKISRVEAEDLGVYFCQGSHPVPTFGGTTKLEIKR 113

RESULT 8
E27888
Ig heavy chain V region (H35-C6) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C;Accession: E27888
R;Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A;Title: Structural and functional implications of a restricted antibody response to a d
A;Reference number: A91043; MUID:86300658; PMID:2427335
A;Accession: E27888
A;Molecule type: DNA
A;Residues: 1-122 <CAT>
A;Experimental source: strain Balb/c
A;Note: This sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 42.3%; Score 557; DB 2; Length 122;
Best Local Similarity 87.7%; Pred. No. 5e-33;
Matches 107; Conservative 8; Mismatches 5; Indels 2; Gaps 2;

Qy 1 EYQLVESGGGLVKPGSLKLSCAAAGFTFSTYTMGVRQTPKRLWEVATISSGGSYTY 60
Db 1 DVKLVESGGGLVKPGSLKLSCAAAGFTFSTYTMGVRQTPKRLWEVATISSGGSYTY 60

Qy 61 PDSVGRFTISRDNKNTLYLQMSLSKSBEDTANYCTRDG-CHGYGS-SFDYWGQGTTLT 118
Db 61 PDSVGRFTISRDNKNTLYLQMSLSKSBEDTANYCTRDG-CHGYGS-SFDYWGQGTTSVT 120

Qy 119 VS 120
Db 121 VS 122

RESULT 9
PT0359
Ig kappa chain V region (R4A.12) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jan-2000
C;Accession: PT0359
R;Shefner, R.; Kleiner, G.; Turken, A.; Papazian, L.; Diamond, B.
J. Exp. Med. 173, 287-296, 1991
A;Title: A novel class of anti-DNA antibodies identified in BALB/c mice.
A;Reference number: PT0352; MUID:91108325; PMID:1988536
A;Accession: PT0359
A;Molecule type: mRNA
A;Residues: 1-118 <SHE>
A;Experimental source: strain BALB/c
C;Comment: This protein is an anti-double-stranded DNA antibody.
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;19-98/Domain: immunoglobulin homology <IMM>

Query Match 42.1%; Score 555; DB 2; Length 118;
Best Local Similarity 90.4%; Pred. No. 6.7e-33;
Matches 103; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 136 SOIVLTQSLPLSVSLGDAQSISCRSSQSIHVHSGNTYLEWYLOKPGQSPKLLIYKVSNR 195
Db 3 SDVMTQTPLSLPLSVSLGDAQSISCRSSQSIHVHSGNTYLEWYLOKPGQSPKLLIYKVSNR 62

Qy 196 FSGVPDRFSGSGGTFTLKISRVEAEDLGVYFCQGSHPVPTFGGTTKLEIKR 249
Db 63 FSGVPDRFSGSGGTFTLKISRVEAEDLGVYFCQGSHPVPTFGGTTKLEIKR 116

RESULT 10
A31807
Ig kappa chain V region (PAC1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 20-Jul-1989 #sequence_revision 20-Jul-1989 #text_change 21-Jan-2000
C;Accession: A31807
R;Taub, R.; Gould, R.J.; Garsky, V.M.; Ciccarone, T.M.; Hoxie, J.; Friedman, P.A.; Shatt
J. Biol. Chem. 264, 259-265, 1989
A;Title: A monoclonal antibody against the platelet fibrinogen receptor contains a sequ
A;Reference number: A31807; MUID:89079661; PMID:2909518
A;Accession: A31807
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <TAU>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 42.1%; Score 554; DB 2; Length 112;
Best Local Similarity 92.8%; Pred. No. 7.5e-33;
Matches 103; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
S26335
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S26335
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26335
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-110 <ST>
A:CROSS-references: EMBL:X59183; NID:952314; PIDN:CAA41893.1; PID:gl3334062
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
Query Match 42.0%; Score 553; DB 2; Length 110;
Best Local Similarity 94.5%; Pred. No. 8.7e-33;
Matches 103; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 138 IVLTQSPISLPVSLGDSQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 197
Db 2 VLMTQTPLSLPVSLGDSQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
QY 198 GVPDKFSGSGGTDFTLKISRVEAEDLGVIYCFQGSHPVPTFGGTTKLEIK 248
Db 62 GVPDRFSGSGGTDFTLKISRVEAEDLGVIYCFQGSHPVPTFGGTTKLEIK 110
RESULT 12
B34904
Ig kappa chain precursor V region (12-40 and 5-14) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 21-Jul-2000
C:Accession: B34904; H34903
R:Bedzyk, W.D.; Herron, J.N.; Edmundson, A.B.; Voss Jr., E.W.
J. Biol. Chem. 265, 133-138, 1990
A:Title: Active site structure and antigen binding properties of idiotypically cross-rea
A:Reference number: A34903; MUID:90094387; PMID:2104617
A:Accession: B34904
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-131 <BBD>
A:CROSS-references: GB:M32384; GB:J05237; GB:J05238; NID:g639656; PID:9
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:35-114/Domain: immunoglobulin homology <IMM>
Query Match 41.8%; Score 550; DB 2; Length 131;
Best Local Similarity 90.3%; Pred. No. 1.7e-32;
Matches 102; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
QY 136 SQIVLTQSPISLPVSLGDSQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNR 195
Db 19 SDVVMQTPTSLPVSLGDSQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNR 78
QY 196 FSGVPDKFSGSGGTDFTLKISRVEAEDLGVIYCFQGSHPVPTFGGTTKLEIK 248
Db 79 FSGVPDRFSGSGGTDFTLKISRVEAEDLGVIYCFQGSHPVPTFGGTTKLEIK 131

RESULT 13
S38719
Ig light chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S38719
R:Cimanis, A.Y.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38719
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <CIM>
A:CROSS-references: EMBL:X76021; NID:g416112; PIDN:CAA53608.1; PID:gl3334264
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
Query Match 41.6%; Score 548; DB 2; Length 112;
Best Local Similarity 93.7%; Pred. No. 2e-32;
Matches 104; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 138 IVLTQSPISLPVSLGDSQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 197
Db 2 IVMTQTPLSLPVSLGDSQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
QY 198 GVPDKFSGSGGTDFTLKISRVEAEDLGVIYCFQGSHPVPTFGGTTKLEIK 248
Db 62 GVPDRFSGSGGTDFTLKISRVEAEDLGVIYCFQGSHPVPTFGGTTKLEIK 112
RESULT 14
A32967
Ig kappa chain V-II region TE33 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 29-Jan-1990 #sequence_revision 29-Jan-1990 #text_change 21-Jan-2000
C:Accession: A32967
R:Levy, R.; Assulin, O.; Scherf, T.; Levitt, M.; Anglister, J.
Biochemistry 28, 7168-7175, 1989
A:Title: Probing antibody diversity by 2D NMR: comparison of amino acid sequences, predi
A:Reference number: A32967; MUID:90057406; PMID:2819059
A:Accession: A32967
A>Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: mRNA
A:Residues: 1-114 <LEV>
A:CROSS-references: GB:M30481; NID:g197157; PIDN:AAA38935.1; PID:gl97158
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
Query Match 41.5%; Score 547; DB 2; Length 114;
Best Local Similarity 90.2%; Pred. No. 2.4e-32;
Matches 101; Conservative 9; Mismatches 2; Indels 0; Gaps 0;
QY 138 IVLTQSPISLPVSLGDSQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 197
Db 2 VLMTQTPLSLPVSLGDSQASISCRSSQSIIVHSNGNTYLEWYLQKPGQSPKLLIYKVSNRFS 61
QY 198 GVPDKFSGSGGTDFTLKISRVEAEDLGVIYCFQGSHPVPTFGGTTKLEIKR 249
Db 62 GVPDRFSGSGGTDFTLKISRVEAEDLGVIYCFQGSHPVPTFGGTTKLEIKR 113
RESULT 15
F27888
Ig heavy chain V region (H158-89H4) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: F27888
R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference number: A91043; MUID:86300658; PMID:2427335

A;Accession: F27888
A;Molecule type: DNA
A;Residues: 1-119 <CAT>
A;Experimental source: strain Balb/c
A;Note: this sequence was determined from the germline gene
C;Comment: This chain was isolated from a hybridoma protein that binds influenza virus h
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMV>

Query Match 41.5%; Score 546.5; DB 2; Length 119;
Best Local Similarity 87.5%; Pred. No. 2.7e-32;
Matches 105; Conservative 7; Mismatches 7; Indels 1; Gaps 1;

Qy	1	EVQLVESGGGLVPRGGSGLKSCAASGFTFSYTMVSRQTPKRLVWVATISSGGSYTY	60
	:		
Db	1	DVKLVESGGGLVPRGGSGLKSCAASGFTFSYTMVSRQTPKRLVWVATISSGGSYTY	60
	:		
Qy	61	PDSVGRFTISRDNKNTLYLQMSLKSSEDAMYYCTRDGGHGYGSSFDYWGQGTTLTWS	120
	:		
Db	61	PDSVKGFTISRDNKNTLYLQMSLKSSEDAMYYCPR-GETYYDYANDYWGQGTSTVTS	119
	:		

Search completed: July 29, 2004, 08:51:48
Job time : 25.3799 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 16.5783 Seconds
(without alignments)
782.073 Million cell updates/sec

Title: US-09-661-992B-84

Sequence: 1 EVQLVESGGGLVPRGGS LKLT.....FQGSHPVWTFGGGTKLEIKR 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	525	39.9	113	1 KV2G_MOUSE	P01631 mus musculus
2	486	36.9	133	1 KV2F_HUMAN	P06310 homo sapien
3	476	36.1	98	1 HV57_MOUSE	P18528 mus musculus
4	466	35.4	117	1 HV55_MOUSE	P18526 mus musculus
5	463	35.2	117	1 KV2E_HUMAN	P06309 homo sapien
6	462.5	35.1	136	1 HV16_MOUSE	P01783 mus musculus
7	461	35.0	117	1 HV54_MOUSE	P18525 mus musculus
8	461	35.0	117	1 HV58_MOUSE	P18529 mus musculus
9	457.5	34.7	97	1 HV56_MOUSE	P18527 mus musculus
10	452	34.3	113	1 KV2D_HUMAN	P01617 homo sapien
11	441.5	33.5	126	1 HV3K_HUMAN	P01772 homo sapien
12	439	33.3	113	1 KV2B_HUMAN	P01615 homo sapien
13	437	33.2	117	1 HV59_MOUSE	P18530 mus musculus
14	435	33.0	113	1 KV2A_MOUSE	P03976 mus musculus
15	433.5	32.9	115	1 KV2E_MOUSE	P01614 homo sapien
16	430.5	32.7	122	1 HV3G_HUMAN	P01768 homo sapien
17	430	32.6	117	1 HV53_MOUSE	P18524 mus musculus
18	429.5	32.6	112	1 KV2C_HUMAN	P01616 homo sapien
19	424	32.2	121	1 HV3J_HUMAN	P01771 homo sapien
20	419	31.8	113	1 KV2F_HUMAN	P01630 mus musculus
21	416	31.6	112	1 KV2D_MOUSE	P01629 mus musculus
22	415.5	31.5	119	1 HV38_MOUSE	P01808 mus musculus
23	414	31.4	118	1 HV39_MOUSE	P01809 mus musculus
24	410.5	31.2	116	1 HV3T_HUMAN	P01781 homo sapien
25	407.5	30.9	111	1 HV35_MOUSE	P01804 mus musculus
26	407	30.8	117	1 HV3C_HUMAN	P01764 homo sapien
27	405.5	30.8	122	1 HV3A_HUMAN	P01762 homo sapien
28	402.5	30.6	122	1 HV3E_HUMAN	P01769 homo sapien
29	402	30.5	115	1 HV3F_HUMAN	P01767 homo sapien
30	401.5	30.5	119	1 HV37_MOUSE	P01807 mus musculus
31	400.5	30.4	114	1 HV3B_HUMAN	P01763 homo sapien
32	400.5	30.4	134	1 KV4C_HUMAN	P06314 homo sapien
33	400	30.4	144	1 HV26_MOUSE	P01795 mus musculus

34 398 30.2 115 1 HV32_MOUSE P01801 mus musculus
35 398 30.2 117 1 HV02_CANFA P01785 canis famil
36 397 30.1 123 1 HV25_MOUSE P01794 mus musculus
37 395 30.0 117 1 HV41_MOUSE P01811 mus musculus
38 393.5 29.9 116 1 HV05_CARAU P19181 carassius a
39 393 29.8 119 1 HV3I_HUMAN P01770 homo sapien
40 392 29.8 115 1 HV3D_HUMAN P01765 homo sapien
41 391.5 29.7 119 1 HV40_MOUSE P01810 mus musculus
42 391 29.7 113 1 HV27_MOUSE P01796 mus musculus
43 391 29.7 113 1 HV30_MOUSE P01799 mus musculus
44 391 29.7 123 1 HV24_MOUSE P01793 mus musculus
45 390 29.6 115 1 HV33_MOUSE P01802 mus musculus

ALIGNMENTS

RESULT 1
KV2G_MOUSE
ID KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody."
RL Biochemistry 22:1153-1158(1983).
- !- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
CC PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KMS26.
DR HSP; P80382; IWHU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 39.9%; Score 525; DB 1; Length 113;
Best Local Similarity 88.4%; Pred. No. 6.6e-34;
Matches 99; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 138 IYLTQSPALPVS LGDQASISCRSSQSI VHSNGNTYLEWY LKQPGQSKLLIYKVSNRFS 197
Db 2 VVMTQPLSLPVS LGDQASISCRSSQSLVHSNGNTYLNWY LKQAGQSPKLLIYKVSNRFS 61
QY 198 GVPDFESGSGSTDFTLKISRVEADLGVYCFQGSHPVWTFGGGTKLEIKR 249
Db 62 GVPDFRSGSGSTDFTLKISRVEADLGLYFCSTHTVPTFGGGTKLEIKR 113

RESULT 2
KV2F_HUMAN

```
ID KV2F HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1998 (Rel. 06, Created)
DT 01-JAN-1998 (Rel. 06, Last sequence update)
DT 15-JUL-1993 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combracio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
   III."
RL Nucleic Acids Res. 13:6499-6513(1985).
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DR EMBL; Z00020; CAA77315.1; -.
DR PIR; A01890; K2HURP.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009BE CRC64;

Query Match 36.9%; Score 486; DB 1; Length 133;
Best Local Similarity 76.9%; Pred. No. 7.8e-31;
Matches 90; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

QY 133 GGGGQIVLTQPLSLPSVLSGDAQISCRSSQIVHSNGNTLYEMVYLPKQPSKLLIYKV 192
Db 17 GSSGIVVNTQPLSLPVTLGQPASISCRSSQIVSDGNTLYLWVQRPQSPRLIYKV 76

QY 193 SNRSGVPDKFSGSGGTDFTLKSRVAEADLVGYCYFCQSHVPTWFGGQTKLEIKR 249
Db 77 SNRDSGVPDFRSGSGGTDFTLKSRVAEADLVGYCYFCQSHVPTWFGGQTKLEIKR 133

RESULT 3
HV57 MOUSE
ID HV57 MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 6.96.
OS Mus musculus (Mouse).
```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RX STRAIN=BALE/CJ;
RA MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
   the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH1783 SUBFAMILY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; J0501; HVMS96.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;

Query Match 36.1%; Score 476; DB 1; Length 98;
Best Local Similarity 92.9%; Pred. No. 3.2e-30;
Matches 91; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 EVLVESGGGLVKGPGSLKSCAASGFTFTYTWVRQTPKRLWVAISSGGSYTY 60
Db 1 EVLVESGGGLVKGPGSLKSCAASGFTFTYTWVRQTPKRLWVAISSGGSYTY 60

QY 61 PDSVGRFTISRDNKNTLYLQMSLKSEDTAMYCYTR 98
Db 61 PDSVGRFTISRDNKNTLYLQMSLKSEDTAMYCYTR 98

RESULT 4
HV55 MOUSE
ID HV55 MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RX STRAIN=BALE/CJ;
RA MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
   the primary immune response."
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH1783 SUBFAMILY.
DR PIR; J0502; HVMS34.
DR HSSP; P01810; 2FBT.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
```

FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;
Query Match 35.4%; Score 466; DB 1; Length 117;
Best Local Similarity 90.8%; Pred. No. 2.3e-29;
Matches 89; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
QY 1 EVQLVESGGGLVKGPGSLKLSCAASGTFSTFTSWVRQTPPEKLEWVATISSGGSYTY 60
Db 20 EVQLVESGGGLVKGPGSLKLSCAASGTFSTFTSWVRQTPPEKLEWVATISSGGSYTY 79
QY 61 PDSVRGFTISRDAKNTLYLQMSLSKSEDTAMYYCTR 98
Db 80 PDTVKGRFTISRDAKNTLYLQMSLSKSEDTAMYYCAR 117

RESULT 5
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain diversity";
RL Nature 309:73-76 (1984).

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CC -----
CC EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON TER 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 5 27 FRAMEWORK-1.
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 58 FRAMEWORK-2.
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 66 97 FRAMEWORK-3.
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 107 116 FRAMEWORK-4.
FT DISULFID 27 97 BY SIMILARITY.
FT NON TER 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DCY19B558B1 CRC64;
Query Match 35.2%; Score 463; DB 1; Length 117;

Best Local Similarity 76.1%; Pred. No. 4e-29;
Matches 89; Conservative 10; Mismatches 18; Indels 0; Gaps 0;
QY 133 GGSQIVLTQSPFLSLPVSIGLQDOASTSCRSSQSVIVSNNGNTYLEWYLOKPEQSPKLIYKV 192
Db 1 GSGDVIWMTQSPFLSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPEQSPQLIYLG 60
QY 193 SNRFSGVPPKFGSGSGSGTDFTLKISRVEAEDLGVVYCFQGSHPVPTFGGGTKLEIKR 249
Db 61 SNRASGVPPRFGSGSGSGTDFTLKISRVEAEDVGVVYCMQGLQTPQTFGGGTKVETKR 117

RESULT 6
HV16_MOUSE STANDARD; PRT; 136 AA.
ID HV16_MOUSE
AC P01783;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region MOPC 21 precursor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Rothwell A.L.M., Paskind M., Rath M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:623-637 (1981).
RN [2]
RP SEQUENCE OF 17-136.
RX MEDLINE=77100368; PubMed=401950;
RA Adetugbo K., Milstein C., Secher D.S.;
RT "Molecular analysis of spontaneous somatic mutants";
RL Nature 265:299-304 (1977).

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CC -----
CC EMBL; J00522; AAD15290.1; -.
DR PIR; E90809; GIMS21.
DR PDB; 1IGC; 03-JUN-95.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; 3D-structure.
FT NON TER 1
FT SIGNAL <1 16
FT CHAIN 17 136 IG HEAVY CHAIN V REGION MOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HVAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON TER 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDF7016 CRC64;
Query Match 35.1%; Score 462.5; DB 1; Length 136;
Best Local Similarity 73.6%; Pred. No. 5.1e-29;
Matches 89; Conservative 14; Mismatches 17; Indels 1; Gaps 1;

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QY 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFTSYMSWVRQTPKEKLEWVAITSSGGSTYY 60
DB 17 DVQLVESGGGLVQPGGSLKLSCAASGFTFTSFGMHVWRQAPKGLWVAITSSGGSTLHY 76
QY 61 PDSVGRGTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGGHGYGSGFDYWGQGTITLVS 120
DB 77 ADTVKGRGTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGGHGYGSGFDYWGQGTITLVS 135
QY 121 S 121
DB 136 S 136

RESULT 7
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RC STRAIN=BALEB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J70505; HVM584.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 59 68 FRAMEWORK-3.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A69861 CRC64;

Query Match 35.0%; Score 461; DB 1; Length 117;
Best Local Similarity 88.8%; Pred. No. 5.6e-29;
Matches 87; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFTSYMSWVRQTPKEKLEWVAITSSGGSTYY 60
DB 20 EVKLVESGGGLVQPGGSLKLSCAASGFTFTSYMSWVRQTPKEKLEWVAITSSGGSTYY 79
QY 61 PDSVGRGTISRDNKNTLYLQMSLSKSEDTAMTYCTR 98
DB 80 PDSVGRGTISRDNKNTLYLQMSLSKSEDTAMTYCAR 117

RESULT 8
HV58_MOUSE
ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RC STRAIN=BALEB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J70504; HVM591.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.

Query Match 35.0%; Score 461; DB 1; Length 117;
Best Local Similarity 88.8%; Pred. No. 5.6e-29;
Matches 87; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFTSYMSWVRQTPKEKLEWVAITSSGGSTYY 60
DB 20 EVKLVESGGGLVQPGGSLKLSCAASGFTFTSYMSWVRQTPKEKLEWVAITSSGGSTYY 79
QY 61 PDSVGRGTISRDNKNTLYLQMSLSKSEDTAMTYCTR 98
DB 80 PDSVGRGTISRDNKNTLYLQMSLSKSEDTAMTYCAR 117

RESULT 9
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RC STRAIN=BALEB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J70504; HVM591.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.

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DE Ig heavy chain V region 5-76 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RC STRAIN=BALEB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J70505; HVM57.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 59 68 FRAMEWORK-3.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 35.0%; Score 461; DB 1; Length 117;
Best Local Similarity 88.8%; Pred. No. 5.6e-29;
Matches 87; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFTSYMSWVRQTPKEKLEWVAITSSGGSTYY 60
DB 20 EVHLVESGGGLVQPGGSLKLSCVYSGFTFNKYAMSWVRQTPKEKLEWVAITSSGGSTYY 79
QY 61 PDSVGRGTISRDNKNTLYLQMSLSKSEDTAMTYCTR 98
DB 80 PDSVGRGTISRDNKNTLYLQMSLSRSEDAMTYCAR 117

RESULT 9
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RC STRAIN=BALEB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J70504; HVM591.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >97 IG-LIKE.
FT NON_TER 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;
Query Match 34.7%; Score 457.5; DB 1; Length 97;
Best Local Similarity 89.8%; Pred. No. 8.4e-29;
Matches 88; Conservative 6; Mismatches 3; Indels 1; Gaps 1;
QY 1 EVLVESGGGLVRFPGGSLKLSCAASGFTFTYMSWVRQTPKRLKLEWATISSGGSYTY 60
Db 1 EVLVESGGGLVRFPGGSLKLSCAASGFTFTYMSWVRQTPKRLKLEWATISSGGSYTY 60
QY 61 PDSVRGFTTISRDNAKNTLYLQMSLKSEDTAMYCTR 98
Db 60 PDSVKGFTTISRDNAKNTLYLQMSLKSEDTAMYCTR 97
RESULT 10
KV2D HUMAN STANDARD; PRT; 113 AA.
ID KV2D HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=7414840; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
FT Primary amyloidosis.";
RL Biochemistry 12:3763-3780 (1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=7316638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
RT patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281 (1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
DR PIR; A90370; K2HUTW.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; Amyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 123 93 BY SIMILARITY.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;
Query Match 34.3%; Score 452; DB 1; Length 113;
Best Local Similarity 76.8%; Pred. No. 2.7e-28;
Matches 86; Conservative 12; Mismatches 14; Indels 0; Gaps 0;
QY 138 IVLTQSPISLPSVSLGDSQASISCRSSQSIIVHNSNGNTYLEWYLOKPGSQSKLLIYKYSNRFS 197
Db 2 IVLTQSPISLPSVTPPEPASISCRSSQSLHSDGPPYLNWYLOKPGSQSZLLIYALSNRAS 61
QY 198 GVPDFKPSGSGGSDTTLTKISRVEADLGVYYCFQGSHPVFTFGGSKLEIKR 249
Db 62 GVPDFKPSGSGGSDTTLTKISRVEADLGVYYCFQGSHPVFTFGGSKLEIKR 113
RESULT 11
HV3K HUMAN STANDARD; PRT; 126 AA.
ID HV3K HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-III region KOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS
RX MEDLINE=82289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747 (1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391 (1980).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02055; GIHUKL.
DR PDB; 2FB4; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; 3D-structure; Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 IG-LIKE.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT STRAND 29 31
FT HELIX 34 39
FT STRAND 41 42
FT TURN 43 51
FT STRAND 53 54
FT TURN 58 60
FT STRAND 62 64
FT HELIX 65 65
FT STRAND 66 67
FT TURN 68 73
FT STRAND 68 73

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FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT TURN 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 116
FT STRAND 120 124
FT NON TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52E16F8776 CRC64;

Query Match 33.5%; Score 441.5; DB 1; Length 126;
Best Local Similarity 66.7%; Pred. No. 1.9e-27;
Matches 84; Conservative 16; Mismatches 21; Indels 5; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSWRQTPKRLKLVATISSGGSYTY 60
DB 1 QVQLVESGGGVQPGSRLLKSCSSGFISSYMYWVRQAPGKLEWVAIIWDGSDQHY 60
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGGHGVGSF-----DYWGQGT 115
DB 61 ADSVKGRTISRDNKNTLYLQMSLSKSEDTAMYCTRDGGHGVGSF-----DYWGQGT 120
QY 116 TLTVSS 121
DB 121 PVTVSS 126

RESULT 12
KV2B HUMAN
ID KV2B HUMAN STANDARD; PRT; 113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 35, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=76253627; PubMed=821524;
RA Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUFR.
DR HSSP; P01607; 1REI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39B46DB96BE CRC64;

Query Match 33.3%; Score 439; DB 1; Length 113;
Best Local Similarity 84.7%; Pred. No. 3.9e-27;
Matches 83; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSWRQTPKRLKLVATISSGGSYTY 60
DB 20 EVKVVESGGGVKPGGSLKLSCEASGFTFSYNGSWVRQTPKRLKLVASISGGVSYTY 79
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTR 98
DB 80 PDSVGRFTISRDNKNTLYLQMSLSKSEDTALYYCAR 117

RESULT 14
KV2E MOUSE
ID KV2E MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.

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Best Local Similarity 72.3%; Pred. No. 2.6e-27;
Matches 81; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 138 IVLTQSPISLPLSVSLGDSQISCRSSQSIHSGNGTYLWYLOKPGSPKLLIYKVSRRFS 197
DB 2 VVMTQSPFLFVLTGEPASIQCRSSQSLVRYRGTYLWYLOKPGSPKLLIYLSYRDS 61
QY 198 GVPDKFSGSGGTFTLTKISRVEAEDLGVVYCFQGSHPWTFFGGTKLEIKR 249
DB 62 GVPDRFSDSGGTFTLTKITRVAEDGVVYCMQATZSPYTFGGTKLZIKR 113

RESULT 13
HV59 MOUSE
ID HV59 MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 7-39 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J70507; HVMS39.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT DOMAIN 20 49
FT DOMAIN 50 54
FT DOMAIN 55 68
FT DOMAIN 69 85
FT DOMAIN 86 117
FT DISULFID 41 115
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; DSCA4167D0F1774F CRC64;

Query Match 33.2%; Score 437; DB 1; Length 117;
Best Local Similarity 84.7%; Pred. No. 3.9e-27;
Matches 83; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTSTYMSWRQTPKRLKLVATISSGGSYTY 60
DB 20 EVKVVESGGGVKPGGSLKLSCEASGFTFSYNGSWVRQTPKRLKLVASISGGVSYTY 79
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTR 98
DB 80 PDSVGRFTISRDNKNTLYLQMSLSKSEDTALYYCAR 117

RESULT 14
KV2E MOUSE
ID KV2E MOUSE STANDARD; PRT; 113 AA.
AC P03976;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 17S29.1.

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Result No.	Score	Query Match	Length	DB ID	Description
1	100	100	100	1	...
2	95	95	95	2	...
3	90	90	90	3	...
4	85	85	85	4	...
5	80	80	80	5	...
6	75	75	75	6	...
7	70	70	70	7	...
8	65	65	65	8	...
9	60	60	60	9	...
10	55	55	55	10	...
11	50	50	50	11	...
12	45	45	45	12	...
13	40	40	40	13	...
14	35	35	35	14	...
15	30	30	30	15	...
16	25	25	25	16	...
17	20	20	20	17	...
18	15	15	15	18	...
19	10	10	10	19	...
20	5	5	5	20	...

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Db 40 QVKLQSGGGLVPGGSLKLSAASGDFGRYVMSVWRQAPGKLEWIGINPDSSTINY 99
Qy 61 PDSVRGRTTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLTVS 120
Db 100 TPLSKDFILSRDNKNTLYLQMSKYSEDTALYYCARASYGHSA--YWGQGTTLTVS 156
Qy 121 SGGGSGGRASGGGSGGQIVITQSPSLPVLGDAQISCRSSOSIVHSNGNTVLEWYLOK 180
Db 157 SGGGSGGSGGSGGSGGDIETQSPASLSASVGTVTITCRASGNI-----HNYLAWYQOK 211
Qy 181 PGQSPKLLIKVSNRFSGVDPKPSGSGSGDTFTLKISRVEAEDLVGVYCFQGSHVPTWG 240
Db 212 QGKSPQLLVNAKTLADGVSRFSGSGSGCTQYSLKINSLQPEDFGSYCHQFHTTPTWG 271
Qy 241 GGTGLEIKR 249
Db 272 GGTGLEIKR 280

RESULT 2
Q7TQM2
ID Q7TQM2 PRELIMINARY; PRT; 243 AA.
AC Q7TQM2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SCFV 6H8 protein (Fragment).
GN SCFV 6H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Peter J.C., Eftekhari P., Billiald P., Wallukat G.;
RA "scfv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ574851; CA00495.1; -.
FT NON TER 1
SQ SEQUENCE 243 AA; 25976 MW; B5FF64D2DC4F76 CRC64;

Query Match 49.3%; Score 649.5; DB 11; Length 243;
Best Local Similarity 51.8%; Pred. No. 8.9e-45;
Matches 130; Conservative 39; Mismatches 65; Indels 17; Gaps 5;

Qy 1 EVQLVESGGGLVPGGSLKLSAASGFTFTSYTMSVWRQTPKRLKLEWATISSGGSYTY 60
Db 1 QVKLQSGGSLVRFSGSVKLSCKASGYTFDTYGMVWYKQAPGKGLKMWGINTYTGEPY 60
Qy 61 PDSVRGRTTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLTVS 120
Db 61 DEKFNKGLITVDTSSTAYMLSSLASDSAVYYCAR--GGRG---LDVWGAGTTLTVS 115
Qy 121 SGGGSGGRASGGGSGGQIVITQSPSLPVLGDAQISCRSSOSIVHSNGNTVLEWYLOK 180
Db 116 SGGGSGGSGGSGGSGGDIQMTQSSSFVSILGRVITTCASDIYNR-----LAWYQOK 170
Qy 181 PGQSPKLLIKVSNRFSGVDPKPSGSGSGDTFTLKISRVEAEDLVGVYCFQGSHVPTWG 237
Db 171 PGNAFRLISGATLETGVSRFSGSGSGDKDYLLISLTQTEDVATYCCQ-----YWSIR 226
Qy 238 TFGGGLKLEIK 248
Db 227 TFGGGLKLEIK 237

RESULT 3
Q921A6
ID Q921A6 PRELIMINARY; PRT; 241 AA.
AC Q921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.-J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819(1997).
DR EMBL; U88067; AAB48044.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00406; IGV_2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 48.5%; Score 638.5; DB 11; Length 241;
Best Local Similarity 50.6%; Pred. No. 6.9e-44;
Matches 128; Conservative 41; Mismatches 67; Indels 17; Gaps 5;

Qy 1 EVQLVESGGGLVPGGSLKLSAASGFTFTSYTMSVWRQTPKRLKLEWATISSGGSYTY 60
Db 1 QVKLQSGGSLVRFSGSVKLSCKASGYTFDTYGMVWYKQAPGKGLKMWGINTYTGEPY 60
Qy 61 PDSVRGRTTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGCHGYGSSFDYWGQGTTLTVS 120
Db 61 ADDPKGRFAFSLTSSASTAYLIQINNKNEDTATYFCARKOLLRY---FDVWGQGTTLTVS 117
Qy 121 SGGGSGGRASGGGSGGQIVITQSPSLPVLGDAQISCRSSOSIVHSNGNTVLEWYLOK 180
Db 118 SGGGSGGSGGSGGSGGDIETQSPSLASISLGGKVTITCKASQDI-----NKYIAWYQHK 172
Qy 181 PGQSPK---LLIYKVSNRFSGVDPKPSGSGSGDTFTLKISRVEAEDLVGVYCFQGSHV 236
Db 173 PKGFSRATLHIYIQ-----PGIPSRFSGSGSGRDYSGFSISNLEPEDIATYICLHYDNL- 227
Qy 237 WTFGGGTGLEIKR 249
Db 228 HTFGGGLKLEIKR 240

RESULT 4
Q925S1
ID Q925S1 PRELIMINARY; PRT; 218 AA.
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRP5 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/C;
RX PubMed=11819679;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]

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RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1;
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
FT NON TER 218 218
SQ SEQUENCE 218 AA; 527B4FA8F7982817 CRC64;

Query Match 45.0%; Score 592; DB 11; Length 218;
Best Local Similarity 53.4%; Pred. No. 3.5e-40;
Matches 119; Conservative 37; Mismatches 57; Indels 10; Gaps 3;

QY 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFSYTWVRQTPPEKLEWVAITSGGSYYT 60
Db 3 QVQLQQSGPELKKPGEIVRISCKASGYFTTAGHWVKQPKGKLGKIGWINTHSGVPKY 62

QY 61 PDVVRGRTISRDNANKNTLYLQMSLSKSEDTAMYCYTRD-GGHGVG--SSFDYWGQGTTL 117
Db 63 AEEFKGRFAFSLSTSASTAVYQIGNLKNEDATYFCMRWDYDGG-----FAYWGQGTTV 116

QY 118 TVSSGGGGGGRASGGGSGQIVLTQSPSLPVS-LGDQASISCRSSQSIIVHS---NGNTY 173
Db 117 TVSSGGGGGGRASGGGSGDVLVLTQSPASLAVSIQGRATISCRASES-VDNIGISFMNWF 175

QY 178 LQKPGQPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVE 220
Db 176 QKQFGQPKLLIYAASQSGVPGAGLLASGSGTDFSLNIYPME 218

RESULT 5
Q99KA4 PRELIMINARY; PRT; 487 AA.
ID Q99KA4
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC004786; AA04786.1; -.
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.
DR PIR; C32248; C32248.
DR PIR; F32530; F32530.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
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DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
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Db      19 SDVWMTQPLSLPVSGLGQASISCRSSQSIHVSNGNTYLEWYLOKPGSPKLLIYKVSNR 78
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RESULT 7
Q920E7 PRELIMINARY; PRT; 119 AA.
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DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope heavy chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the idiotope of Pterin-Mimicking Antibodies Expressed
RT in Mammalian Cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF307937; AAL09421.1; -.
DR PIR; C25913; C25913.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 119
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Query Match 41.0%; Score 540; DB 11; Length 119;
Best Local Similarity 86.0%; Pred. No. 2.7e-36;
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Db 1 EVQLVESGDLVKGSLKLSCAASGTFSSYGNVWRQPKRLWVAIISGGSYTY 60
QY 61 PDSVGRGRTISRDNKNTLYLQMSLSKSEDTAMTYCTRQGHGYSYFDYWGQGLTLTVS 120
Db 61 PDSVKGRTISRDNKNTLYLQMSLSKSEDTAMTYCARHGDYDVG--FAYWGQGLTLTVS 118
QY 121 S 121
Db 119 A 119

RESULT 8
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AC Q9VC16;
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DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Colon;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC019760; AAH19760.1; -.
DR PIR; A27887; A27887.

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KW Hypothetical protein.
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Query Match 41.0%; Score 540; DB 11; Length 238;
Best Local Similarity 89.5%; Pred. No. 6.4e-36;
Matches 102; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 136 SQIVTQPLSLPVSGLGQASISCRSSQSIHVSNGNTYLEWYLOKPGSPKLLIYKVSNR 195
Db 19 SDVWMTQPLSLPVSGLGQASISCRSSQSLVHSNGNTYHMYLOKPGSPKLLIYKVSNR 78
QY 196 FSGVDPKESGSGGTDFTLKISRVEADLGVYCFQGSHPVWTFGGTKLEIKR 249
Db 79 FSGVDPKESGSGGTDFTLKISRVEADLGVYCFQGSHPVWTFGGTKLEIKR 132

RESULT 9
Q8VC55 PRELIMINARY; PRT; 239 AA.
AC Q8VC55;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Colon;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC021781; AAH21781.1; -.
DR PIR; A33933; A33933.
DR PDB; 1KC5; 24-JUL-02.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.

```


ID	Q91Z07	PRELIMINARY;	PRT;	486 AA.
AC	Q91Z07;			
DT	01-DEC-2001	(TrEMBLrel. 19, Created)		
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE		Hypothetical protein.		
OS		Mus musculus (Mouse).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX		NCBI_TaxID=10090;		
RN		[1]		
RP		SEQUENCE FROM N.A.		
EA		Strausberg R.;		
RL		Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL;	BC010324; AAH10324.1; -		
DR	InterPro;	IPR007110; Ig_LIKE.		
DR	InterPro;	IPR003006; Ig_MHC.		
DR	InterPro;	IPR003596; Ig_v.		
DR	Pfam;	PF00047; Ig; 4.		
DR	SMART;	SM00406; IGv; 1.		
DR	PROSITE;	PS00835; IG_LIKE; 4.		
DR	PROSITE;	PS00290; IG_MHC; 2.		
KW		Hypothetical protein.		
SK		SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;		
Query Match 38.3%; Score 505; DB 11; Length 486;				
BestLocal Similarity 50.08; Pred.No. 1.1e-32;				
Matches 121; Conservative 22; Mismatches 55; Indels 44; Gaps 3;				
Qy	1	EVQLVESGGGLVPGGSLKSCAAAGFTFSYITMSWVRQTPKRLKRWVATISGGSYTY 60		
Db	20	EVHLVESGGGLVPGGSLKSCVVSFGSFTSDMSWVRQTPERRLEWVAATISGNN-TYY 78		
Qy	61	PDSVRGHFTISRDNKNTLYLQWSSLKSEDTAMYYCTRDGGHG- --GSSFDYWGQGTLL 117		
Db	79	PDNVKGFHTSRDNKNTLYLQWSSLKSEDTAMYYCVRPIPIYYSGSYFDSWGQGTII 138		
Qy	118	TVSSGGGSGGRASGGGSGIVLTQSPSLSPVSL-GDQASISCRSSOSIVHS---NGNTY 173		
Db	139	TVSSESARNP-----TIYPLTLPRALSSDPVIIGC-----LIHDYFPSPGTMN 180		
Qy	174	LEWYLPQGQSPKLLIYKVNRRSGVPDKFSGSGSGTGDTFLKISRVEADLGVIYCFQGS 233		
Db	181	VTW-----GKSGKDI-----TTVNFPPALASGGGYTSSQLTLPAVE-----CPEGE 222		
Qy	234	HV 235		
Db	223	SV 224		
RESULT 12				
Q91WP5		PRELIMINARY;	PRT;	479 AA.
ID	Q91WP5			
AC	Q91WP5;			
DT	01-DEC-2001	(TrEMBLrel. 19, Created)		
DT	01-DEC-2001	(TrEMBLrel. 19, Last sequence update)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)		
DE		Hypothetical protein.		
OS		Mus musculus (Mouse).		
OC		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX		NCBI_TaxID=10090;		
RN		[1]		
RP		SEQUENCE FROM N.A.		
RC		TISSUE=Colon;		
RA		Strausberg R.;		
RL		Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL;	BC013656; AAH13656.1; -		
DR	InterPro;	IPR007110; Ig_LIKE.		
DR	InterPro;	IPR003006; Ig_MHC.		
DR	InterPro;	IPR003596; Ig_v.		
DR	Pfam;	PF00047; Ig; 4.		
DR	SMART;	SM00406; IGv; 1.		

DR PROSITE; PS00835; IG LIKE; 4.
KW PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein_182
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 36.6%; Score 482.5; DB 11; Length 479;
Best Local Similarity 55.3%; Pred. No. 7.1e-31;
Matches 105; Conservative 16; Mismatches 36; Indels 33; Gaps 6;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYVMSWVRQTEKLEWVATISSGGSYTY 60
DB 20 EVQLVESGGGLVPGGSLKLSVCAASGLTFSYVMSWVRQTEKLEWVATISSGGSYTY 79
QY 61 PDSVGRFTISRDNAKNTLYLQMSLKSEDATAMYYCTRDGGHGYGSSPDYWGQGTTLTVS 120
DB 80 SDTMKGRFTISRDNAKNTLYLQMSLKSEDATAFYICVR-----GGYEDVWAGTAVTVS 133
QY 121 SGSGSGGPRASGGGSGQIVLTQSPSLPVSL-GDQASISCRSSQSIHVS---NGNTYLEW 176
DB 134 SEFAREP-----TIYPLTFFQALSSDPVITGC-----LIHDYFPGGMNVTW 175
QY 177 YLQKPGQSPK 186
DB 176 -----GKSGK 180

RESULT 13
QY1205 PRELIMINARY; PRT; 473 AA.
AC Q91205; (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -
DR MGD; MGI:2144967; AU044919.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR00345; CytC_heme_BS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME C; 1.
DR PROSITE; PS00835; IG LIKE; 4.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CPG25F008932AF12 CRC64;

Query Match 36.1%; Score 475.5; DB 11; Length 473;
Best Local Similarity 48.2%; Pred. No. 2.6e-30;
Matches 109; Conservative 23; Mismatches 43; Indels 51; Gaps 6;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYVMSWVRQTEKLEWVATISSGGSYTY 60
DB 20 EVQLVESGGGLVPGGSLKLSVCAASGFTFSYVMSWVRQTEKLEWVATISSGGSYTY 79
QY 61 PDSVGRFTISRDNAKNTLYLQMSLKSEDATAMYYCTRDGGHGYGSSPDYWGQGTTLTVS 120
DB 80 SDTMKGRFTISRDNAKNTLYLQMSLKSEDATAFYICVR-----GGYEDVWAGTAVTVS 136
QY 121 S-----GGGSGGGR-----SGGSGSQI-----VLITQS 143

Db 137 SAKTTPSYVPLAPGCGDTTGSSTVLGCLVKGYPFESVTVTWNSGLSSSVHTFPALLOS 196
QY 144 PL-----SLPVSLGDQASISCRSSQSIHVSNGNTYLEWYLQKPG 182
DB 197 GLYTMSSSVTFSSWPSQTVC-----SVAHPASSTTVDKLEPSG 238

RESULT 14
Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0; (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -
DR PIR; S34095; S34095.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match 35.9%; Score 473; DB 4; Length 239;
Best Local Similarity 75.2%; Pred. No. 1.7e-30;
Matches 88; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 133 GGSQIVLTQSPSLFVSLGDAQSISCRSSQSIHVSNGNTYLEWYLQKPGSPKLLIYKV 192
DB 17 GSSGDVMTQSPSLFVTLGQPASISCRSTQSLVSDGNTYLNWFOQRPGSPRLIYKV 76
QY 193 SNRFGVPDKFSGSGSGTDFTLKISRVEAEDLGVVYCCPGSHVPTFGGTGLEIKR 249
DB 77 SNRDSGVPDRFSGSGSGTDFTLKISRVEAEDGVVYFCMGQTHWPTFGGTGLEIKR 133

RESULT 15
Q91XE1 PRELIMINARY; PRT; 480 AA.
AC Q91XE1; (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE Hypothetical protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010798; AAH10798.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 4.

Thu Jul 29 11:08:05 2004

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DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 2.
DR Hypothetical protein.
FT NON TER
SQ SEQUENCE      480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Query Match          35.9%; Score 472.5; DB 11; Length 480;
Best local similarity 55.3%; Fred. No. 4.6e-30;
Matches 105; Conservative 20; Mismatches 34; Indels 31; Gaps 7;

QY      1 EVLVESGGGLVFPGGSKLSCAASGTFSTYTMSWVRQTPEKLELVAATISSGGSYTY 60
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      19 DVLVESGGGLVFPGGSRLRSCAASGFIFNSYMSWRQTPEKLELVAATISSGYATHY 78

QY      61 PDSVRGRFTISRDNAKNTLYLQSSLSKSEBTAMYCTRDGCHGVGSSFDFWQGQTTLTVS 120
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      79 PDSMKGRFTISRDNAQNVTLLQMTSLNSEATAVYICTR-GDYWY---FDYMGAGTTTIVS 134

QY      121 SGCGGGSGRASGGGGSIVLTQTGPLSPVSL-GDQASISCRSSQSIVHS---NGNITYLEW 176
       :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      135 SEPAREP-----TIPLTPFOALSDPDVILGC-----LIHDYFPSTGMNVTW 176

QY      177 YLOKPQQSPK 186
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Db      177 -----GKSGK 181

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Search completed: July 29, 2004, 08:50:23
Job time : 52.3851 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 76.7154 Seconds
(without alignments) 917.082 Million cell updates/sec

Title: US-09-661-992B-84
 Perfect score: 1317
 Sequence: 1 EVOLVESSGGIVKPGGSLKL.....FQGSHPVPTFGGTYKLEIKR 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Database :
A_Geneseq_29Jan04.*
1: Genesep1980s.*
2: Genesep1990s.*
3: Genesep2000s.*
4: Genesep2001s.*
5: Genesep2002s.*
6: Genesep2003as.*
7: Genesep2003bs.*
8: Genesep2004s.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	length			
1	1317	100.0	249	4	AAB20434	Aab20434 Anti-Fix/
2	1072	81.4	247	2	AAR32091	Aar32091 H and L c
3	1072	81.4	249	2	AAR32090	Aar32090 H and L c
4	1072	81.4	249	2	AAR95213	Aar95213 Heavy and
5	1029	78.1	249	2	AAR21262	Aar21262 pscFvNq1.1
6	994.5	75.5	233	2	AAR93013	Aar93013 Lewis-Y a
7	989	75.1	281	2	AAR27560	Aar27560 Consensus
8	985	74.8	253	2	AAR72599	Aar72599 Anti-Fix/
9	982	74.6	249	4	AAB20436	Aab20436 Anti-Fix/
10	976	74.1	268	2	AAY08983	Aay08983 SCFv4155
11	976	74.1	408	2	AAY08990	Aay08990 Llama pro
12	976	74.1	409	2	AAY08989	Aay08989 Llama pro
13	975	74.0	234	4	AAB20442	Aab20442 Anti-Fix/
14	975	74.0	732	4	AAB20437	Aab20437 Anti-Fix/
15	971	73.7	325	4	AAB20438	Aab20438 Anti-Fix/
16	970.5	73.7	262	5	ABP46070	Abp46070 Human Bly
17	963	73.1	249	4	AAB20435	Anti-Fix/
18	960.5	72.9	244	5	ABP45980	Abp45980 Human Bly
19	949.5	72.1	573	4	AAG64459	Aag64459 Mouse 6D9
20	946.5	71.9	252	4	AAU07497	Synthetic
21	942.5	71.6	247	5	AAU90900	Insulin/i
22	937	71.1	249	1	AAAP80154	Aap80154 Biosynthe
23	937	71.1	289	2	AAY06132	Monoclonal
24	937	71.1	289	4	AAM50158	Type II c
25	935.5	71.0	269	4	AAM50158	Type II c
26	935.5	71.0	269	4	AAB61541	3DX sfv p

ALIGNMENTS

RESULT 1

AAB20434
ID AAB20434 standard: protein: 249 AA.

AA
AC

DT 21-JUN-2001 (first entry)

Anti-FIX/FIXa antibody 193/K2 scFv.

Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
 Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

OS Mus musculus.

OS Synthetic.

os chimeric.

FH	Key	Location/Qualifiers
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FT	Protein	1. .121

FT /label=

FT	Region	98.	.110

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120  /label= Link
121  /label= Link
122  /label= Link

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Protein 136: .249

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      / LABEL= VL
      230  238
      position
      238  238

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region
230.: 238
/label = CDR3

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XXIX

AA PN W0200119992-A2.

XX
XX
FROM
TO
DATE

PD 22-MAR-2001.

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PF	13-SEP-2000; 2000WO-EF008936.
XX	
PR	14-SEP-1999; 99AT-00001576.
XX	
FA	(BAXT) BAXTER AG.
XX	
PI	Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;
XX	
XX	
DR	WPI: 2001-290358/30.
DR	N-PSDB; AAF30724.
XX	
PT	New factor IX/factor IXa antibodies and their derivatives useful for
PT	increasing amidolytic activity of factor IXa, and for treating blood
PT	coagulation disorders such as hemophilia A and hemorrhagic diathesis
PT	

XX PS Claim 10; Fig 15; 138pp; English.

XX CC The present sequence is that of a single chain Fv (scFv) derivative of

CC antibody 193/K2, comprising the heavy (VH) and light (VL) chain variable

CC regions of 193/K2 joined by an artificial, flexible linker peptide. The

CC scFv was obtained by PCR amplification of cDNAs for 193/K2 VH and VL

CC regions and cloning in vector pDAP2. 193/K2 is an example of anti-human

CC Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.

CC Anti-FIX/FIXa and their derivatives, including scFv and CDR3 fragments,

CC have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity.

CC Administration leads to an increase in the procoagulant activity of FIXa,

CC even in the presence of FVIIIa inhibitors. This allows for rapid blood

CC coagulation even in the absence of FVIII or FVIIIa, and in the case of

CC FVIII inhibitor patients. The antibodies and derivatives are used in a

CC claimed pharmaceutical composition for treating patients with blood

CC coagulation disorders, especially haemophilia A and haemorrhagic

CC diathesis

XX CC

SQ Sequence 249 AA;

Query Match 100.0%; Score 1317; DB 4; Length 249;

Best Local Similarity 100.0%; Pred. No. 2.3e-86;

Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFTSTYMSWVRQTPKRLWVAITSSGGSVYY 60

DB 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFTSTYMSWVRQTPKRLWVAITSSGGSVYY 60

QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSDTAMTYCTRDGGHGVGSSFDYWGQTTLTVS 120

DB 61 PDSVGRFTISRDNKNTLYLQMSLSKSDTAMTYCTRDGGHGVGSSFDYWGQTTLTVS 120

QY 121 SGGGSGGGRASGGGSGQIVLTQSPSLFVSLGDAQISCRSSQIVHSNGNTYLEWTLQK 180

DB 121 SGGGSGGGRASGGGSGQIVLTQSPSLFVSLGDAQISCRSSQIVHSNGNTYLEWTLQK 180

QY 181 PQSPKLLIYKVNRFSGVPDKFSTGTFTTYSWVRQTPKRLWVAITSSGGSVYY 240

DB 181 PQSPKLLIYKVNRFSGVPDKFSTGTFTTYSWVRQTPKRLWVAITSSGGSVYY 240

QY 241 GGTGLEIKR 249

DB 241 GGTGLEIKR 249

RESULT 2

AAR32091

ID AAR32091 standard; protein; 247 AA.

XX AC AAR32091;

XX DT 25-MAR-2003 (revised)

XX DT 17-DEC-2001 (revised)

XX DT 08-JUN-1993 (first entry)

XX DE H and L chain Fv region from mAb B3.

XX immunotoxin; monoclonal antibody; cancer; tumour; neoplasm;

KW tumour regression; anti-tumour agent; anti-cancer agent; carcinoma.

XX OS Mus musculus.

XX FH Key Location/Qualifiers

FT Region 1..120

FT /label= Fv H chain

FT Region 121..135

FT /label= linker

FT Region 136..247

FT /label= Fv light chain

XX USN767331-N.

PD 15-DEC-1992.

XX PF 30-SEP-1991; 91US-00767331.

XX PR 12-OCT-1990; 90US-00576289.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICE.

XX PI Pastan I, Willingham M, Fitzgerald D, Brinkmann U, Pai L;

XX WPI; 1993-058410/07.

XX N-PSDB; AAQ35955.

XX New recombinant immuno:toxin(s) B3(FV)-PB40 and B3(FV)-PB38 KDEL - used

PT in treatment of mammalian cancer, giving rapid tumour regression using

PT only small amt. of immuno:toxin.

XX PS Disclosure; Fig 2; 25pp; English.

XX CC This sequence represents the heavy and light chain Fv region of murine

CC mAb B3. The first amino acid encoded by the cloned heavy chain Fv gene is

CC Asp instead of Glu due to the primer used - at nucleotide posn. 456-465

CC is the region where the PCR cloning artifact was repaired. The coding

CC sequence encodes the same amino acids as the original B3 L chain

CC (AAQ35954) but uses other codons (see AAQ35955). The MAb recognises an

CC antigen present on many carcinoma cells and may be useful for the

CC treatment of various types of cancer. The heavy and light chain regions

CC are connected by a flexible linker (Gly4Ser)3. The coding gene can also

CC be fused to sequences encoding two different truncated forms of the PE

CC molecule to obtain single chain B3(Fv) immunotoxins. (Note: Revised entry

CC submitted to correct the patent number format of US Government-owned NTIS

CC applications to prevent clashes with ongoing US granted patent numbers.

CC For further information please visit the Derwent web site at

CC www.derwent.com/awpi/updates/ntis_us.html.) (Updated on 25-MAR-2003 to

CC correct PF field.)

XX SQ Sequence 247 AA;

Query Match 81.4%; Score 1072; DB 2; Length 247;

Best Local Similarity 83.1%; Pred. No. 7.3e-69;

Matches 206; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFTSTYMSWVRQTPKRLWVAITSSGGSVYY 60

DB 2 DVKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYVVRQTPKRLWVAITSSGGSVYY 61

QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSDTAMTYCTRDGGHGVGSSFDYWGQTTLTVS 120

DB 62 SDTVKGRFTISRDNKNTLYLQMSLSKSDTAMTYCTRDGGHGVGSSFDYWGQTTLTVS 119

QY 121 SGGGSGGGRASGGGSGQIVLTQSPSLFVSLGDAQISCRSSQIVHSNGNTYLEWTLQK 180

DB 120 SGGGSGGGRASGGGSGQIVLTQSPSLFVSLGDAQISCRSSQIVHSNGNTYLEWTLQK 179

QY 181 PQSPKLLIYKVNRFSGVPDKFSTGTFTTYSWVRQTPKRLWVAITSSGGSVYY 240

DB 180 PQSPKLLIYKVNRFSGVPDKFSTGTFTTYSWVRQTPKRLWVAITSSGGSVYY 239

QY 241 GGTGLEIKR 248

DB 240 GGTGLEIKR 247

RESULT 3

AAR32090

ID AAR32090 standard; protein; 249 AA.

XX AC AAR32090;

XX DT 25-MAR-2003 (revised)

XX DT 17-DEC-2001 (revised)

XX DT 08-JUN-1993 (first entry)

XX

DE H and L chain Fv region from mAb B3.
 XX immunotoxin; monoclonal antibody; cancer; tumour; neoplasm;
 KW tumour regression; anti-tumour agent; anti-cancer agent; carcinoma.
 XX OS Mus musculus.
 XX FH Key Location/Qualifiers
 FT Region 1. .120
 FT /label= Fv H chain
 FT Region 121. .135
 FT /label= linker
 FT Region 136. .249
 FT /label= Fv light chain
 XX USN7767331-N.
 XX 15-DEC-1992.
 XX 30-SEP-1991; 91US-00767331.
 XX 12-OCT-1990; 90US-00576289.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICE.
 XX Pastan I, Willingham M, Fitzgerald D, Brinkmann U, Pai L;
 PI WPI; 1993-058410/07.
 DR N-PSDB; AAQ35954.
 XX New recombinant immunotoxin(s) B3(FV)-PE40 and B3(FV)-PE38 KBEL - used
 FT in treatment of mammalian cancer, giving rapid tumour regression using
 PT only small amt. of immuno:toxin.
 XX Disclosure; Fig 2; 25pp; English.
 XX This sequence represents the heavy and light chain Fv region of murine
 CC MAB B3. The first amino acid encoded by the cloned heavy chain Fv gene is
 CC Asp instead of Glu due to the primer used - at nucleotide posn. 456-465
 CC is the region where the PCR cloning artifact was repaired. The MAB
 CC recognises an antigen present on any carcinoma cells and may be useful
 CC for the treatment of various types of cancer. The heavy and light chain
 CC regions are connected by a flexible linker (Gly4Ser)3. The coding gene
 CC can also be fused to sequences encoding two different truncated forms of
 CC the PE molecule to obtain single chain B3(Fv) immunotoxins. (Note:
 CC Revised entry submitted to correct the patent number format of US
 CC Government-owned NTIS applications to prevent clashes with ongoing US
 CC granted patent numbers. For further information please visit the Derwent
 CC web site at www.derwent.com/dwpi/updates/ntis_us.html.) (Updated on 25-
 CC MAR-2003 to correct PF field.)
 XX SQ Sequence 249 AA;
 Query Match 81.4%; Score 1072; DB 2; Length 249;
 Best Local Similarity 83.1%; Pred. No. 7.4e-69;
 Matches 206; Conservative 16; Mismatches 24; Indels 2; Gaps 1;
 QY 1 EVQLVESGGGLVPGGSLKLCASAGFTFFSYTWVSRVQTPEKLEWVAITSSGGSTYY 60
 Db 2 DVKLVESGGGLVPGGSLKLCASAGFTFFSYTWVSRVQTPEKLEWVAITSSGGSTYY 61
 QY 61 PDSVGRFTISRDAKNTLYIQMPSLKSEDTAMYYCTRDGCHGYSFDPYWGQGTTLTVS 120
 Db 62 SDTVKGRFTISRDAKNTLYIQMPSLKSEDTAMYYCTRDGCHGYSFDPYWGQGTTLTVS 119
 QY 121 SGGSGSGRAGSGGSGIVLTQSPSLFVSLGDSQASISCRSSQIVHSNGNTYLEWYLQK 180
 Db 120 SGGSGSGGSGGSGGSDVLTQSPSLFVSLGDSQASISCRSSQIVHSNGNTYLEWYLQK 179
 QY 181 FCQSPKLLIYKSNRFGVPDPKPSGSGSGTFTLKISRVEAEDLGVYFCQGSHPVTFG 240
 Db 180 FCQSPKLLIYKSNRFGVPDPKPSGSGSGTFTLKISRVEAEDLGVYFCQGSHPVTFG 239

QY 241 GGTGLEIK 248
 Db 240 SGTGLEIK 247
 RESULT 4
 AAR95213
 ID AAR95213 standard; protein; 249 AA.
 XX AAR95213;
 AC AAR95213;
 XX 16-DEC-1996 (first entry)
 DT Heavy and light chain Fv region of monoclonal antibody B3.
 XX Antibody; fusion protein; single chain; inhibition; tumour; diagnosis;
 KW detection; imaging; immunotoxin; targeting; assay; immunoassay;
 KW Lewis(Y) carbohydrate antigen.
 XX Mus musculus.
 XX Key Location/Qualifiers
 FT Region 2. .119
 FT /label= Fv Heavy chain.
 FT Region 120. .135
 FT /label= Linker.
 FT Region 136. .249
 FT /label= Fv light chain.
 XX WO9613594-A1.
 XX 09-MAY-1996.
 XX 26-OCT-1995; 95WO-US013811.
 XX 28-OCT-1994; 94US-00331396.
 PR 28-OCT-1994; 94US-00331397.
 PR 28-OCT-1994; 94US-00331398.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Pastan I, Benhar I, Padlan EA, Jung S, Lee B, Willingham M;
 PI Fitzgerald D, Brinkmann U, Pai L;
 DR WPI; 1996-251462/25.
 DR N-PSDB; AAT27991.
 XX Single chain fusion proteins and antibodies - useful to diagnose and
 PT treat cancer, specifically bind Lewis(Y) related carbohydrate antigen.
 XX Disclosure; Fig 2; 116pp; English.
 XX A novel recombinant DNA molecule which encodes a single chain fusion
 CC protein or antibody comprising the Fv region of both the light and heavy
 CC chains of an antibody (Ab) fused together, and an effector molecule,
 CC where the fusion protein or Ab has the binding specificity of monoclonal
 CC Ab (MAB) B1, B3 or B5, can be used for the production of such fusion
 CC proteins or antibodies. The fusion proteins can be used in compositions
 CC as an immunotoxin to inhibit tumour cell growth. The single chain
 CC antibody can be used to detect the presence or absence of cells bearing a
 CC Lewis(Y) carbohydrate antigen in a patient. The antibodies are also
 CC useful as multiple targeting moieties, providing at least 2 kinds of
 CC biological activity. They can also be used in diagnostic assays and for
 CC the imaging of tumours when attached to a radiolabel and for the
 CC pathological diagnosis of tumours. Humanised antibodies are less
 CC immunogenic than the mouse MABs B1, B3 and B5, making them more suitable
 CC for long term treatment
 XX SQ Sequence 249 AA;
 Query Match 81.4%; Score 1072; DB 2; Length 249;
 Best Local Similarity 83.1%; Pred. No. 7.4e-69;
 Matches 206; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

QY	1	EVOLVESGGGLVYPGGSILKLSCAASGFTFSTYTHSWVROTPPKRLEWVAIISGGSYTY	60
Db	2	DYKLVESGGGLVQPGGSLKLSCATSGFTFSDYYMYVYRQTPKRLEWVAIISNDDSSAA	61
QY	61	PDSVGRFTIISRDNAKNTLYIQMSSLKSEDTAMYYCTRDGCHGYGSSFDYWGQTTLTVS	120
Db	62	STTVKGRFTIISRDNAKNTLYIQMSELKSEDTAIVSCAR--GLAWGAFVAWGQTTLTVS	119
QY	121	SGGGSGGGRASGGGSGQIVLTQSPSLPVSIGDQASISCRSSQSIIVHSNGNTYLEWYLOK	180
Db	120	SGGGSGGGSGGGSGGSDVLTQSPSLPVSIGDQASISCRSSQSIIVHSNGNTYLEWYLOK	179
QY	181	PGQSPKLLIYKVSNSFGVPDKFSCSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFG	240
Db	180	PGQSPKLLIYKVSNSRFGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCFQGSHPVPTFG	239
QY	241	GGTKLEIK 248	
Db	240	SGTKLEIK 247	
RESULT 5			
AAR21262			
ID	AAR21262	standard; protein; 249 AA.	
XX	AAR21262;		
XX			
DT	21-MAY-1992	(first entry)	
XX			
XX		pscFYNQ11 encoding anti-oxazalone antibody.	
KW	Pd; bacteriophage; gene III; filamentous; phagemid; capsid; coat; pilus;		
KW	G3p; binding; adsorption; gene VIII; diverse repertoire;		
KW	specific binding pairs; replicable genetic display package;		
KW	immunoglobulin; ss.		
XX			
OS	Synthetic.		
XX			
Key		Location/Qualifiers	
FT	Protein	1..118	
FT		/label= VH	
FT	Peptide	119..138	
FT		/label= linker	
FT	Protein	139..249	
FT		/label= VL	
XX			
PN	W09201047-A.		
XX			
PD	23-JAN-1992.		
XX			
XX	10-JUL-1990;	90GB-00015198.	
XX			
PR	10-JUL-1990;	90GB-00015198.	
PR	19-OCT-1990;	90GB-00022845.	
PR	12-NOV-1990;	90GB-00024503.	
PR	06-MAR-1991;	91GB-00004744.	
PR	15-MAY-1991;	91GB-00010549.	
XX			
PA	{CAMB-}	CAMBRIDGE ANTIBODY TECHNOLOGY.	
PA	{MEDI-}	MED RES COUNCIL.	
PI	McCafferty J, Pope AR, Johnson KS, Hoogenboom HRJ, Griffiths AD;		
PI	Jackson RH, Holliger KP, Marks JD;		
XX			
DR	WPI; 1992-056862/07.		
DR	N-PSDB; AAQ21098.		
XX			
XX			
PT	Producing members of specific binding pairs - by expression in		
PT	recombinant host cells with a secreting replicable genetic display		
PT	package.		
XX			
XX	Example 9; Fig 13; 209pp; English.		


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PA (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Yelton D, Glaser S, Huse W, Rosok MJ;
XX
XX WPI; 1996-129723/14.
XX
XX N-PSDB; AAT16700.
XX
XX Mutant complementarity determining region BR96 poly:peptide(s) - having
XX amino acid changes to improve affinity binding, used for detection and
XX therapy of tumours and cancers.
XX
XX Disclosure; Fig 1; 108pp; English.
XX
XX The sequence represents the variable region heavy and light chains of
XX wild-type anti-Lewis-Y tumour-associated antigen mouse monoclonal
XX antibody BR96. Antibody engineering may be used to form an Fv single
XX chain antibody or mutants with altered complementarity determining region
XX sequences (AAR93008-12) in Escherichia coli. The mutant antibodies have
XX increased affinity for the Lewis-Y antigen, which is expressed by
XX carcinomas and some differentiated epithelial cells, as compared to BR96,
XX and may be used in cancer diagnosis, or in an antitumour conjugate
XX immunotoxin
XX
XX SQ Sequence 233 AA;
Query Match 75.5%; Score 994.5; DB 2; Length 233;
Best Local Similarity 77.9%; Pred. No. 2.4e-63;
Matches 194; Conservative 14; Mismatches 24; Indels 17; Gaps 2;
QY 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFSYTMISWVRQTPKRLKLEWVAISGGSYTY 60
Db 1 EVNLVESGGGLVQPGGSLKLSVTSFTSDYIMYWRQTPKRLKLEWVAISQGGDITDY 60
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCYTRDGHGYSDFYWGQTTLTYS 120
Db 61 PDTVKGRFTISRDNKNTLYLQMSLSKSEDTAMYCYCAR--GLDGFANFAWQGTTLTVS 118
QY 121 SGSGSGGRASGGGSIQVLTQSPSLPVSLGDAQSISCRSSQIVHNSNGNTYLEWYLOK 180
Db 119 -----VDVLTQIPVSLPVSLGDAQSISCRSSQIVHNSNGNTYLEWYLOK 163
QY 181 PGQSPKLLIYKSNRFGVDPKFGSGSGTDFTLKISRVEADLGVYVCFQGSHPVPTFG 240
Db 164 PGQSPQLLIYKSNRFGVDPKFGSGSGTDFTLKISRVEADLGVYVCFQGSHPVPTFG 223
QY 241 GGTGLEIKR 249
Db 224 SGTGLEIKR 232
RESULT 7
AAW27560
ID AAW27560 standard; protein; 281 AA.
XX
XX AAW27560;
XX
XX 23-JAN-1998 (first entry)
XX
XX Consensus single chain fragment VH3-V-kappa-2.
XX
XX Human; antibody; preparation; library; VH3; variable region; light chain;
XX heavy chain; V-kappa-2; single chain; consensus.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..21
XX Peptide /label= sig_peptide
XX Peptide 22..281
XX Peptide /label= mat_peptide
XX
XX WO9708320-A1.

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XX
XX 06-MAR-1997.
XX
XX 19-AUG-1996; 96WO-EP003647.
XX
XX 18-AUG-1995; 95EP-00113021.
XX
XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
XX
XX Knappik A, Pack P, Ilag V, Ge L, Moroney S, Plueckthun A;
XX
XX WPI; 1997-179277/16.
XX
XX N-PSDB; AAT67958.
XX
XX Preparation of human derived antibody gene library - using synthetic
XX consensus sequences, and signal consensus antibody gene as universal
XX framework for highly diverse antibody libraries.
XX
XX Example 2; Fig 8; 436pp; English.
XX
XX The present sequence is the consensus single chain fragment VH3-V-kappa-
XX 2. VH3-V-kappa-2, which comprises the human antibody heavy and light
XX chain variable region consensus sequences VH3 and V-kappa-2, was used in
XX the preparation of a human derived antibody gene library
XX
XX SQ Sequence 281 AA;
Query Match 75.1%; Score 989; DB 2; Length 281;
Best Local Similarity 75.6%; Pred. No. 7.1e-63;
Matches 192; Conservative 23; Mismatches 33; Indels 6; Gaps 2;
QY 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFSYTMISWVRQTPKRLKLEWVAISGGSYTY 60
Db 26 EVQLVESGGGLVQPGGSLKLSCAASGFTFSYTMISWVRQTPKRLKLEWVAISGGSYTY 85
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCYTRDGHGYSDFYWGQTTLTYS 120
Db 86 ADSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYCYCARWGGDGF-YAMDYWGQGTTLTVS 144
QY 121 -----SGSGSGGRASGGGSIQVLTQSPSLPVSLGDAQSISCRSSQIVHNSNGNTYLE 175
Db 145 SAGSGSGSGSGSGSGSGGSDIVMTQSPFLSLPVPFGEPAISCRSSQSLHSGNYILD 204
QY 176 WYLQKPGQSPKLLIYKSNRFGVDPKFGSGSGTDFTLKISRVEADLGVYVCFQGSHPV 235
Db 205 WYLQKPGQSPQLLIYLGNSNRASGVDFRFGSGSGTDFTLKISRVEADLGVYVCFQGHYTT 264
QY 236 PWTFGGTTKLEIKR 249
Db 265 PPTFGGTTKLEIKR 278
RESULT 8
AAR72599
ID AAR72599 standard; protein; 253 AA.
XX
XX AAR72599;
XX
XX 25-MAR-2003 (revised)
XX
XX 03-JUL-1996 (first entry)
XX
XX Anti-dansyl single chain antibody.
XX
XX Single chain antibody; dansyl; SCAB; bispecific; tetraivalent;
XX immunoglobulin; heavy chain; light chain; primer.
XX
XX Synthetic.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Peptide 126..140
XX Peptide /note= "Flexible linker"
XX
XX

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PN WO9509917-A1.
 PD 13-APR-1995.
 XX
 PF 07-OCT-1994; 94WO-US011411.
 XX
 PR 07-OCT-1993; 93US-00134556.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Morrison SL, Coloma MJ;
 XX
 DR WPI; 1995-155258/20.
 DR N-PSDB; AAQ86755.
 XX
 PT Prodn. of bi-specific, tetra-valent antibodies - by recombinant
 PT expression of DNA encoding variable heavy and light immunoglobulin
 FT chains.
 FT
 PS
 SS Example 1; Page 19; 33pp; English.
 CC The anti-dansyl single chain antibody was produced using PCR to join two
 CC variable regions by overlap extension. A flexible linker region
 CC consisting of three gly-gly-gly-ser repeats was used to connect the C
 CC -terminus of the heavy chain variable region (Vh) and the N-terminus of
 CC the light chain variable region (Vl) in order to maximise flexibility
 CC while minimising steric hindrance during protein folding. For the PCR
 CC reaction, the 3' primer for Vh (AAQ86751) and the 5' primer for Vl
 CC (AAQ86752) were designed to have a complementary region in the linker
 CC portion. The Vh and Vl regions were independently amplified, followed by
 CC a second PCR reaction in which these products were used as templates. The
 CC complementary sequences in the linker were hybridised, joining the V
 CC regions and two primers (AAQ86753, AAQ86754) were then used to amplify
 CC the single chain antibody. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 253 AA;

Query Match 74.8%; Score 985; DB 2; Length 253;
 Best Local Similarity 74.9%; Pred. No. 1.2e-62;
 Matches 188; Conservative 28; Mismatches 31; Indels 4; Gaps 2;
 QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMISWVRQTPKRLWVATII--SSGSYT 58
 DB 5 EVKLEESGGGLVPGGSKLSCATSGFTFSDAWMDVWRQSPKGLWVAIRKANNHAT 64
 QY 59 YPDQSVRGRFTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGHHGYSDFYWGQGTTLT 118
 DB 65 YYAIPSVKGRFTISRDSKRRVYLQMTLRADDTGIYCT--GIYHYFPWYAWGQGTLT 122
 QY 119 VSSGGSGGSGRASGGGSGOIVLTQSLPVLSDQASISCRSSQSIVHNGNTYLEWYL 178
 DB 123 VSAGGGSGGSGGSGGSDVVMTUTPLSLPVLNGQASISCRSSQSIVHNGNTYLEWYL 182
 QY 179 QKPGQSKLLIYKSNRFPSPGVPDPSGSGGSDFTLKISRVEADPLGVYCFQGSHPVPT 238
 DB 183 QKPGQSKLLIYKSNRFPSPGVPDPSGSGGSDFTLKISRVEADPLGVYCFQGSHPVPT 242
 QY 239 FGGGTKLEIKR 249
 DB 243 FGGGTKLEIKR 253

RESULT 9
 AAB20436
 ID AAB20436 standard; protein; 249 AA.
 XX
 AC AAB20436;
 XX
 DT 21-JUN-2001 (first entry)
 XX
 DE Anti-FIX/FIXa antibody 198/A1 scFv.
 XX
 KW Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;

KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
 XX
 OS Mus musculus.
 OS Synthetic.
 OS Chimeric.
 XX
 PH Key
 FT Protein
 FT /label= VH
 FT Region
 FT /label= CDR3
 FT Peptide
 FT /label= Linker
 FT Protein
 FT /label= VL
 FT Misc-difference 142
 FT /note= "encoded by ACN"
 FT Misc-difference 224
 FT /note= "encoded by GCN"
 FT Region
 FT /label= CDR3
 XX WO200119992-A2.
 PD 22-MAR-2001.
 XX
 PF 13-SEP-2000; 2000WO-EP008936.
 XX
 PR 14-SEP-1999; 99AT-00001576.
 XX
 PA (BAXT) BAXTER AG.
 PI Scheifflinger F, Kerschbaumer R, Falkner F, Dorner F;
 DR WPI; 2001-290358/30.
 DR N-PSDB; AAF30726.
 XX
 PT New factor IX/factor IXa antibodies and their derivatives useful for
 PT increasing amidolytic activity of factor IXa, and for treating blood
 PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
 XX
 PS Example 10; Fig 17; 138pp; English.
 CC The present sequence is that of a single chain Fv (scFv) derivative of
 CC antibody 198/A1, comprising the heavy (VH) and light (VL) chain variable
 CC regions of 198/A1 joined by an artificial, flexible linker peptide. The
 CC scFv was obtained by PCR amplification of cDNAs for 198/A1 VH and VL
 CC regions and cloning in vector pDAP2. 198/A1 is an example of anti-human
 CC Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.
 CC Anti-FIX/FIXa and their derivatives, including scFv and CDR3 fragments,
 CC have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity.
 CC Administration leads to an increase in the procoagulant activity of FIXa,
 CC even in the presence of FVIIIa inhibitors. This allows for rapid blood
 CC coagulation even in the absence of FVIII or FVIIIa, and in the case of
 CC FVIII inhibitor patients. The antibodies and derivatives are used in a
 CC claimed pharmaceutical composition for treating patients with blood
 CC coagulation disorders, especially haemophilia A and haemorrhagic
 CC diathesis
 XX
 SQ Sequence 249 AA;

Query Match 74.6%; Score 982; DB 4; Length 249;
 Best Local Similarity 77.2%; Pred. No. 2e-62;
 Matches 193; Conservative 20; Mismatches 35; Indels 2; Gaps 2;
 QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMISWVRQTPKRLWVATIISSGSYTY 60
 DB 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYTMISWVRQTPKRLWVATIISSGSSTY 60
 QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGHHGYS-SFDYWGQGTTLTV 119
 DB 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGHHGYS-SFDYWGQGTTLTV 120

QY 120 SSGGGSGRAGGGGQIVLTQSLPVLSDQASISCRSSQSIHVSNGNTYLEWYLO 179
 Db 121 SSGGGSGRAGGGGQIVLTQSLPVLSDQASISCRSSQSIHVSNGNTYLEWYLO 179
 QY 180 KPGQPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVAEDLGVYFCQSGHVPWTF 239
 Db 180 KPGQPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVAEDLGVYFCQSGHVPWTF 239
 QY 240 GGTGKLEIKR 249
 Db 240 GGTGKLEIKR 249

RESULT 10

AA08983
 ID AAY08983 standard; protein; 268 AA.

XX AAY08983;

XX 20-AUG-1999 (first entry)

XX ScFv4155 anti-E3G antibody fragment construct protein.

XX Analytical device; electrically conductive solid support; immobilisation;
 KW electroactive; analysis; peptide hormone; steroid; disease marker;
 KW diagnostic indicator; antibody; bacteria; virus; fungi; yeast.

XX Synthetic.

XX WO9927356-A1.

XX 03-JUN-1999.

XX 23-NOV-1998; 98WO-GB003495.

XX 21-NOV-1997; 97EP-00309425.

XX (UNIL) UNILEVER PLC.

XX (UNIL) UNILEVER NV.

XX Porter RA, Badley RA;

XX WPI; 1999-385228/32.

XX N-PSDB; AAX78155.

XX Analytical device including electrochemically active compound on solid support.

XX Example 6; Page 66-64; 78pp; English.

XX This invention describes a novel component for an analytical device
 CC comprising an electrically conductive solid support on which a compound
 CC (I) is immobilized which has an electroactive part (EA) with an
 CC electrochemical property that can be modulated in a detectable manner by
 CC binding it to a specific binding partner (II). Compounds used in the
 CC method of the invention include those with the formula R = hydrogen,
 CC hydroxy, 1-14C alkyl, aryl, alkenyl or alkoxy (all optionally
 CC substituted), halo, amido, or amino; optionally one or more positions on
 CC the heteroaromatic rings are substituted by alkyl, aryl, alkenyl or
 CC alkoxy (all optionally substituted), acid groups (organic or inorganic),
 CC halo, amido or amino. Devices that contain the component of the invention
 CC are used for qualitative and quantitative analysis of e.g. nucleic acid,
 CC hormones (peptide or steroid), disease markers, diagnostic indicators
 CC etc., e.g. antibodies, bacteria, viruses, fungi or yeast. These devices
 CC can be used with turbid solutions (whole blood, milk, culture liquids
 CC etc.), unlike conventional colourimetric methods. This sequence
 CC represents a scFv anti-E3G antibody fragment construct which is used in
 CC the method of the invention

XX Sequence 268 AA;

XX Query Match

74.1%; Score 976; DB 2; Length 268;

Best Local Similarity 76.7%; Pred. No. 5.8e-62;
 Matches 191; Conservative 16; Mismatches 40; Indels 2; Gaps 1;
 QY 1 EVQLVSGGGLVPGGSLKLSCAASGFTFTSTYMSWVRQTPKRLLEWVATISSGGSYTY 60
 Db 1 QVQLQSGGGGLVNLGGMTLSCVASGFTFTNTYMSWVRQTPKRLLEWVATISSGGSYTY 60
 QY 61 PDSVRGRFTISRDNKNTLYLQMSLKSSEDTAMVYCTRDGGHGYGSGFDYWGOGTTLTVS 120
 Db 61 PDLKGRVTISRDNKNTLYLQMSLKSSEDTAMVYCTRDGGHGYGSGFDYWGOGTTLTVS 118
 QY 121 SGGGSGGGRASGGGSGIIVLTQSLPVLSDQASISCRSSQSIHVSNGNTYLEWYLOK 180
 Db 119 SGGGSGGSGGGGGGSDIELTQTPPSLPVSLGQVDSISCRSSQSLVNNRNYLHWYLOK 178
 QY 181 PGQSPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVAEDLGVYFCQSGHVPWTF 240
 Db 179 PGQSPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVAEDLGVYFCQSGHVPWTF 238
 QY 241 GGTGKLEIKR 249
 Db 239 GGTGKLEIKR 247

RESULT 11

AA08990

ID AAY08990 standard; protein; 408 AA.

XX AAY08990;

XX 20-AUG-1999 (first entry)

XX Llama protein construct pPIC.scFv4155-link-HCV24-His2t.

XX Analytical device; electrically conductive solid support; immobilisation;
 KW electroactive; analysis; peptide hormone; steroid; disease marker; HCV24;
 KW diagnostic indicator; antibody; bacteria; virus; fungi; yeast; llama.

XX Lama glama.

XX Synthetic.

XX WO9927356-A1.

XX 03-JUN-1999.

XX 23-NOV-1998; 98WO-GB003495.

XX 21-NOV-1997; 97EP-00309425.

XX (UNIL) UNILEVER PLC.

XX (UNIL) UNILEVER NV.

XX Porter RA, Badley RA;

XX WPI; 1999-385228/32.

XX Analytical device including electrochemically active compound on solid support.

XX Example 6.4; Page 72-73; 78pp; English.

XX This invention describes a novel component for an analytical device
 CC comprising an electrically conductive solid support on which a compound
 CC (I) is immobilized which has an electroactive part (EA) with an
 CC electrochemical property that can be modulated in a detectable manner by
 CC binding it to a specific binding partner (II). Compounds used in the
 CC method of the invention include those with the formula R = hydrogen,
 CC hydroxy, 1-14C alkyl, aryl, alkenyl or alkoxy (all optionally
 CC substituted), halo, amido, or amino; optionally one or more positions on
 CC the heteroaromatic rings are substituted by alkyl, aryl, alkenyl or
 CC alkoxy (all optionally substituted), acid groups (organic or inorganic),
 CC halo, amido or amino. Devices that contain the component of the invention
 CC are used for qualitative and quantitative analysis of e.g. nucleic acid,

CC hormones (peptide or steroid), disease markers, diagnostic indicators
 CC etc., e.g. antibodies, bacteria, viruses, fungi or yeast. These devices
 CC can be used with turbid solutions (whole blood, milk, culture liquids
 CC etc.), unlike conventional colourimetric methods. This sequence
 CC represents a protein construct pPIC.scFv4155-link-HCV3-His2t which
 CC contains the llama HC-V fragment, HCV3 which is used in the method of the
 CC invention
 XX
 SQ Sequence 408 AA;

Query Match 74.1%; Score 976; DB 2; Length 408;
 Best Local Similarity 76.7%; Pred. No. 9e-62;
 Matches 191; Conservative 16; Mismatches 40; Indels 2; Gaps 1;
 QY 1 EVOLVESGGGLVKGSGSLKSCAASGFTFTSTYMSWVRQTPKEKLEWVATISSGGSYTY 60
 DB 1 QVQLQESGGGLVNLGGSMTLSCVASGFTFTNTYMSWVRQTPKEKLELVAAINSDGEPIY 60
 QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 DB 61 PDLKGRVTISRDNKNTLYLQMSLSLNFEDTALYVCARLTAVYVG--MDYWGQGTTLTVS 118
 QY 121 SGGGSGGGRASGGGSGQIVLTQSPSLPVSGLDQASISCRSSQSIHVSNGNTYLEWYLOK 180
 DB 119 SGGGSGGSGGSGGSGGSDIELTQTTPSPVSLGDQVSISSCRSSQSLVSNRRNRYLHWYLOK 178
 QY 181 PQQSPKLLIYKVSNRFPKFGSGSGTDTFTLKISRVEAEDLGVYCYFGSHVPWTFG 240
 DB 179 PQQSPKLLIYKVSNRFPKFGSGSGTDTFTLKISRVEAEDLGVYCYFGSHVPWTFG 238
 QY 241 GGTKEIKR 249
 DB 239 SGTKEIKR 247

RESULT 12

AA08989
 ID AAY08989 standard; protein; 409 AA.

AC AAY08989;

DT 20-AUG-1999 (first entry)

DE Llana protein construct pPIC.scFv4155-link-HCV3-His2t.

XX Analytical device; electrically conductive solid support; immobilisation;
 KW electroactive; analysis; peptide hormone; steroid; disease marker; HCV3;
 KW diagnostic indicator; antibody; bacteria; virus; fungi; yeast; llama.

OS Lama glama.
 OS Synthetic.

XX WO9927356-A1.

PN 03-JUN-1999.

PD 23-NOV-1998; 98WO-GB003495.

XX 21-NOV-1997; 97EP-00309425.

PR (UNIL) UNILEVER PLC.
 PA (UNIL) UNILEVER NV.

XX Porter RA, Badley RA;

XX WPI; 1999-385228/32.

XX Analytical device including electrochemically active compound on solid
 PT support.

XX Example 6.4; Page 70-71; 78pp; English.

XX This invention describes a novel component for an analytical device

CC comprising an electrically conductive solid support on which a compound
 CC (I) is immobilized which has an electroactive part (EA) with an
 CC electrochemical property that can be modulated in a detectable manner by
 CC binding it to a specific binding partner (II). Compounds used in the
 CC method of the invention include those with the formula R = hydrogen,
 CC hydroxy, 1-14C alkyl, aryl, alkenyl or alkoxy (all optionally
 CC substituted), halo, amido, or amino; optionally one or more positions on
 CC the heteroaromatic rings are substituted by alkyl, aryl, alkenyl or
 CC alkoxy (all optionally substituted), acid groups (organic or inorganic),
 CC halo, amido or amino. Devices that contain the component of the invention
 CC are used for qualitative and quantitative analysis of e.g. nucleic acid,
 CC hormones (peptide or steroid), disease markers, diagnostic indicators
 CC etc., e.g. antibodies, bacteria, viruses, fungi or yeast. These devices
 CC can be used with turbid solutions (whole blood, milk, culture liquids
 CC etc.), unlike conventional colourimetric methods. This sequence
 CC represents a protein construct pPIC.scFv4155-link-HCV3-His2t which
 CC contains the llama HC-V fragment, HCV3 which is used in the method of the
 CC invention
 XX
 SQ Sequence 409 AA;

Query Match 74.1%; Score 976; DB 2; Length 409;
 Best Local Similarity 76.7%; Pred. No. 9.1e-62;
 Matches 191; Conservative 16; Mismatches 40; Indels 2; Gaps 1;

QY 1 EVOLVESGGGLVKGSGSLKSCAASGFTFTSTYMSWVRQTPKEKLEWVATISSGGSYTY 60
 DB 1 QVQLQESGGGLVNLGGSMTLSCVASGFTFTNTYMSWVRQTPKEKLELVAAINSDGEPIY 60
 QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGGHGYGSSFDYWGQGTTLTVS 120
 DB 61 PDLKGRVTISRDNKNTLYLQMSLSLNFEDTALYVCARLTAVYVG--MDYWGQGTTLTVS 118
 QY 121 SGGGSGGGRASGGGSGQIVLTQSPSLPVSGLDQASISCRSSQSIHVSNGNTYLEWYLOK 180
 DB 119 SGGGSGGSGGSGGSGGSDIELTQTTPSPVSLGDQVSISSCRSSQSLVSNRRNRYLHWYLOK 178
 QY 181 PQQSPKLLIYKVSNRFPKFGSGSGTDTFTLKISRVEAEDLGVYCYFGSHVPWTFG 240
 DB 179 PQQSPKLLIYKVSNRFPKFGSGSGTDTFTLKISRVEAEDLGVYCYFGSHVPWTFG 238
 QY 241 GGTKEIKR 249
 DB 239 SGTKEIKR 247

RESULT 13

AA020442
 ID AAB20442 standard; protein; 294 AA.

XX AAB20442;

XX 21-JUN-2001 (first entry)

DE Anti-FIX/Fixa antibody 198/B1-myc-tag fusion.

XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; myc-tag.

XX Mus musculus.

OS Synthetic.

OS Escherichia coli.

XX Chimeric.

XX Key Location/Qualifiers
 FT Peptide 1..22
 FT Protein /label= signal_peptide
 FT Protein 23..294
 FT Protein /label= Mature_protein
 FT Protein 23..271
 FT Protein /label= scFv
 FT Region 23..144

FT FT /label= VH
FT Misc-difference 76
FT /note= "encoded by GGN"
FT Peptide 145..159
FT /label= Linker
FT Region 160..271
FT /label= VL
FT Peptide 272..274
FT /label= Spacer
FT Protein 275..296
FT /label= Myc_tag
FT Peptide 287..288
FT /label= Spacer
FT Peptide 289..294
FT /label= His_tag
XX
XX
XX WO200119992-A2.
XX
XX
XX PD 22-MAR-2001:
XX
XX PF 13-SEP-2000; 2000WO-EP008936.
XX
XX PR 14-SEP-1999; 99AT-00001576.
XX
XX PA (BAXT) BAXTER AG.
XX
XX PI Scheifflinger F, Kerschbaumer R, Falkner F, Dornier F;
XX
XX DR N-PSDB; AAF30732.
XX
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Example 18; Fig 34; 138pp; English.
XX
XX The present sequence is that of a fusion protein comprising: a PelB
CC leader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising
CC the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by
CC an artificial, flexible linker peptide; a spacer; a Myc-tag peptide; a
CC spacer; and a C-terminal this affinity tail. 198/B1 is an example of anti
CC -human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the
CC invention. Anti-FIX/FIXa antibodies and their derivatives, including scFv
CC fragments, have FvIIa cofactor activity or FIXa activating activity.
CC Administration leads to an increase in the procoagulant activity of FIXa,
CC even in the presence of FvIIa inhibitors. This allows for rapid blood
CC coagulation even in the absence of FvIII or FvIIa, and in the case of
CC FvIII inhibitor patients. The antibodies and derivatives are used in a
CC claimed pharmaceutical composition for treating patients with blood
CC coagulation disorders, especially haemophilia A and haemorrhagic
CC diathesis. The scFv-myc-tag fusion was expressed in E. coli. It exhibited
CC FvIII-like activity
XX
XX Sequence 294 AA;
Query Match 74.0%; Score 975; DB 4; Length 294;
Best Local Similarity 76.5%; Pred. No. 7.5e-62;
Matches 192; Conservative 23; Mismatches 32; Indels 4; Gaps 3;
QY 1 EVQLVESGGGLVAPGQSLKLSCAASGFTFTSYTMSWRQTPPEKLEWATISSGGSYYY 60
Db 23 EVKLVESGGGLVAPGQSLKLSCAASGFTFTSYTMSWRQTPPEKLEWATISSGGSYYY 82
QY 61 PDSVGRFTISRDAKNTLYIQMSSLKSEDTAMYYCTRDGGHGYGSS--FDYWGQGTLLT 118
Db 83 PDSVGRFTISRDAKNTLYIQMSSLKSEDTAMYYCTREGG-GFTVNWYFDVWGAGFSVT 141
QY 119 VSSGGGGGGRASGGGSGQIVLTQSLPLSPVSLGDAQSISCRSSQSIHNSGNTYLEWYL 178
Db 142 VSSGGGGGGRASGGGSDIVLTQSPASLAVSLQGRATISCRASES-VDSVGYNFHMYQ 200
QY 179 QKPGQSPKLLIYKYNRPSGVDPDFSGSGSGTDFTLKISRVEAEDLGVYFCFGSHVPWT 238

Db 201 QIFGQPPKLLIYRASNLGGIPARFSGSGSRDFTLTINFEADDVATYYCQSQNEDPLT 260
QY 239 FGGGTKLEIKR 249
Db 261 FGTGTRLEIKR 271
RESULT 14
AAB20437
ID AAB20437 standard; protein; 732 AA.
XX
XX AAB20437;
XX
XX 21-JUN-2001 (first entry)
XX
XX Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion.
XX
XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW hemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW alkaline phosphatase.
XX
XX Mus musculus.
OS Synthetic.
OS Escherichia coli.
OS Chimeric.
XX
XX Key Location/Qualifiers
FT Peptide 1..22
FT /label= Signal_peptide
FT Protein 23..732
FT /label= Mature_protein
FT Protein 23..271
FT /label= scFv
FT Region 23..144
FT /label= VH
FT
FT Misc-difference 76
FT /note= "encoded by GGN"
FT Peptide 145..159
FT /label= Linker
FT Region 160..271
FT /label= VL
FT Peptide 272..275
FT /label= Spacer
FT Protein 276..725
FT /label= Alkaline_phosphatase
FT Peptide 726..732
FT /label= His_tag
XX
XX WO200119992-A2.
XX
XX PD 22-MAR-2001.
XX
XX 13-SEP-2000; 2000WO-EP008936.
XX
XX 14-SEP-1999; 99AT-00001576.
XX (BAXT) BAXTER AG.
XX
XX Scheifflinger F, Kerschbaumer R, Falkner F, Dornier F;
XX
XX WPI; 2001-290358/30.
XX
XX N-PSDB; AAB30727.
XX
XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX Example 16; Fig 26; 138pp; English.
XX
XX The present sequence is that of a fusion protein comprising: a PelB
CC leader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising

CC the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by
 CC an artificial, flexible linker peptide; a spacer; Escherichia coli
 CC alkaline phosphatase; and a C-terminal 6His affinity tail. 198/B1 is an
 CC example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
 CC antibodies of the invention. Anti-FIX/FIXa antibodies and their
 CC derivatives, including scFv fragments, have FVIIIa cofactor activity or
 CC FIXa activating activity. Administration leads to an increase in the
 CC procoagulant activity of FIXa, even in the presence of FVIIIa inhibitors.
 CC This allows for rapid blood coagulation even in the absence of FVIII or
 CC FVIIIa, and in the case of FVIII inhibitor patients. The antibodies and
 CC derivatives are used in a claimed pharmaceutical composition for treating
 CC patients with blood coagulation disorders, especially haemophilia A and
 CC haemorrhagic diathesis. The scFv-alkaline phosphatase was expressed in E.
 CC coli. It exhibited FVIII-like activity
 XX
 SQ Sequence 732 AA;

Query Match 74.0%; Score 975; DB 4; Length 732;
 Best Local Similarity 76.5%; Pred. No. 2e-61;
 Matches 192; Conservative 23; Mismatches 32; Indels 4; Gaps 3;

QY 1 EVLVESGGGLVKGSGSLKLSAASGFTFSYTMWVROTPEKLEWVATISSGGSYTY 60
 DB 23 EVKLVSAGGLVKGSGSLKLSAASGFTFSYTMWVROTPEKLEWVATISSGGSYTY 82
 QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGGHGYGSS--FDYWGQGTTLT 118
 DB 83 PDSVKGRTISRDNKNTLYLQMSLSRSEDTAMYCTREGG-GFTVNVYFDVWGAGTSVT 141
 QY 119 VSSGGGGSGGRASGGGGQIVLTQSLPLVSLGDAQISCRSQSIVHNGNTYLEWYL 178
 DB 142 VSSGGGGSGGRASGGGGQIVLTQSPASLAVSLGQATISCRASES-VDSYGYNFMHWYQ 200
 QY 179 QKPGQSKLLIYKVSNRFSVPDRKFGSGSGTDFTLKTSRVEADLGVYCFQGSHPWT 238
 DB 201 QIPGQPKLLIYASNLSESGIPARFSGSGSRDFTLTPNVEADVATYCCQSNEDPLT 260
 QY 239 FGGGPKLEIKR 249
 DB 261 FGTGRLBIKR 271

RESULT 15
 ID AAB20438 standard; protein; 325 AA.
 XX
 AC AAB20438;
 XX
 DT 21-JUN-2001 (first entry)
 XX
 DE Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody.
 XX
 KW Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
 KW bivalent antibody; plasmid pZip-198AB2#102.
 XX
 OS Mus musculus.
 OS Synthetic.
 OS Escherichia coli.
 OS Chimeric.

XX
 FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /label= Signal_peptide
 FT /note= "pe1B leader"
 FT Protein 23..325
 FT /label= Mature_protein
 FT Protein 23..271
 FT /label= scfv
 FT Region 23..144
 FT /label= VH
 FT Misc-difference 76

FT Peptide /note= "encoded by GGN"
 FT 145..159
 FT /label= Linker
 FT Region 160..271
 FT /label= VL
 FT Misc-difference 166
 FT /note= "encoded by TNT"
 FT Misc-difference 181
 FT /note= "encoded by TCN"
 FT Peptide 272..274
 FT /label= Spacer
 FT Protein 275..284
 FT /label= Hinge
 FT Protein 285..319
 FT /label= Helix
 FT Peptide 320..325
 FT /label= His_tag

XX WO200119992-A2.
 PN 22-MAR-2001.
 XX 13-SEP-2000; 2000WO-EP008936.
 PF 14-SEP-1999; 99AT-00001576.
 XX (BAXT) BAXTER AG.
 XX Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;
 XX WPI; 2001-290358/30.
 DR N-PSDB; AAF30728.
 XX
 PT New factor IX/factor IXa antibodies and their derivatives useful for
 PT increasing amidolytic activity of factor IXa, and for treating blood
 PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
 XX
 PS Example 16; Fig 28; 138pp; English.
 XX
 CC The present sequence is that of a bivalent miniantibody comprising a Pe1B
 CC leader peptide, the single chain Fv (scFv) fragment of antibody 198/B1
 CC (subclone AB2), an amphipathic helical structure and a C-terminal 6His
 CC tag. The protein was expressed in Escherichia coli from plasmid
 CC pZip198AB2#102 (see AAF30728). Antibody 198/B1 is an example of anti-
 CC human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the
 CC invention. Anti-FIX/FIXa antibodies and their derivatives have FVIIIa
 CC cofactor activity or FIXa activating activity. Administration leads to an
 CC increase in the procoagulant activity of FIXa, even in the presence of
 CC FVIIIa inhibitors. This allows for rapid blood coagulation even in the
 CC absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients.
 CC The antibodies and derivatives are used in a claimed pharmaceutical
 CC composition for treating patients with blood coagulation disorders,
 CC especially haemophilia A and haemorrhagic diathesis. The bivalent
 CC miniantibody exhibited FVIII-like activity
 XX
 SQ Sequence 325 AA;

Query Match 73.7%; Score 971; DB 4; Length 325;
 Best Local Similarity 76.1%; Pred. No. 1.6e-61;
 Matches 191; Conservative 23; Mismatches 33; Indels 4; Gaps 3;

QY 1 EVLVESGGGLVKGSGSLKLSAASGFTFSYTMWVROTPEKLEWVATISSGGSYTY 60
 DB 23 EVKLVSAGGLVKGSGSLKLSAASGFTFSYTMWVROTPEKLEWVATISSGGSYTY 82
 QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYCTRDGGHGYGSS--FDYWGQGTTLT 118
 DB 83 PDSVKGRTISRDNKNTLYLQMSLSRSEDTAMYCTREGG-GFTVNVYFDVWGAGTSVT 141
 QY 119 VSSGGGGSGGRASGGGGQIVLTQSLPLVSLGDAQISCRSQSIVHNGNTYLEWYL 178
 DB 142 VSSGGGGSGGRASGGGGQIVLTQSPASLAVSLGQATISCRASES-VDSYGYNFMHWYQ 200

QY 179 QKPGQSPKLLIYKVSÑRFSQVDPDKFSGSGGTDFTLKISRVEABDLGVYICFQGSHPVWT 238
| | | | | : | | : | | | | | | | : | | : | |
Db 201 QIPGQPPKLLIYRASNLSEGI PARPSGSGSRTDFTLINPVEADDVATYYCQSQNEDEPLT 260
| | | | | : | | : | | | | | | | : | | : | |
QY 239 FGGGTKLEIKR 249
| | | | | : | | : | | | | | | | : | | : | |
Db 261 FGTGTRLEIKR 271
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.
OM protein - protein search, using sw model
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Scoring table:
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1291235

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	976	74.1	268	16	US-10-353-721-2
2	976	74.1	408	16	US-10-353-721-15
3	976	74.1	409	16	US-10-353-721-14
4	970.5	73.7	262	10	US-09-880-748-2081
5	970.5	73.7	262	12	US-10-293-418-2081
6	960.5	72.9	244	10	US-09-880-748-1991
7	960.5	72.9	244	12	US-10-293-418-1991
8	946.5	71.9	252	14	US-10-169-351-49
9	944.5	71.7	269	13	US-10-027-770-5
10	935.5	71.0	269	13	US-10-027-770-2
11	924	70.2	263	14	US-10-153-401-66
12	915.5	69.5	507	12	US-10-239-656-47
13	915.5	69.5	510	12	US-10-239-656-48
14	915.5	69.5	510	12	US-10-239-656-49
15	909	69.0	381	9	US-09-822-698A-5

898	68.2	271	12	US-10-257-864A-91	Sequence 91, Appl
898	68.2	271	12	US-10-221-131-95	Sequence 95, Appl
898	68.2	271	12	US-10-221-131-96	Sequence 96, Appl
898	68.2	271	14	US-10-138-505-30	Sequence 30, Appl
898	68.2	271	16	US-10-399-518-120	Sequence 120, Appl
898	68.2	274	12	US-10-257-864A-90	Sequence 90, Appl
898	68.2	274	14	US-10-138-505-26	Sequence 26, Appl
898	68.2	274	16	US-10-399-518-119	Sequence 119, Appl
896	68.0	240	9	US-09-782-504-4	Sequence 4, Appl
896	68.0	240	12	US-10-336-672-4	Sequence 92, Appl
892	67.7	274	12	US-10-257-864A-92	Sequence 92, Appl
892	67.6	245	12	US-10-257-864A-95	Sequence 95, Appl
890	67.6	245	12	US-10-221-131-100	Sequence 100, Appl
890	67.6	245	14	US-10-138-505-40	Sequence 40, Appl
890	67.6	245	16	US-10-399-518-124	Sequence 124, Appl
890	67.6	271	12	US-10-257-864A-93	Sequence 93, Appl
890	67.6	271	12	US-10-221-131-98	Sequence 98, Appl
890	67.6	271	14	US-10-138-505-34	Sequence 34, Appl
890	67.6	271	16	US-10-399-518-122	Sequence 122, Appl
890	67.6	274	12	US-10-221-131-97	Sequence 97, Appl
890	67.6	274	14	US-10-138-505-32	Sequence 32, Appl
890	67.6	274	16	US-10-399-518-121	Sequence 121, Appl
890	67.6	533	12	US-10-257-864A-96	Sequence 96, Appl
890	67.6	533	12	US-10-221-131-101	Sequence 101, Appl
890	67.6	533	16	US-10-399-518-125	Sequence 125, Appl
884	67.1	237	10	US-03-880-748-1906	Sequence 1906, Ap
884	67.1	237	10	US-09-880-748-2104	Sequence 2104, Ap
884	67.1	237	12	US-10-293-418-1906	Sequence 1906, Ap
884	67.1	237	12	US-10-293-418-2104	Sequence 2104, Ap
881	66.9	237	10	US-09-880-748-2020	Sequence 2020, Ap

ALIGNMENTS

RESULT 1

US-10-353-721-2
; Sequence 2, Application US/10353721
; Publication No. US20040020791A1
; GENERAL INFORMATION:
; APPLICANT: Porter, Robert A
; APPLICANT: Badley, Robert A
; TITLE OF INVENTION: Electroactive Surfaces
; FILE REFERENCE: IMIN.P-036
; CURRENT APPLICATION NUMBER: US/10/353,721
; CURRENT FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: US/09/554,765
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: PCT/GB98/03495
; PRIOR FILING DATE: 1998-11-23
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 268
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: anti-B3G antibody fragment
US-10-353-721-2

Query Match	74.1%;	Score 976;	DB 16;	Length 268;
Best Local Similarity	76.7%;	Pred. NO. 8.5e-68;		
Matches 191;	Conservative 16;	Mismatches 40;	Indels 2;	Gaps 1;
QY	1	EVQLVESGGLVKPGGSLKCAASGFTFSYTWMSVRCTPEKRLQWATVSSGGSYTY 60		
Db	1	QVQLVESGGLVNLCGSMILSCVSGFTFNYYMSWVQTPEKTLLELVAINSDGEPIY 60		
QY	61	PDVSRGRTISRDNKNTLYLQMSLKSEDTAMYYCTDGGHGYSFDTWQGGTTLTVS 120		
Db	61	PDTLGRVTRISRDNKNTLYLQMSLNFDATLYCARLTAVYGV-MDYWGQGTTLTVS 118		
QY	121	SGGSGSGGRASGGGSGQIVLTQSPVLSLQDQASISCRSSQSIHNGNTYLEWYLOK 180		


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Db 1 QVQLVQSGGGLVPGGSLRLSCAASGFTIYNIYSNNWVRQAPGKLEWVSISSSSVIYY 60
QY 61 PDSVRGRFTISRDNKNTLYIQMSLSKSDTAMYYCTRDGG-----HGYGSS 107
Db 61 ADSVKGRFTISRDNKNTLYIQMSLSKSDTAMYYCTRDGG-----HGYGSS 118
QY 108 FDYWGQGTTLTVSSGGGSGGRASGGGGS--QIVLTQSPSLPVSIGDQASISCRSSQSI 165
Db 119 MDVWGKGTITVSSGGGSGGRASGGGGSLEIVMTQSPSLPVPDGPASISCRSSQSL 178
QY 166 VHSNGNTLYEYLQKPGQSPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVEADLG 225
Db 179 LHSNGNYLDWYLQKPGQSPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVEADLG 238
QY 226 VYCFQSGSHVPTFGGKLEIKR 249
Db 239 VYICWQALQTLPTFGGKLEIKR 262

RESULT 5
US-10-293-418-2081
; Sequence 2081, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3247
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-2081

Query Match 73.7%; Score 970.5; DB 12; Length 262;
Best Local Similarity 71.2%; Pred. No. 2,2e-67;
Matches 188; Conservative 29; Mismatches 30; Indels 17; Gaps 3;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFTSYTMSWVRQTPKRLIEWATISSGGSYTY 60
Db 1 QVQLVQSGGGLVPGGSLRLSCAASGFTIYNIYSNNWVRQAPGKLEWVSISSSSVIYY 60
QY 61 PDSVRGRFTISRDNKNTLYIQMSLSKSDTAMYYCTRDGG-----HGYGSS 107
Db 61 ADSVKGRFTISRDNKNTLYIQMSLSKSDTAMYYCTRDGG-----HGYGSS 118
QY 108 FDYWGQGTTLTVSSGGGSGGRASGGGGS--QIVLTQSPSLPVSIGDQASISCRSSQSI 165
Db 119 MDVWGKGTITVSSGGGSGGRASGGGGSLEIVMTQSPSLPVPDGPASISCRSSQSL 178
QY 166 VHSNGNTLYEYLQKPGQSPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVEADLG 225
Db 179 LHSNGNYLDWYLQKPGQSPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVEADLG 238
QY 226 VYCFQSGSHVPTFGGKLEIKR 249

RESULT 6
US-09-880-748-1991
; Sequence 1991, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1991
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1991

Query Match 72.9%; Score 960.5; DB 10; Length 244;
Best Local Similarity 74.9%; Pred. No. 1,2e-66;
Matches 188; Conservative 27; Mismatches 27; Indels 9; Gaps 4;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFTSYTMSWVRQTPKRLIEWATISSGGSYTY 60
Db 1 EVQLVQSGGGLVPGGSLRLSCAASGFTFSSYTMNWRQAPGKLEWVSISSSSHIYY 60
QY 61 PDSVRGRFTISRDNKNTLYIQMSLSKSDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
Db 61 ADSVKGRFTISRDNKNTLYIQMSLSKSDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 114
QY 121 SGGGSGSGGRASGGGGS--QIVLTQSPSLPVSIGDQASISCRSSQSI VHSNGNTLYEYLW 178
Db 115 SGGGSGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSG 174
QY 179 QPQSGSPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVEADLG VYICFQSGSHVPT 238
Db 175 QPQSGSPRLIYKVNRFSGVPDKFSGSGGTDFTLKISRVEADLVGVYICFQSGSHVPT 233
QY 239 FGGGKLEIKR 249
Db 234 FGGKLEIKR 244

RESULT 7
US-10-293-418-1991
; Sequence 1991, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
```

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Db 239 VYICWQALQTLPTFGGKLEIKR 262

RESULT 6
US-09-880-748-1991
; Sequence 1991, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1991
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1991

Query Match 72.9%; Score 960.5; DB 10; Length 244;
Best Local Similarity 74.9%; Pred. No. 1,2e-66;
Matches 188; Conservative 27; Mismatches 27; Indels 9; Gaps 4;

QY 1 EVQLVESGGGLVPGGSLRLSCAASGFTFTSYTMSWVRQTPKRLIEWATISSGGSYTY 60
Db 1 EVQLVQSGGGLVPGGSLRLSCAASGFTFSSYTMNWRQAPGKLEWVSISSSSHIYY 60
QY 61 PDSVRGRFTISRDNKNTLYIQMSLSKSDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
Db 61 ADSVKGRFTISRDNKNTLYIQMSLSKSDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 114
QY 121 SGGGSGSGGRASGGGGS--QIVLTQSPSLPVSIGDQASISCRSSQSI VHSNGNTLYEYLW 178
Db 115 SGGGSGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSGGSG 174
QY 179 QPQSGSPKLLIYKVNRFSGVPDKFSGSGGTDFTLKISRVEADLG VYICFQSGSHVPT 238
Db 175 QPQSGSPRLIYKVNRFSGVPDKFSGSGGTDFTLKISRVEADLVGVYICFQSGSHVPT 233
QY 239 FGGGKLEIKR 249
Db 234 FGGKLEIKR 244

RESULT 7
US-10-293-418-1991
; Sequence 1991, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
```

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; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1991
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1991

Query Match          72.9%; Score 960.5; DB 12; Length 244;
Best Local Similarity 74.9%; Pred. No. 1.2e-66;
Matches 188; Conservative 27; Mismatches 27; Indels 9; Gaps 4;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPDKRLEWVATISSGGSYTY 60
DB 1 EVQLVQSGGGLVPGGSLRLSCAASGFTFSYSNWRQAPGKLEWVSSISSSHIYY 60
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGGHGYGSGFDYWGQGTILTVS 120
DB 61 ADSVKGRTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGGHGYGSGFDYWGQGTILTVS 114
QY 121 SGGSGSGGRASGGGSG--QIVLTQSLPLSVSLGDOASISCRSSQSIIVHNGNTYLEWYL 178
DB 115 SGGSGSGGGGGSGGSDLVVMTQSPSLPVLTPGQPSISCRSSQSLVHSDGNTYLNWVQ 174
QY 179 QKPGQSPKLLIYKVNRFSGVPEDFKFGSGSGTDFTLKISRVEAEDLGVYCFQGSHPWT 238
DB 175 QRPQSPRLIYKVNRFSGVPEDFKFGSGSGTDFTLKISRVEAEDLGVYCFQGSHPWT 233
QY 239 FGGGTGLEIKR 249
DB 234 FGGGTGLEIKR 244

RESULT 8
US-10-169-351-49
; Sequence 49, Application US/10169351
; Publication No. US20030157090A1
; GENERAL INFORMATION:
; APPLICANT: BENVENUTO, EUGENIO
; APPLICANT: FRANCONI, ROSELLA
; APPLICANT: DESIDERIO, ANGIOLA
; APPLICANT: TAVLADORAKI, PARASKEVI
; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
; FILE REFERENCE: 4161-4
; CURRENT APPLICATION NUMBER: US/10/169,351
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/IT00/00554
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: IT RM99A000803
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 49
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv(F8)
; OTHER INFORMATION: amino acid sequence
US-10-169-351-49

Query Match          71.9%; Score 946.5; DB 14; Length 252;
Best Local Similarity 72.7%; Pred. No. 1.5e-65;
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Matches 186; Conservative 22; Mismatches 37; Indels 11; Gaps 3;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPDKRLEWVATISSGGSYTY 60
DB 1 QVQLQESGGDLVPGGSLKLSCAASGFTFSYGYMSWRVQTPDKRLELVAIVNSGSGTFY 60
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRD-----GHHGVGSSFDYWGQ 113
DB 61 PDSVKGRTISRDNKNTLYLQMSLSKSEDTAMYYCARRRNPYYVSGRGY---FDYWGQ 117
QY 114 GTTLTVSSGGSGGGRASGGGSGIIVLTQSLPLSVSLGDOASISCRSSQSIIVHNGNTY 173
DB 118 GTTVTVSSGGSGGSGGSGGSDIELTQSPASLAVSLGQRATISCRASES-VDSYGNPF 176
QY 174 LEWYLQKPGQSPKLLIYKVNRFSGVPEDFKFGSGSGTDFTLKISRVEAEDLGVYCFQGS 233
DB 177 MHWYQKPGQPPKLLIYFRLNLESGIPARFSGSGSRDFTLTINPVEADVVATYYCQSN 236
QY 234 HVPWTFGGGTGLEIKR 249
DB 237 EDPWTFGGGTGLEIKR 252

RESULT 9
US-10-027-770-5
; Sequence 5, Application US/10027770
; Publication No. US20020151684A1
; GENERAL INFORMATION:
; APPLICANT: MAYER, BRUCE
; APPLICANT: SAKSELA, KALLE
; APPLICANT: KIRCHAUSEN, TOMAS
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10 with site directed mutagenesis
US-10-027-770-5

Query Match          71.7%; Score 944.5; DB 13; Length 269;
Best Local Similarity 72.2%; Pred. No. 2.4e-65;
Matches 184; Conservative 24; Mismatches 40; Indels 7; Gaps 2;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPDKRLEWVATISSGGSYTY 60
DB 6 EVKLIVSGGDLVPGGSLKLSCAASGFTFSHYGMSWRVQTPDKRLEWVATISGRGTTHY 65
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRD-----GHHGVGSSFDYWGQ 114
DB 66 PDSVKGRTISRDNKNTLYLQMSLSKSEDTAMYYCARRRNPYYVSGRGY---FDYWGQ 125
QY 115 TTLTVSSGGSGGGRASGGGSGIIVLTQSLPLSVSLGDOASISCRSSQSIIVHNGNTYL 174
DB 126 ASVTVSSGGSGGSGGSGGSDIVLTQSPASLAVSLGQRATISCRASES-VDSYGNPF 184
QY 175 EHWYLQKPGQSPKLLIYKVNRFSGVPEDFKFGSGSGTDFTLKISRVEAEDLGVYCFQGS 234
DB 185 NWFQKPGQPPKLLIYAIISNRSGVGPARGFSGSGSGTDFTSLNIHPVEEDDPAMYFCQOTKE 244
QY 235 VFWTFGGGTGLEIKR 249
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Db 245 VPWTFGGGKLEIKR 259

RESULT 10

US-10-027-770-2

Sequence 2, Application US/10027770

Publication No. US20020151684A1

GENERAL INFORMATION:

APPLICANT: MAYER, BRUCE

APPLICANT: SAKSELA, KALLE

APPLICANT: KIRCHAUSEN, TOMAS

TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF

FILE REFERENCE: 701039-050001-C

CURRENT APPLICATION NUMBER: US/10/027,770

CURRENT FILING DATE: 2002-06-13

PRIOR APPLICATION NUMBER: PCT/US00/17929

PRIOR FILING DATE: 2000-06-29

PRIOR APPLICATION NUMBER: 60/141,896

PRIOR FILING DATE: 1999-06-30

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 2

LENGTH: 269

TYPE: PRT

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: 3dx, a

OTHER INFORMATION: second-generation ScFv derived from monoclonal

OTHER INFORMATION: antibody 9810

US-10-027-770-2

Query Match 71.0%; Score 935.5; DB 13; Length 269;

Best Local Similarity 71.4%; Pred. No. 1.2e-64;

Matches 182; Conservative 25; Mismatches 41; Indels 7; Gaps 2;

Qy 1 EVQVVESSGGGLVPGGSLKLSCAASGFTFTYMSWVRQTPKRLWVATISSGGSYTY 60

Db 6 EVKLVEGGDLVKEGSLKLSCAASGFTFHYGNSWVRQTPKRLWVATISSGGSYTY 65

Qy 61 PDSVGRFTISRDNKNTLYLQMSLSKSDTAMYYCTRD-----GGHVGSSPFDYWGQ 114

Db 66 PDSVKGRTISRDNKNTLYLQMSLSKSDTAMYYCTRD-----GGHVGSSPFDYWGQ 125

Qy 115 TTLVSSGGGGGGRASGGGSOVLVLTQSPLSLPVSLGDOASISCRSSQSIHNSGNTYL 174

Db 126 ASVTSSGGGGGGGGGGSDVLVLTQSPASLAVSLGQRTATISCRASES-VDNYGFSEF 184

Qy 175 EWLQKPGQPKLLIYKVNRFSGVPDKFSGSGGTFTLKISRVEAEDLGVYFCQGS 234

Db 185 NWFOQKPGQPKLLIYKVNRFSGVPDKFSGSGGTFTLKISRVEAEDLGVYFCQGTKE 244

Qy 235 VPWTFGGGKLEIKR 249

Db 245 VPWTFGGGKLEIKR 259

RESULT 11

US-10-153-401-66

Sequence 66, Application US/10153401

Publication No. US20030114398A1

GENERAL INFORMATION:

APPLICANT: Chatterjee, Malaya

APPLICANT: Foon, Kenneth A.

APPLICANT: Chatterjee, Sunil K.

TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE

TITLE OF INVENTION: TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORRISON & FOERSTER

STREET: 755 PAGE MILL ROAD

CITY: PALO ALTO

STATE: CA

COUNTRY: USA

Zip: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/153,401

FILING DATE: 27-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/293,533

FILING DATE: 1999-04-15

APPLICATION NUMBER: US 08/372,676

FILING DATE: 1995-01-17

APPLICATION NUMBER: US 08/591,196

FILING DATE: 1996-01-16

ATTORNEY/AGENT INFORMATION:

NAME: Catherine M. Polizzi

REGISTRATION NUMBER: 40,130

REFERENCE/DOCKET NUMBER: 304142000202

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 705141

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 263 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 66:

US-10-153-401-66

Query Match 70.2%; Score 924; DB 14; Length 263;

Best Local Similarity 69.8%; Pred. No. 9e-64;

Matches 173; Conservative 34; Mismatches 37; Indels 4; Gaps 2;

Qy 1 EVQLVESGGGLVPGGSLKLSCAASGFTFTYMSWVRQTPKRLWVATISSGGSYTY 60

Db 20 QVQVKEGPFLLVPPSQSLITCTVSGFSLTTYGVSWIRQPPGKGLWLGAIWGDGT-TNY 78

Qy 61 PDSVGRFTISRDNKNTLYLQMSLSKSDTAMYYCTRDGGHVGSSPFDYWGQTTLTVS 120

Db 79 HGLAISRLISIKNSKQVFLKNSLQDDTATYYCAKLGNY---DALDYWGQGSVTVS 135

Qy 121 SGGGGSGGRASGGGSGQIVLTQSPLSLPVSLGDOASISCRSSQSIHNSGNTYLEWYLQK 180

Db 136 SGGGGSGGGGGGGSDVLVLTQSPLSLPVSLGDOASISCRSSQSIHNSGNTYLEWYLQK 195

Qy 181 PQQSPKLLIYKVNRFSGVPDKFSGSGGTFTLKISRVEAEDLGVYFCQGSHPVWTFG 240

Db 196 PQQSPNLLIYFVSNRFGVDPDRFSGSGGTFTLKISRVEAEDLGVYFCQGSHPVWTFG 255

Qy 241 GGTKLEIK 248

Db 256 GGTKLEIK 263

RESULT 12

US-10-239-656-47

Sequence 47, Application US/10239656

Publication No. US20040038339A1

GENERAL INFORMATION:

APPLICANT: KOEHLER, PETER

APPLICANT: RIETHMULLER, GERT

APPLICANT: LUTTERBEUSE, RALF

APPLICANT: BORSCHERT, KATRIN

APPLICANT: KISCHEL, ROMAN

APPLICANT: MAYER, MONIKA

APPLICANT: HOFMEISTER, ROBERT

TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE

TITLE OF INVENTION: TO AN EPITOPE OF THE NK2D RECEPTOR COMPLEX

Db 368 TVSSGGGGGGGGGGGGSELVMTQTPLSLPVSIGDOASISCRSSQSLVHSNGNTYLHWY 427
Qy 178 LQKFCQSPKLLIYKVSNRFSQVDPKFSQSGSGTDFTLKISRVEAEDLGVYFCQSHVPW 237
Db 428 LQKFCQSPKLLIYKVSNRFSQVDPKFSQSGSGTDFTLKISRVEAEDLGVYFCQSHVPY 487
Qy 238 TFGGGTKLEIKR 249
Db 488 TFGGGTKLEIKR 499

RESULT 15
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; Patent No. US20020146750A1
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bivPHI-IL-2
US-09-822-698A-5

Query Match 59.0%; Score 909; DB 9; Length 381;
Best Local Similarity 69.9%; Pred. No. 2e-62;
Matches 174; Conservative 28; Mismatches 37; Indels 10; Gaps 1;

Qy 1 EVQLVESGGGLVQPGGSLKLSCAASGFTSTYTWVRQTPKEKLEWVATISSGGSYTY 60
Db 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWTRQAPGKLEWVSGISSGGSTYY 60

Qy 61 PDVVRGFTTISRDNKNTLYLQMSLKSDEDTAMYCTRDGHHGYGSSFDYWGQGTTLTVS 120
Db 61 ADSVKGRFTTISRDNKNTLYLQMSLRAEDTAVVYCAKHTGGGVWDPIYWGQGTTLTVS 120

Qy 121 SGGGSGGRASGGGSGOIVLTQSLPVSIGDOASISCRSSQSLVHSNGNTYLEWYLOK 180
Db 121 -----SGGGALEIVLTQSLPVSIPVTFGEPAISCRSSQSLHNSGTYLDWYLOK 170

Qy 181 PGQSPKLLIYKVSNRFSQVDPKFSQSGSGTDFTLKISRVEAEDLGVYFCQSHVPWTFG 240
Db 171 PGQSPQLLIYSGSHRASQVDPKFSQSVSGTDFTLISRVEAEDGVVYCMQGLQSPFTFG 230

Qy 241 GGTKLEIKR 249
Db 231 PGTKVDIKR 239

Search completed: July 29, 2004, 09:12:26
Job time : 62.1123 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:27 ; Search time 22.4295 Seconds
(without alignments)
573.123 Million cell updates/sec

Title: US-09-661-992B-84
Perfect score: 1317
Sequence: 1 EVQLVESGGGLVKGSSLK.....PQSHVPTFGGKLEIKR 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1072	81.4	247	3	US-09-227-693-34
2	1072	81.4	248	1	US-08-331-398A-34
3	1072	81.4	248	2	US-08-331-397B-34
4	1072	81.4	248	2	US-08-759-804A-34
5	989	75.1	281	4	US-09-025-769B-178
6	976	74.1	268	4	US-09-554-765-2
7	976	74.1	408	4	US-09-554-765-15
8	976	74.1	409	4	US-09-554-765-14
9	937	71.1	289	3	US-03-184-658-63
10	937	71.1	289	4	US-09-504-262D-63
11	928	70.5	228	5	PCT-US92-08257-9
12	924	70.2	263	2	US-08-752-844-66
13	924	70.2	263	4	US-09-293-533-66
14	920	69.9	282	2	US-08-860-174A-10
15	907.5	68.9	239	2	US-08-553-497A-18
16	896	68.0	240	2	US-08-459-354-4
17	896	68.0	240	2	US-08-077-253-4
18	896	68.0	240	3	US-08-333-840-4
19	876	66.5	245	4	US-08-918-148-75
20	873	66.3	245	4	US-08-918-148-78
21	860.5	65.3	301	2	US-08-661-052-14
22	860.5	65.3	301	3	US-08-188-082-14
23	860.5	65.3	301	4	US-09-364-088-14
24	860.5	65.3	301	4	US-09-102-716-14
25	860.5	65.3	553	3	US-08-661-052-16
26	860.5	65.3	553	3	US-09-188-082-16
27	860.5	65.3	553	4	US-09-364-088-16

28 860.5 65.3 553 4 US-09-102-716-16 Sequence 16, Appl
29 856 65.0 284 3 US-08-564-164A-2 Sequence 2, Appl
30 833 63.2 245 4 US-08-918-148-76 Sequence 76, Appl
31 831.5 63.1 244 4 US-08-918-148-77 Sequence 77, Appl
32 827 62.8 277 2 US-08-256-790-2 Sequence 2, Appl
33 823.5 62.5 535 4 US-08-983-035A-38 Sequence 38, Appl
34 823 62.5 246 1 US-08-257-341-7 Sequence 7, Appl
35 823 62.5 252 1 US-08-133-804-4 Sequence 4, Appl
36 823 62.5 252 1 US-08-461-838-4 Sequence 4, Appl
37 823 62.5 252 2 US-08-461-386-4 Sequence 4, Appl
38 823 62.5 367 1 US-08-257-341-5 Sequence 5, Appl
39 819.5 62.2 365 3 US-08-875-811-53 Sequence 53, Appl
40 819.5 62.2 366 3 US-08-875-811-55 Sequence 55, Appl
41 818.5 62.1 348 4 US-09-646-028-12 Sequence 12, Appl
42 818.5 62.1 361 4 US-09-646-028-14 Sequence 14, Appl
43 817 62.0 240 1 US-08-488-113B-148 Sequence 148, App
44 817 62.0 240 1 US-08-477-484B-148 Sequence 148, App
45 817 62.0 240 2 US-08-646-360-148 Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-227-693-34
; Sequence 34, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-09-227-693-34
Query Match      81.4%; Score 1072; DB 3; Length 247;
Best Local Similarity 83.1%; Pred. No. 7.3e-81;
Matches 206; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVXPGGSLKLSAASGFTFTSYTMSVWVQTPKRLWVAISSGGSYTY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 DVKLVEGGGLVQPGGSLKLSAASGFTFTSYTMSVWVQTPKRLWVAISSGGSYTY 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PDSVREGRTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGGHGYGSSFDYWGQTTLTVS 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SDTVKGRFTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGGHGYGSSFDYWGQTTLTVS 119
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 SGGGSGGGRASGGGSGQIVLTQSPLSLPSVSLGDOASISCRSSQSIIVHSGNTYLEWYLOK 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 SGGGSGGGRASGGGSGQIVLTQSPLSLPSVSLGDOASISCRSSQSIIVHSGNTYLEWYLOK 179
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 PQQSPKLLIYKVSNNRFGVPDKFSGSGSGTDTFTLKISRVEADLGVYVCFQGSHPVPTFG 240
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 PQQSPKLLIYKVSNNRFGVPDKFSGSGSGTDTFTLKISRVEADLGVYVCFQGSHPVPTFG 239
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 GGTLEIK 248
   :|||||:
Db 240 SGTLEIK 247
   :|||||:

RESULT 2
US-08-331-398A-34
; Sequence 34, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid

US-09-661-992b-84.ra1
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-331-398A-34
Query Match      81.4%; Score 1072; DB 1; Length 248;
Best Local Similarity 83.1%; Pred. No. 7.3e-81;
Matches 206; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

QY 1 EVLVESGGGLVXPGGSLKLSAASGFTFTSYTMSVWVQTPKRLWVAISSGGSYTY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 DVKLVEGGGLVQPGGSLKLSAASGFTFTSYTMSVWVQTPKRLWVAISSGGSYTY 61
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 PDSVREGRTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGGHGYGSSFDYWGQTTLTVS 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SDTVKGRFTISRDNKNTLYLQMSLSKSEDTAMTYCTRDGGHGYGSSFDYWGQTTLTVS 119
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 SGGGSGGGRASGGGSGQIVLTQSPLSLPSVSLGDOASISCRSSQSIIVHSGNTYLEWYLOK 180
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 SGGGSGGGRASGGGSGQIVLTQSPLSLPSVSLGDOASISCRSSQSIIVHSGNTYLEWYLOK 179
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 181 PQQSPKLLIYKVSNNRFGVPDKFSGSGSGTDTFTLKISRVEADLGVYVCFQGSHPVPTFG 240
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 180 PQQSPKLLIYKVSNNRFGVPDKFSGSGSGTDTFTLKISRVEADLGVYVCFQGSHPVPTFG 239
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 241 GGTLEIK 248
   :|||||:
Db 240 SGTLEIK 247
   :|||||:

RESULT 3
US-08-331-397B-34
; Sequence 34, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331.397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
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; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-759-804A-34

Query Match 81.4%; Score 1072; DB 2; Length 248;
Best Local Similarity 83.1%; Pred. No. 7.3e-81;
Matches 206; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

QY 1 EVOLVSGGLVKPGGSLKLSCAASGFTPTSTMVWVROTPEKRLWVATISSGGSYTY 60
DQ 2 DVKLVSGLVQPGGSLKLSGATGFTPTSDYMYWVROTPEKRLWVATISSGGSAA 61
QY 61 PDSVVRGFTISRDNANTLYLQMSLKSDEDTAMYYCTRDGHHGSSFDYWGQGLT 120
DQ 62 SDTVKGRFTISRDNANTLYLQMSRLKSEDTAIYSCAR--GLAWGAWFAWYWGQGLT 119
QY 121 SGGGSGGSRASGGGQIVLTQSPSLPVSGLDQASISCRSSQSIIVHNGNTYLEWY 180
DQ 120 SGGGSGGSGGGGSDVLTQSPSLPVSGLDQASISCRSSQSIIVHNGNTYLEWY 179
QY 181 PGQSPKLLIYKVSNRPSGVDPKFGSGSGTDFTLKISRVEADLGVYCFQGSHP 240
DQ 180 PGQSPKLLIYKVSNRPSGVDPKFGSGSGTDFTLKISRVEADLGVYCFQGSHP 239
QY 241 GGTGLEIK 248
DQ 240 SGTGLEIK 247

RESULT 4
US-08-759-804A-34
; Sequence 34, Application US/08759804A
; Patent No. 590296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 248 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-759-804A-34

Query Match 81.4%; Score 1072; DB 2; Length 248;
Best Local Similarity 83.1%; Pred. No. 7.3e-81;
Matches 206; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

QY 1 EVOLVSGGLVKPGGSLKLSCAASGFTPTSTMVWVROTPEKRLWVATISSGGSYTY 60
DQ 2 DVKLVSGLVQPGGSLKLSGATGFTPTSDYMYWVROTPEKRLWVATISSGGSAA 61
QY 61 PDSVVRGFTISRDNANTLYLQMSLKSDEDTAMYYCTRDGHHGSSFDYWGQGLT 120
DQ 62 SDTVKGRFTISRDNANTLYLQMSRLKSEDTAIYSCAR--GLAWGAWFAWYWGQGLT 119
QY 121 SGGGSGGSRASGGGQIVLTQSPSLPVSGLDQASISCRSSQSIIVHNGNTYLEWY 180
DQ 120 SGGGSGGSGGGGSDVLTQSPSLPVSGLDQASISCRSSQSIIVHNGNTYLEWY 179
QY 181 PGQSPKLLIYKVSNRPSGVDPKFGSGSGTDFTLKISRVEADLGVYCFQGSHP 240
DQ 180 PGQSPKLLIYKVSNRPSGVDPKFGSGSGTDFTLKISRVEADLGVYCFQGSHP 239
QY 241 GGTGLEIK 248
DQ 240 SGTGLEIK 247

RESULT 5
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Illeg, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:

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SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-035-769B-178

Query Match 75.1%; Score 989; DB 4; Length 281;
Best Local Similarity 75.6%; Pred. No. 5.8e-74;
Matches 192; Conservative 23; Mismatches 33; Indels 6; Gaps 2;
QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMVSRQTPKLEWVAITSSGGSYTY 60
DB 26 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMVSRQTPKLEWVAITSSGGSYTY 85
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGGHGYGGSFDYWGQGTTLTVS 120
DB 86 ADSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGGHGYGGSFDYWGQGTTLTVS 144
QY 121 -----SGGGSGGRASGGGSGQIVLTQSPSLPVSLGPDQASISCRSSQSIHVSNGTYLE 175
DB 145 SAGGSGGGGGGGGGGGGGGDIWMTQSPSLPVTPGPASISCRSSQSLHNSGNYLD 204
QY 176 WYLOKPGSPKLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYCFQGS 235
DB 205 WYLOKPGSPKLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYCFQGS 264
QY 236 PWTGGGKLEIKR 249
DB 265 PPTFGGKVEIKR 278

RESULT 6

US-09-554-765-2

Query Match 74.1%; Score 976; DB 4; Length 268;
Best Local Similarity 76.7%; Pred. No. 6.4e-73;
Matches 191; Conservative 16; Mismatches 40; Indels 2; Gaps 1;
GENERAL INFORMATION:
APPLICANT: Porter, Robert A
TITLE OF INVENTION: Electroactive Surfaces
FILE REFERENCE: IMIN.P-036
CURRENT APPLICATION NUMBER: US/09/554,765
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent in version 3.2
SEQ ID NO 2
LENGTH: 268
TYPE: PRT
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: anti-E3G antibody fragment
US-09-554-765-2

Query Match 74.1%; Score 976; DB 4; Length 268;
Best Local Similarity 76.7%; Pred. No. 6.4e-73;
Matches 191; Conservative 16; Mismatches 40; Indels 2; Gaps 1;
QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMVSRQTPKLEWVAITSSGGSYTY 60
DB 1 QVQLQESGGGLVNGGSLTSCVASGFTFTNYMSWRQTPKLELVAAINDSGEPIYY 60
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGGHGYGGSFDYWGQGTTLTVS 120
DB 61 PDLKGRVTISRDNKNTLYLQMSLSKSEDTALYYCARLYAVYG--MDYWGQGTTLTVS 118
QY 121 SGGGSGGRASGGGSGQIVLTQSPSLPVSLGPDQASISCRSSQSIHVSNGTYLEWYLOK 180
DB 119 SGGGSGGGGGGGGGGDIETQTPPSLPVSLGQVSISSCRSSQSLVSNRRNRYLHWYLOK 178
QY 181 PQSPKLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYCFQGSHPVPTFG 240

DB 179 PQSPKLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVAEADLGLYFCSSSHVPLTFG 238
QY 241 GGTKLEIKR 249
DB 239 SGTKLEIKR 247

RESULT 7

US-09-554-765-15
Sequence 15, Application US/09554765
Patent No. 6551495
GENERAL INFORMATION:
APPLICANT: Porter, Robert A
APPLICANT: Badley, Robert A
TITLE OF INVENTION: Electroactive Surfaces
FILE REFERENCE: IMIN.P-036
CURRENT APPLICATION NUMBER: US/09/554,765
CURRENT FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: PCT/GB98/03495
PRIOR FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent in version 3.2
SEQ ID NO 15
LENGTH: 408
TYPE: PRT
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: expression product of pPIC.scFv4155-link-HCV4.HIS2t
US-09-554-765-15

Query Match 74.1%; Score 976; DB 4; Length 408;

Best Local Similarity 76.7%; Pred. No. 1.1e-72;
Matches 191; Conservative 16; Mismatches 40; Indels 2; Gaps 1;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMVSRQTPKLEWVAITSSGGSYTY 60
DB 1 QVQLQESGGGLVNGGSLTSCVASGFTFTNYMSWRQTPKLELVAAINDSGEPIYY 60
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGGHGYGGSFDYWGQGTTLTVS 120
DB 61 PDLKGRVTISRDNKNTLYLQMSLSKSEDTALYYCARLYAVYG--MDYWGQGTTLTVS 118
QY 121 SGGGSGGRASGGGSGQIVLTQSPSLPVSLGPDQASISCRSSQSIHVSNGTYLEWYLOK 180
DB 119 SGGGSGGGGGGGGGGDIETQTPPSLPVSLGQVSISSCRSSQSLVSNRRNRYLHWYLOK 178
QY 181 PQSPKLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVEAEDLGVYCFQGSHPVPTFG 240
DB 179 PQSPKLLIYKVSNRFSGVDPDRFSGSGSGTDFTLKISRVAEADLGLYFCSSSHVPLTFG 238
QY 241 GGTKLEIKR 249
DB 239 SGTKLEIKR 247

RESULT 8

US-09-554-765-14
Sequence 14, Application US/09554765
Patent No. 6551495
GENERAL INFORMATION:
APPLICANT: Porter, Robert A
APPLICANT: Badley, Robert A
TITLE OF INVENTION: Electroactive Surfaces
FILE REFERENCE: IMIN.P-036
CURRENT APPLICATION NUMBER: US/09/554,765
CURRENT FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: PCT/GB98/03495
PRIOR FILING DATE: 1998-11-23
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patent in version 3.2
SEQ ID NO 14
LENGTH: 409
TYPE: PRT

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; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: expression product of pPIC.scFv4 155-link-HCV3.HIS2t
US-09-554-765-14

Query Match 74.1%; Score 976; DB 4; Length 409;
Best Local Similarity 76.7%; Pred.No.1.le-72;
Matches 191; Conservative 16; Mismatches 40; Indels 2; Gaps 1;

QY 1 EYLVESGGGLVKGSGSLKSLCAASGFTFTYTMVSRQTPKRLKLEWATISSGGSYTY 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 QVOLQESGGGLVNLGGSMTLSCVASGFTFTYTMVSRQTPKRLKLEWATISSGGSYTY 60
QY 61 PDSVREGRTTISRDAKNTLYLQMSLAKSDEDTAMVYCTRDGGHGYGSSSEPDYMGQGTLLTVS 120
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 PDLTKGRVTISRDAKNTLYLQMSLNFEDTALYYCARITYAVYG--MDYWGQGTTVTVS 118
QY 121 SGGGSGGGRASGGGGGSGTIVLTQSPSLPVSILGDAQISCRSSQSIVHNSNGNTYLEWYLQK 180
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
119 SGGGSGGSGGGGGGGSDIELTQTTPSLPVSILGQVQVSISSRSGSLVSNRRNLYLHWYLQK 178
QY 181 PQGSKLLIYKVSNRFGVDPKFGSGSGGTDFTLKISRVEADLGYVYCFQGSHPVPTFG 240
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
179 PQGSKLLIYKVSNRFGVDPKFGSGSGGTDFTLKISRVAADLGLYFCQGSHPVPTFG 238
QY 241 GGTGLEIKR 249
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
239 GGTGLEIKR 247

RESULT 9
US-09-184-658-63
; Sequence 63, Application US/09184658
; Patent No. 6030792
; GENERAL INFORMATION:
; APPLICANT: Otterness, Ivan G.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Downs, James T.
; APPLICANT: Johnson, Kimberly S.
; TITLE OF INVENTION: Assays for Measurement of Protein Fragments in
; TITLE OF INVENTION: Biological Media
; FILE REFERENCE: PC9946-A
; CURRENT APPLICATION NUMBER: US/09/184,658
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/065,423
; EARLIER FILING DATE: 1997-11-13
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 63
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: 5109 VH - VL
; OTHER INFORMATION: scFv.
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(22)
; OTHER INFORMATION: pCANTAB6 signal peptide; Val at position 1 is most
; OTHER INFORMATION: likely initiator Met.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (23)..(138)
; OTHER INFORMATION: 5109 VH domain.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (139)..(154)
; OTHER INFORMATION: 16 amino acid linker.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (155)..(266)
; OTHER INFORMATION: 5109 VL domain.
; FEATURE:

```

LOCATION: (155)..(266)
OTHER INFORMATION: 5109 VL domain.
FEATURE:
NAME/KEY: SITE
LOCATION: (270)..(279)
OTHER INFORMATION: myc tag.
FEATURE:
NAME/KEY: SITE
LOCATION: (284)..(289)
OTHER INFORMATION: His tag.
US-09-504-262D-63

Query Match 71.1%; Score 937; DB 4; Length 289;

Best Local Similarity 73.1%; Pred. No. 1.1e-69; Indels 6; Gaps 3;
Matches 182; Conservative 27; Mismatches 34;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFTSYTMSWVRQTPKRLKLEWVATISSGGSYTY 60
DB 23 EVQLVESGGGVQPGGSLKLSCAASGFTFTSYTMSWVRQTPKRLKLEWVATISSGGGLTFY 82
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
DB 83 ADSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 137
QY 121 SGGGSGGSGRAGSGGGG-SQIVLTQSLPLSVSLGDSQASISCRSSQSIIVHSNGNTYLEWYLQ 179
DB 138 SGGGSGGSGGSGGSDVMTQPTLTLSTVIGQSASISCKSSQSLGSDGLTYLIWLLQ 197
QY 180 KPGSPKLLIYKVNRFSGVPDKFSGSGGTDFTLTKISRVEAEDLGVIYCFQGSHPVPTF 239
DB 198 RFGSPKRLIFLVSELDGVPDRFTGSGGTDFTLTKISRVEAEDLGVIYCFQGSHPVPTF 257
QY 240 GGTGKLEIK 248
DB 258 GAGTKLEIK 266

RESULT 11

PCT-US92-08257-9
Sequence 9, Application PC/TUS9208257
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: Fitzgerald, David
APPLICANT: Brinkmann, Uli
APPLICANT: Pai, Lee
TITLE OF INVENTION: Recombinant Immunotoxins
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08257
FILING DATE: 19920929
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/737,331
FILING DATE: 30-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 15280-20-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600

TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 228 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-08257-9

Query Match 70.5%; Score 928; DB 5; Length 228;

Best Local Similarity 73.4%; Pred. No. 4.7e-69;
Matches 182; Conservative 17; Mismatches 27; Indels 22; Gaps 2;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFTSYTMSWVRQTPKRLKLEWVATISSGGSYTY 60
DB 2 DVKLVESGGGLVQPGGSLKLSCATSGFTFSDYMYWVRQTPKRLKLEWVATISSNDSSAY 61
QY 61 PDSVGRFTISRDNKNTLYLQMSLSKSEDTAMYYCTRDGGHGYGSSFDYWGQGTTLTVS 120
DB 62 SDTVGRFTISRDNKNTLYLQMSLSKSEDTATYSCAR-GLAWGAWFAYWGQGTTLTVFS 119
QY 121 SGGGSGGSGRAGSGGSGQIVLTQSLPLSVSLGDSQASISCRSSQSIIVHSNGNTYLEWYLQ 180
DB 120 SGGGSGGSGGSGGSDVMTQPTLTLSTVIGQSASISCKSSQSLGSDGLTYLIWLLQ 179
QY 181 KPGSPKLLIYKVNRFSGVPDKFSGSGGTDFTLTKISRVEAEDLGVIYCFQGSHPVPTF 240
DB 180 KPGSPKLLIYKVNRFSGVPDRFSGSGGTDFTLTKISRVEAEDLGVIYCFQGSHPVPTF 219
QY 241 GGTGKLEIK 248
DB 220 SGTGKLEIK 227

RESULT 12

US-08-752-844-66
Sequence 66, Application US/08752844
Patent No. 5935821
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
APPLICANT: Chatterjee, Sunil K.
TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/752,844
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Schiff, J. Michael
REGISTRATION NUMBER: 40,253
REFERENCE/DOCKET NUMBER: 30414-20002.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
TYPE: amino acid

```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-752-844-66

Query Match      70.2%; Score 924; DB 2; Length 263;
Best Local Similarity 69.8%; Pred. No. 1.2e-68;
Matches 173; Conservative 34; Mismatches 37; Indels 4; Gaps 2;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMVSRQTPKRLKLEWVATSSGGSYTY 60
Db 20 QVQVKESGPFLLPPPSQSLITCTVSGFSLTTYGVSMIRQPPGKLEWLGAIWGDGT-TNY 78
QY 61 PDSVRGRFTISRDNKNTLYLQMSLSKSEDTAMYCYCTRDGGHGYGSSFDYWGQGTTLTVS 120
Db 79 HSALISRLSISKDNKSQVFLKLSLQTDATYYCAKLGNY--DALDYMGGQTSVTVS 135
QY 121 SGGGSGGGRASGGGSGQIVLTQSPSLPVSIGLDQASISCRSSQSIHNSNGNTYLEWYLOK 180
Db 136 SGGGSGGGRASGGGSGQIVLTQSPSLPVSIGLDQASISCRSSQSIHNSNGNTYLEWYLOK 195
QY 181 PQQSPKLLIYKVSNRFGVDPKFSGGSGGTDFTLKISRVEADLGVYCYFQGSHPVPTFG 240
Db 196 PQQSPNLLIYFVSNRFGVDPKFSGGSGGTDFTLKISRVEADLGVYCYFQGSHPVPTFG 255
QY 241 GGTKLEIK 248
Db 256 GGTKLEIK 263

RESULT 13
US-09-293-533-66
; Sequence 66, Application US/09293533
; Patent No. 6509016
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; APPLICANT: Foon, Kenneth A.
; APPLICANT: Chatterjee, Sunil K.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY 1A7 AND USE FOR THE
; TREATMENT OF MELANOMA AND SMALL CELL CARCINOMA
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/293,533
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,844
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schiff, J. Michael
; REGISTRATION NUMBER: 40,253
; REFERENCE/POCKET NUMBER: 30414-20002.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 66:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 263 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

Query Match      70.2%; Score 924; DB 2; Length 263;
Best Local Similarity 69.8%; Pred. No. 1.2e-68;
Matches 173; Conservative 34; Mismatches 37; Indels 4; Gaps 2;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMVSRQTPKRLKLEWVATSSGGSYTY 60
Db 20 QVQVKESGPFLLPPPSQSLITCTVSGFSLTTYGVSMIRQPPGKLEWLGAIWGDGT-TNY 78
QY 61 PDSVRGRFTISRDNKNTLYLQMSLSKSEDTAMYCYCTRDGGHGYGSSFDYWGQGTTLTVS 120
Db 79 HSALISRLSISKDNKSQVFLKLSLQTDATYYCAKLGNY--DALDYMGGQTSVTVS 135
QY 121 SGGGSGGGRASGGGSGQIVLTQSPSLPVSIGLDQASISCRSSQSIHNSNGNTYLEWYLOK 180
Db 136 SGGGSGGGRASGGGSGQIVLTQSPSLPVSIGLDQASISCRSSQSIHNSNGNTYLEWYLOK 195
QY 181 PQQSPKLLIYKVSNRFGVDPKFSGGSGGTDFTLKISRVEADLGVYCYFQGSHPVPTFG 240
Db 196 PQQSPNLLIYFVSNRFGVDPKFSGGSGGTDFTLKISRVEADLGVYCYFQGSHPVPTFG 255
QY 241 GGTKLEIK 248
Db 256 GGTKLEIK 263

RESULT 14
US-08-860-174A-10
; Sequence 10, Application US/08860174A
; Patent No. 5989830
; GENERAL INFORMATION:
; APPLICANT: DAVIS, Paul James
; APPLICANT: VAN DER LOGT, Cornelis Paul Erik
; APPLICANT: VERHOEIJEN, Martine Elisa
; APPLICANT: WILSON, Steve
; TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
; ANTIBODY FRAGMENT ANALOGUE
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
; STREET: 1100 New York Avenue, N.W.
; CITY: WASHINGTON, D.C.
; STATE:
; COUNTRY: UNITED STATES
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS DOS Text
; SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/860,174A
; FILING DATE: June 16, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95307332.7
; FILING DATE: October 16, 1995
; APPLICATION NUMBER: PCT/EP/96/03605
; FILING DATE: August 14, 1996
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 282 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-860-174A-10

Query Match      69.9%; Score 920; DB 2; Length 282;
Best Local Similarity 71.6%; Pred. No. 2.8e-68;
Matches 179; Conservative 23; Mismatches 46; Indels 2; Gaps 2;

QY 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMVSRQTPKRLKLEWATISSGGSYTY 60
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Db      23 QVQVQSGDGLVKGPGSLTLSCATSGFTFSSYAFSWVRQTSDKSLVWVATISDTTYTYY 82
QY      61 PDSVGRFTISRDNKNTLYLQMSLKSSEDAMYYCTRDGGHGYGSGFDYWGQGTTLTVS 120
Db      83 SDNVKGRFTISRDNKNTLYLQMSLKSSEDAMYYCAHGYGKG-YFDYWGQGTTLTVS 141
QY      121 SGGGGSGGRASGGGSGQIVLQSPVLSLQDQASISCRSSQSIHVS-NGNTYLEWYLQ 179
Db      142 SGGGGSGGSGGGSGGSDIELTQSPFLTVTAGEKVTWCKSGQSLNSVQRYLTYQQ 201
QY      180 KPGQSPKLLIYKVNRFSGVDPKFSGGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVWTF 239
Db      202 KPGQPKLLIYKVNRFSGVDPKFSGGSGGTDFTLKISRVEAEDLGVYYCNDYTPPTF 261
QY      240 GGGTKLEIKR 249
Db      262 GGGTKLEIKR 271

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RESULT 15

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US-08-553-497A-18
; Sequence 18, Application US/08553497A
; Patent No. 5844093
; GENERAL INFORMATION:
; APPLICANT: KETTLEBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCESCA
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCESC
; APPLICANT: PIULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553.497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104150.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid

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; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-497A-18
Query Match      68.9%; Score 907.5; DB 2; Length 239;
Best Local Similarity 73.1%; Pred. No. 2.4e-67;
Matches 177; Conservative 23; Mismatches 39; Indels 3; Gaps 2;
QY      1 EVQLVESGGGLVKGPGSLKSLSCAASGFTFSTYTMSEWVRQTPEKRLVWVATISSGSYTY 60
Db      1 EVKIQESGGDLVKGPGSLKSLSCAASGFTFSSYGMSWVRQTPEKRLVWVATISSGGAIYY 60
QY      61 PDSVGRFTISRDNKNTLYLQMSLKSSEDAMYYCTRDGGHGYGSGFDYWGQGTTLTVS 120
Db      61 PDSVGRFTISRDNKNTLYLQMSLKSSEDAMYYCARLETGDTY--ALDYWGQGTTLTVS 118
QY      121 SGGGGSGGRASGGGSGQIVLQSPVLSLQDQASISCRSSQSIHVSNGNTYLEWYLQK 180
Db      119 SGGGGSGGSGGGSGGSDIELTQSPASLAVSLGQRATIFCKSQSYDY-DGDSYMNWYQK 177
QY      181 PQGSPKLLIYKVNRFSGVDPKFSGGSGGTDFTLKISRVEAEDLGVYYCFQGSHPVWTFG 240
Db      178 PQGPPKLLIYARNSLNSGVDPKFSGGSGGTDFTSLNHPVEEDIAMYFCQSRKVPWSFG 237
QY      241 GG 242
Db      238 GG 239

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Search completed: July 29, 2004, 08:53:08
Job time : 23.4295 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:27 ; Search time 24.3799 Seconds
(without alignments)
982.436 Million cell updates/sec

Title: US-09-661-992B-86
Perfect score: 1309
Sequence: 1 EVQLQESGGGLVPGGSLKL.....QQSNEDPLTGTGTRLEIKR 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: Pirl1.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	56.2	233	JC5322	p53 specific singl
2	696.5	53.2	268	A56446	Ig heavy chain v r
3	686	52.4	249	S41374	single chain Fv an
4	539.5	41.2	122	E27888	Ig kappa chain v r
5	532	40.6	111	KVMS37	Ig heavy chain v r
6	518	39.6	112	S26327	Ig heavy chain v r
7	517.5	39.5	117	PL0249	Ig heavy chain v r
8	517	39.5	107	S26343	Ig kappa chain v r
9	516	39.4	119	F27888	Ig heavy chain v r
10	514.5	39.3	120	S55336	Ig heavy chain v r
11	514.5	39.3	120	S55337	Ig heavy chain v r
12	514.5	39.3	138	S09258	Ig heavy chain v r
13	514	39.3	115	S63596	Ig kappa chain v r
14	514	39.3	121	I27887	Ig heavy chain v r
15	513	39.2	107	S26344	Ig kappa chain v r
16	512	39.1	131	KVMSM6	Ig kappa chain pre
17	510.5	39.0	117	PL0252	Ig heavy chain v r
18	509	38.9	119	D27889	Ig heavy chain v r
19	508.5	38.8	120	S55339	Ig heavy chain v r
20	508	38.8	121	H27888	Ig heavy chain v r
21	505.5	38.6	548	S38864	Ig epsilon chain C
22	501.5	38.3	120	S55338	Ig heavy chain v r
23	501	38.3	111	D45722	anti-glycoprotein
24	500.5	38.2	119	PH0098	Ig heavy chain v r
25	500.5	38.2	124	D27888	Ig heavy chain v r
26	500	38.2	119	S27888	Ig heavy chain v r
27	498	38.0	118	PH0097	Ig heavy chain v r
28	497	38.0	118	PH0096	Ig heavy chain v r
29	496	37.9	254	B31790	Ig heavy chain v r

ALIGNMENTS

RESULT 1

JC5322

p53 specific single-chain antibody Fab421 - human

C:Species: Homo sapiens (man)

C>Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997

C/Accession: JC5322

R/Jannot, C.B.; Hynes, N.E.

Biochem. Biophys. Res. Commun. 230, 242-246, 1997

A/Title: Characterization of scFv-421, a single-chain antibody targeted to p53.

A/Reference number: JC5322; MUID:97168950; PMID:9016757

A/Accession: JC5322

A/Molecule type: mRNA

A/Residues: 1-233 <JAN>

A/Experimental source: hydricloma cell

C/Comment: This protein specifically binds the tumor suppressor protein p53. It restores

Query Match 56.2%; Score 736; DB 2; Length 233;

Best Local Similarity 61.2%; Pred No. 1.3e-46;

Matches 150; Conservative 26; Mismatches 55; Indels 14; Gaps 4;

QY	5	QESGGGLVPGGSLKLSCAAGFTFSYTMVSRVOTPEKRLFWATI--SGSGSSTYYPD	62
DB	1	QESGAELVRSGASVKLSCTTSGFNINDYMHVKKRPEQGLEWIGRIDPENGADWTRSS	60
QY	63	SVKGRFTISRDNKNTLYIQMSSLESDTAMYYCTREGGGFTVWYFDVWNGTILVTYSA	122
DB	61	GVKA--TMDTSSNTAYLQSSLTSETAVYIC-----NAGMDYWGQGITVTYSS	109
QY	123	GGGGSGGRASGGGSENVLTQSPASLAVSLGORATISCRASESVDSYGVNFMHWYQQIPG	182
DB	110	GGGGSGGRASGGGSDIELTQSPASLAVSLGORATISCRASKSVTSYGVNFMHWYQQXP	169
QY	183	QPKLLIYRASNLSEGIIPARFGSGSRDFTILTNFVADDDVATYVCCQSNEDPLTFTG	242
DB	170	QPKLLIYLVSNLSEGVIPARFGSGSGDFTILNHFVEEDAATYVCOHIRELTSEG-G	228
QY	243	TRLEI 247	
DB	229	TKLEI 233	

RESULT 2

A56446

Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C:Species: Mus musculus (house mouse)

C>Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C/Accession: A56446

R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical

A/Reference number: A56446; MUID:95229583; PMID:7713873

A/Accession: A56446

QY 200 PARFSGSGSRDFTLTINPVEADDVATYYCOOSNEDPLTFTGTRLEIK 248
Db 63 PARFSGSGSRDFTLTINPVEADDVATYYCOOSNEDPYTFGGTKLEIK 111

RESULT 6
S26327
Ig heavy chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
C/Accession: S26327
R/Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A/Title: Antibodies that are specific for a single amino acid interchange in a protein e
A/Reference number: S26309; MUID:91341421; PMID:1908510
A/Accession: S26327
A/Molecule type: mRNA
A/Residues: 1-112 <STA>
A/Cross-references: EMBL:X59192
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:9-91/Domain: immunoglobulin homology <IMM>

Query Match 39.6%; Score 518; DB 2; Length 112;
Best Local Similarity 87.1%; Pred. No. 4.3e-31;
Matches 101; Conservative 4; Mismatches 7; Indels 4; Gaps 2;

QY 7 SGGGLVPGGSLKLSCAASGFTSSYTMVWVROTPEKRLWVATISSGGSSTYYPDSVKG 66
Db 1 SGGGLVPGGSLKLSCAASGFTSSYTMVWVROTPEKRLWVATISSGGSSTYYPDSVKG 59

QY 67 RFTISRDNKNTLYLQMSLSRSEDATMYCTREGGFTVNWYFDVWGAGTLVTVA 122
Db 60 RFTISRDNKNTLYLQMSLSRSEDATMYCARLYGNY--WYFDVWGAGTLVTVSS 112

RESULT 7
PL0249
Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C/Accession: PL0249
R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
J. Exp. Med. 171, 265-297, 1990
A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
A/Reference number: PL0231; MUID:90111618; PMID:2104919
A/Accession: PL0249
A/Molecule type: mRNA
A/Residues: 1-117 <SHL>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-49/Region: framework 2
F:50-66/Region: complementarity-determining 2
F:67-98/Region: framework 3
F:99-108/Region: complementarity-determining 3
F:109-117/Region: framework 4

Query Match 39.5%; Score 517.5; DB 2; Length 117;
Best Local Similarity 83.3%; Pred. No. 4.9e-31;
Matches 100; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYTMVWVROTPEKRLWVATISSGGSSTYY 60
Db 1 EVKLVESGGGLVPGGSLKLSCAASGFTFSYTMVWVROTPEKRLWVATISSRGGSTYY 60

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDATMYCTREGGFTVNWYFDVWGAGTLVTV 120
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDATMYCARRDYS---HWFDVWGAGTLVTV 117

RESULT 8
S26343
Ig kappa chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C/Accession: S26343
R/Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A/Title: Antibodies that are specific for a single amino acid interchange in a protein e
A/Reference number: S26309; MUID:91341421; PMID:1908510
A/Accession: S26343
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-107 <STA>
A/Cross-references: EMBL:X59207; NID:952334; PID:CAA41917.1; PID:91334073
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-93/Domain: immunoglobulin homology <IMM>

Query Match 39.5%; Score 517; DB 2; Length 107;
Best Local Similarity 92.5%; Pred. No. 4.8e-31;
Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 140 VLTQSPASLVSLGQRATISCRASESDVSYGNFMHWYQQIPGQPPLLIYRASNLSEGI 199
Db 2 VMTQTPASLVSLGQRATISCRASESDVSYGNFMHWYQQKPGQPPKLLIYRASNLSEGI 61

QY 200 PARFSGSGSRDFTLTINPVEADDVATYYCOOSNEDPLTFTGTRPL 245
Db 62 PARFSGSGSRDFTLTINPVEADDVATYYCOOSNEDPFTFGSGTKL 107

RESULT 9
F27888
Ig heavy chain V region (H158-89H4) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C/Accession: F27888
R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerthard, W.
EMBO J. 5, 1577-1587, 1986
A/Title: Structural and functional implications of a restricted antibody response to a
A/Reference number: A91043; MUID:86300658; PMID:2427335
A/Accession: F27888
A/Molecule type: DNA
A/Residues: 1-119 <CAT>
A/Experimental source: strain Balb/c
A/Note: This sequence was determined from the germline gene
C/Comment: This chain was isolated from a hybridoma protein that binds influenza virus
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 39.4%; Score 516; DB 2; Length 119;
Best Local Similarity 84.3%; Pred. No. 6.4e-31;
Matches 102; Conservative 5; Mismatches 12; Indels 2; Gaps 1;

QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYTMVWVROTPEKRLWVATISSGGSSTYY 60
Db 1 DVKLVESGGGLVPGGSLKLSCAASGFTFSYTMVWVROTPEKRLWVATISSGGSSTYY 60

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDATMYCTREGGFTVNWYFDVWGAGTLVTV 120
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDATMYCPR--GETYYDYANDWYQGTSVTV 118

QY 121 S 121
Db 119 S 119

RESULT 10
S55536
Ig heavy chain V region pe20 - mouse (fragment)
C/Species: Mus musculus (house mouse)

C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C/Accession: S55536

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using mutations in the variable region genes.

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55536

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-120 <BOE>

A/Cross-references: EMBL:X82589; NID:g854304; PIDN:CAA57925.1; PID:g854305

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 514.5; DB 2; Length 120;
Best Local Similarity 84.3%; Pred. No. 8.3e-31;
Matches 102; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

Qy 2 VQLQESGGGLVKGPGSLKLSCAASGFTFSYTSWVRQTPKEKLEWVAITSSGGSSTYYP 61

Db 1 VQLQESGGGLVKGPGSLKLSCAASGFTFSYTSWVRQTPKEKLEWVAITSSGGSSTYYP 60

Qy 62 DSVKGRFTISRDNKNTLYLQMSLSRSEDYTSYCTREGGFTVNNYFDVWGAGTLTVTS 121

Db 61 DSVKGRFTISRDNKNTLYLQMSLSRSEDYTSYCTREGGFTVNNYFDVWGAGTLTVTS 119

Qy 122 A 122

Db 120 S 120

RESULT 11

Ig heavy chain V region pe21 - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999

C/Accession: S55537

R/Boettger, V.; Boettger, A.; Lane, E.B.; Spruce, B.A.

J. Mol. Biol. 247, 932-946, 1995

A/Title: Comprehensive epitope analysis of monoclonal anti-proenkephalin antibodies using mutations in the variable region genes.

A/Reference number: S55528; MUID:95239763; PMID:7536850

A/Accession: S55537

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-120 <BOE>

A/Cross-references: EMBL:X82590; NID:g854306; PIDN:CAA57926.1; PID:g854307

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:14-97/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 514.5; DB 2; Length 120;
Best Local Similarity 85.1%; Pred. No. 8.3e-31;
Matches 103; Conservative 3; Mismatches 14; Indels 1; Gaps 1;

Qy 2 VQLQESGGGLVKGPGSLKLSCAASGFTFSYTSWVRQTPKEKLEWVAITSSGGSSTYYP 61

Db 1 VQLQESGGGLVKGPGSLKLSCAASGFTFSYTSWVRQTPKEKLEWVAITSSGGSSTYYP 60

Qy 62 DSVKGRFTISRDNKNTLYLQMSLSRSEDYTSYCTREGGFTVNNYFDVWGAGTLTVTS 121

Db 61 DSVKGRFTISRDNKNTLYLQMSLSRSEDYTSYCTREGGFTVNNYFDVWGAGTLTVTS 119

Qy 122 A 122

Db 120 S 120

RESULT 12

Ig heavy chain V region precursor - mouse (fragment)

S09258

C/Species: Mus musculus (house mouse)

C/Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999

C/Accession: S09258

R/Hanada, H.; Maerawa, K.; Tsuruo, T.

Nucleic Acids Res. 18, 1900, 1990

A/Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK

A/Reference number: S09258; MUID:90245594; PMID:2110659

A/Accession: S09258

A/Molecule type: DNA

A/Residues: 1-138 <HAM>

A/Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545

C/Genetics:

A/Introns: 16/1

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 514.5; DB 2; Length 138;
Best Local Similarity 83.6%; Pred. No. 9.6e-31;
Matches 102; Conservative 4; Mismatches 13; Indels 3; Gaps 1;

Qy 1 EVQLQESGGGLVKGPGSLKLSCAASGFTFSYTSWVRQTPKEKLEWVAITSSGGSSTYYP 60

Db 20 EVILVESGGGLVKGPGSLKLSCAASGFTFSYTSWVRQTPKEKLEWVAITSSGGSSTYYP 79

Qy 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYTSYCTREGGFTVNNYFDVWGAGTLTVT 120

Db 80 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYTSYCTREGGFTVNNYFDVWGAGTLTVT 136

Qy 121 SA 122

Db 137 SA 138

RESULT 13

S63596

Ig kappa chain V region - mouse

C/Species: Mus musculus (house mouse)

C/Date: 28-Oct-1986 #sequence_revision 13-Mar-1997 #text_change 21-Jan-2000

C/Accession: S63596

R/Verdaguer, N.; Mateu, M.G.; Bravo, J.; Domingo, E.; Pita, I.

J. Mol. Biol. 256, 364-376, 1996

A/Title: Induced pocket to accommodate the cell attachment Arg-Gly-Asp motif in a neutral

A/Reference number: S63596; MUID:96174482; PMID:8594203

A/Accession: S63596

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-115 <VER>

A/Cross-references: GS:S81196; NID:g1336821; PIDN:AAB36171.1; PID:g1336822

C/Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-94/Domain: immunoglobulin homology <IMM>

Query Match 39.3%; Score 514; DB 2; Length 115;
Best Local Similarity 90.0%; Pred. No. 8.6e-31;
Matches 99; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 140 VITQSPASLAVSLGQRTATISCRASESDSYGNFMHYQQIPGQPKLLIYRASNLSEGI 199

Db 3 VITQSPASLAVSLGQRTATISCRASESDSYGNFMHYQQIPGQPKLLIYRASNLSEGI 62

Qy 200 PARFSGSGSRDFTLTINPVEADVDVATYCCQSNEDLTFTGTRLEIKR 249

Db 63 PDRFSGSGSRDFTLTIDPVEADVDVATYCCQSNEDLTFTGTRLEIKR 112

RESULT 14

I27887

Ig heavy chain V region (H37-45) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C/Accession: I27887

R/Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to a d
A:Reference: A91043; PMID:86300658; PMID:2427335
A:Accession: J27887
A:Molecule type: DNA
A:Residues: 1-121 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match	39.3%; Score 514; DB 2; Length 121;
Best Local Similarity	85.5%; Pred. No. 9.le-31;
Matches 101; Conservative	3; Mismatches 17; Indels 0; Gaps 0;
QY	1 EVQVQESGGGLVKGPGSLKLSCAASGFTSSIVTMSWVROTPEKRLIEWATISSGGSSTYY 60
Db	1 EVMVVESGGGLVKGPGSLKLSCAASGFTSIYAMSWVROTPEKRLIEWATISSGGSSTYY 60
QY	61 PDSVKGRFTISRDNAKNTLYLQMSLRSEDAMYCTREGGGFTVNWFVDVWGAGTLVT 120
Db	61 PDSVKGRFTISRDNAKNTLYLQMSLRSEDAMYCAREGLRLEDYANDYWGGQTSTVT 120
QY	121 S 121
Db	121 S 121

RESULT 15
S26344
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Jun-2000
C:Accession: S263344
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421; PMID:1908510
A:Accession: S26344
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <STA>
A:Cross-references: EMBL:X59209; NID:G52336; PIDN:CAA41919.1; PID:g1334074
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
I:15-93/Domain: immunoglobulin homology <IMW>

Query Match	39.2%	Score 513;	DB 2;	Length 107;
Best Local Similarity	92.5%;	Pred. No. 9.4e-31;		
Matches 98; Conservative 4;	Mismatches 4;	Indels 0;	Gaps 0;	
<hr/>				
OY	140	VLTQSPASLVGLQRATISCRASESVDSYGYNFMHWYQQIIPGQPPELLIVRASNLSEGI	199	
	:	:	:	:
Ddb	2	VMTQTASLVGLQRATISCRASESVDSYGNSFMHWYQKPGQPKLLIVRASNLSEGI	61	
	:	:	:	:
<hr/>				
OY	200	PARSGGSRTDFTLINPVEADVATYYCOOSNEDPLTFGTGTL	245	
	:	:	:	:
Ddb	62	PARSGGSRTDFTLINPVEADVATYYCOOSNEDPYTGGGTKL	107	
	:	:	:	:

Search completed: July 29, 2004, 08:51:48
Job time : 24.3799 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 16.5783 Seconds
(without alignments)
782.073 Million cell updates/sec

Title: US-09-661-992B-86
Perfect score: 1309
Sequence: 1 EVQLQESGGGIVKFGSGSLK.....QQSNEDPLTFTGTTRLEIKR 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	532	40.6	111	1 KV3H_MOUSE	P01650 mus musculus
2	517	39.5	111	1 KV3K_MOUSE	P01663 mus musculus
3	512	39.1	111	1 KV3J_MOUSE	P01662 mus musculus
4	512	39.1	131	1 KV3I_MOUSE	P01661 mus musculus
5	493	37.7	132	1 KV3F_MOUSE	P01658 mus musculus
6	483	36.9	112	1 KV3G_MOUSE	P01659 mus musculus
7	469	35.8	117	1 HV55_MOUSE	P18526 mus musculus
8	468	35.8	111	1 KV3N_MOUSE	P01686 mus musculus
9	467	35.7	111	1 KV3M_MOUSE	P01685 mus musculus
10	465	35.5	111	1 KV3O_MOUSE	P01667 mus musculus
11	464	35.4	117	1 HV54_MOUSE	P18525 mus musculus
12	462	35.3	98	1 HV57_MOUSE	P18528 mus musculus
13	462	35.3	111	1 KV3S_MOUSE	P01671 mus musculus
14	460.5	35.2	97	1 HV56_MOUSE	P18527 mus musculus
15	458	35.0	111	1 KV3Q_MOUSE	P01689 mus musculus
16	457	34.9	111	1 KV3L_MOUSE	P01684 mus musculus
17	456	34.8	111	1 KV3R_MOUSE	P01670 mus musculus
18	456	34.8	111	1 KV3T_MOUSE	P01672 mus musculus
19	453	34.6	117	1 HV58_MOUSE	P18529 mus musculus
20	450	34.4	111	1 KV3U_MOUSE	P01673 mus musculus
21	441	33.7	136	1 HV16_MOUSE	P01783 mus musculus
22	440.5	33.7	110	1 KV3P_MOUSE	P01688 mus musculus
23	440	33.6	111	1 KV3A_MOUSE	P01654 mus musculus
24	439	33.5	111	1 KV3D_MOUSE	P03977 mus musculus
25	433	33.1	117	1 HV53_MOUSE	P18524 mus musculus
26	432.5	33.0	112	1 KV3C_MOUSE	P01655 mus musculus
27	431	32.9	111	1 KV3B_MOUSE	P01656 mus musculus
28	426	32.5	117	1 HV59_MOUSE	P18530 mus musculus
29	422	32.2	108	1 KV3V_MOUSE	P01674 mus musculus
30	419	32.0	117	1 HV3C_HUMAN	P01764 homo sapien
31	417	31.9	122	1 HV3G_HUMAN	P01768 homo sapien
32	416	31.8	119	1 HV38_MOUSE	P01808 mus musculus
33	413	31.6	114	1 HV3B_HUMAN	P01763 homo sapien

34	412	31.5	111	1 KV3E_MOUSE	P01657 mus musculus
35	411	31.4	122	1 HV20_MOUSE	P01789 mus musculus
36	409.5	31.3	121	1 HV3J_HUMAN	P01771 homo sapien
37	404.5	30.9	115	1 HV32_MOUSE	P01801 mus musculus
38	404	30.9	116	1 HV3T_HUMAN	P01781 homo sapien
39	402.5	30.7	123	1 HV18_MOUSE	P01787 mus musculus
40	402	30.7	122	1 HV21_MOUSE	P01790 mus musculus
41	402	30.7	126	1 HV3K_HUMAN	P01772 homo sapien
42	401.5	30.7	123	1 HV19_MOUSE	P01788 mus musculus
43	401.5	30.7	142	1 HV01_RAT	P01805 rattus norv
44	400.5	30.6	117	1 HV02_CANFA	P01785 canis famil
45	400.5	30.6	123	1 HV22_MOUSE	P01791 mus musculus

ALIGNMENTS

```
RESULT 1
KV3H_MOUSE
ID KV3H_MOUSE STANDARD; PRT; 111 AA.
AC P01660;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region PC 3741/TPC 111.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (PC 3741).
RX MEDLINE=79012520; PubMed=99744;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
RT diversity.";
RL Nature 276:785-790(1978).
RN [2]
RP SEQUENCE (TEPC 111).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
RT related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).
CC -I- MISCELLANEOUS: THE PC 3741 AND TPC 111 SEQUENCES ARE IDENTICAL.
DR PIR; A93204; KMS37.
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 54 60
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 61 92
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 93 101
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
FT BY SIMILARITY.
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;
Query Match 40.6%; Score 532; DB 1; Length 111;
Best Local Similarity 94.5%; Pred. No. 3.9e-35;
Matches 103; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 140 VLTQSPASLVSLGQRATISCRASESVDSYGVNFWHTQCIIPGQPPKLLIYRASNLSEGI 199
Db 3 VLTQSPASLVSLGQRATISCRASESVDSYGVNFWHTQCIIPGQPPKLLIYRASNLSEGI 62
QY 200 PARFSGSGSRDTFTLTINPVEADVVATYYCOQSNEDPLTFTGTGTRLEIK 248
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Db 63 PARFSGSGSRDFTLTINPVEADDVATVYCOQSNEDPVTGCGTKLEIK 111
RESULT 2
KV3K_MOUSE STANDARD; PRT; 111 AA.
ID KV3K_MOUSE STANDARD; PRT; 111 AA.
AC P01663;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR HSSP; P01679; 2FB7.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DE Ig kappa chain V-III region PC 4050.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
DR HSSP; P01679; 2FB7.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12005 MW; 39D87619313453CB CRC64;

Query Match 39.5%; Score 517; DB 1; Length 111;
Best Local Similarity 89.9%; Pred. No. 5.7e-34;
Matches 98; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 140 VLTQSPASVLSLQGRATISCRASESDSYGNFMHWYQQIPGQPPLIYRASNLSEGI 199
Db 3 VLTQSPASVLSLQGRATISCRASESDSYGNFMHWYQQIPGQPPLIYRASNLSEGV 62
QY 200 PARFSGSGSRDFTLTINPVEADDVATVYCOQSNEDPVTGCGTKLEIK 248
Db 63 PARFSGSGSRDFTLTIDPVEADDAATVYCOQNNEDPVTGCGTKLEIK 111
RESULT 3
KV3J_MOUSE STANDARD; PRT; 111 AA.
ID KV3J_MOUSE STANDARD; PRT; 111 AA.
AC P01662;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region ABPC 22/PC 9245.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE (ABPC 22).
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).
RN [2]

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RP SEQUENCE (PC 9245).
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.
DR HSSP; P01679; 2FB7.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 39.1%; Score 512; DB 1; Length 111;
Best Local Similarity 89.9%; Pred. No. 1.4e-33;
Matches 98; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 140 VLTQSPASVLSLQGRATISCRASESDSYGNFMHWYQQIPGQPPLIYRASNLSEGI 199
Db 3 VLTQSPASVLSLQGRATISCRASESDSYGNFMHWYQQIPGQPPLIYRASNLSEGV 62
QY 200 PARFSGSGSRDFTLTINPVEADDVATVYCOQSNEDPVTGCGTKLEIK 248
Db 63 PARFSGSGSRDFTLTIDPVEADDAATVYCOQNNEDPVTGCGTKLEIK 111
RESULT 4
KV3I_MOUSE STANDARD; PRT; 131 AA.
ID KV3I_MOUSE STANDARD; PRT; 131 AA.
AC P01661;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region MOPC 63 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-35.
RX MEDLINE=78235887; PubMed=98179;
RA Burstein Y., Schechter I.;
RT "Primary structures of N-terminal extra peptide segments linked to
the variable and constant regions of immunoglobulin light chain
precursors: implications on the organization and controlled
expression of immunoglobulin genes.";
RL Biochemistry 17:2392-2400 (1978).
RN [2]
RP SEQUENCE OF 21-131.
RX MEDLINE=73140225; PubMed=4691517;
RA McKean D.J., Potter M., Hood L.E.;
RT "Mouse immunoglobulin chains. Pattern of sequence variation among
RT kappa chains with limited sequence differences.";
RL Biochemistry 12:760-771 (1973).
RN [3]
RP REVISIONS.
RX MEDLINE=79012520; PubMed=99744;
RA McKean D.J., Bell M., Potter M.;
RT "Mechanisms of antibody diversity: multiple genes encode structurally
related mouse kappa variable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917 (1978).

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DR PIR: B90412; KVM5M6.
 DR HSP; P01679; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 DR Immunoglobulin V region; Signal.
 KW SIGNAL 1 20
 FT CHAIN 21 131 IG KAPPA CHAIN V-III REGION MOPC 63.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 59 73 FRAMEWORK-2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 81 112 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-4.
 FT DOMAIN 122 131 BY SIMILARITY.
 FT DISULFID 43 112
 FT NON TER 131 131
 SQ SEQUENCE 131 AA; 14291 MW; D212EC9F08DC880A CRC64;
 Query Match 39.1%; Score 512; DB 1; Length 131;
 Best Local Similarity 86.1%; Pred. No. 1.7e-33;
 Matches 99; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
 QY 134 GGSSENVLTQSPASVAVSLGQRATISCRASESDSYGNFMHWYQQIPGPPKLLIYRAS 193
 Db 17 GSTGNVLTQSPASVAVSLGQRATISCRASESDSYGNFMHWYQQIPGPPKLLIYRAS 76
 QY 194 NLESGIPARFSGSGSRDTFTLTINPVEADDAVATYYCOQSNEDPLTFTGTGLEIKR 249
 Db 77 NLESGVPAFSGSGSRDTFTLTIDPVEADDAATYYCOQNNEDPWTGGTKLEIK 131
 RESULT 5
 KV3F_MOUSE
 ID KV3F_MOUSE STANDARD; PRT; 132 AA.
 AC P01658;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region MOPC 321 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-37.
 RX MEDLINE=78235887; PubMed=98179;
 RA Burstein Y., Schechter I.;
 RT "Primary structures of N-terminal extra peptide segments linked to
 RT the variable and constant regions of immunoglobulin light chain
 RT precursors: implications on the organization and controlled
 RT expression of immunoglobulin genes.";
 RL Biochemistry 17:2392-2400(1978).
 RN [2]
 RP SEQUENCE OF 21-132.
 RX MEDLINE=73140224; PubMed=4120629;
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse immunoglobulin chains. Partial amino acid sequence of a kappa
 RT chain.";
 RL Biochemistry 12:749-759(1973).
 CC -1- MISCELLANEOUS: THE PARTIAL SEQUENCE OF THE C REGION OF THIS
 CC BENCE-JONES PROTEIN WAS ALSO DETERMINED. IT DIFFERS FROM THAT
 CC REPORTED FOR MOLEC MOPC 21 ONLY IN THE TRANSPOSITION OF TWO NEARBY
 CC RESIDUES.
 DR PIR: A90412; KVM532.
 DR HSP; P01679; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.

KW Immunoglobulin V region; Bence-Jones protein; Signal.
 KW SIGNAL 1 20
 FT CHAIN 21 132 IG KAPPA CHAIN V-III REGION MOPC 321.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 59 73 FRAMEWORK-2.
 FT DOMAIN 74 80 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 81 112 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 113 121 COMPLEMENTARITY-DETERMINING-4.
 FT DISULFID 43 112 BY SIMILARITY.
 FT NON TER 132 132
 SQ SEQUENCE 132 AA; 14523 MW; 9F3B809BB773FBE9 CRC64;
 Query Match 37.7%; Score 493; DB 1; Length 132;
 Best Local Similarity 75.0%; Pred. No. 5.3e-32;
 Matches 87; Conservative 21; Mismatches 8; Indels 0; Gaps 0;
 QY 134 GGSSENVLTQSPASVAVSLGQRATISCRASESDSYGNFMHWYQQIPGPPKLLIYRAS 193
 Db 17 GSTGDIVLTQSPASVAVSLGQRATISCRASKSVNTYGNFMZWYZZKFGZPKLLIYRAS 76
 QY 194 NLESGIPARFSGSGSRDTFTLTINPVEADDAVATYYCOQSNEDPLTFTGTGLEIKR 249
 Db 77 NLZSGIPARFSGSGSRDTFTLTIBVZABDVATYFCZSBZBPMWTFGSGTKLEIKR 132
 RESULT 6
 KV2G_MOUSE
 ID KV2G_MOUSE STANDARD; PRT; 112 AA.
 AC P01659;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region TEPIC 124.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=73140225; PubMed=4691517;
 RA McKean D.J., Potter M., Hood L.E.;
 RT "Mouse immunoglobulin chains. Pattern of sequence variation among
 RT kappa chains with limited sequence differences.";
 RL Biochemistry 12:760-771(1973).
 DR HSP; P01679; 2FBJ.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 39 53 FRAMEWORK-2.
 FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 61 92 FRAMEWORK-3.
 FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 102 111 FRAMEWORK-4.
 FT DISULFID 23 92 BY SIMILARITY.
 FT NON TER 112 112
 SQ SEQUENCE 112 AA; 12339 MW; 7CFD328DBE8E9D71 CRC64;
 Query Match 36.9%; Score 483; DB 1; Length 112;
 Best Local Similarity 78.2%; Pred. No. 2.6e-31;
 Matches 86; Conservative 18; Mismatches 6; Indels 0; Gaps 0;
 QY 140 VLTQSPASVAVSLGQRATISCRASESDSYGNFMHWYQQIPGPPKLLIYRASL2SGI 199
 Db 3 VLTQSPASVAVSLGQRATISCRASVSNVYGNFMZWYZZKFGZPKLLIYRASL2SGI 62
 QY 200 PARFSGSGSRDTFTLTINPVEADDAVATYYCOQSNEDPLTFTGTGLEIKR 249

Query Match 35.7%; Score 457; DB 1; Length 111;
Best Local Similarity 82.6%; Pred. No. 4.7e-30;
Matches 90; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 140 VLTQSPASLAVSLQQRATISCRASESDSYGNFMHWYQIQPGPPKLLIYRASNLSEGI 199
Db 3 VLTQSPASLAVSLQQRATISCRASQSDYDGDSDYNNWYQKPGPPKLLIYASNLSEGI 62

Qy 200 PARFSGSGSRDFTLTINPVEADVAITYCQSNEDPLTGTGTRLEIK 248
Db 63 PARFSGSGSGDFTLTINHPVEEADAITYCQSNEDPFTGSGTKLEIK 111

RESULT 10
KV30_MOUSE
ID KV30_MOUSE STANDARD; PRT; 111 AA.
AC P01657;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region PC 6308.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.B.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity";
RL Nature 276:785-790(1978).
DR PIR; C01937; KMS08.
DR HSSP; P80362; LMTL.
DR InterPro; IPR007110; Ig-like.
DR SMART; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 38
FT DOMAIN 39 53
FT DOMAIN 54 60
FT DOMAIN 61 92
FT DOMAIN 93 101
FT DOMAIN 102 111
FT DISULFID 23 92
FT NON TER 111 111
SQ SEQUENCE 111 AA; 12071 MW; 7A4ADE4D6C256D29 CRC64;

Query Match 35.5%; Score 465; DB 1; Length 111;
Best Local Similarity 82.6%; Pred. No. 6.7e-30;
Matches 90; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 140 VLTQSPASLAVSLQQRATISCRASESDSYGNFMHWYQIQPGPPKLLIYRASNLSEGI 199
Db 3 VLTQSPASLAVSLQQRATISCRASQSDYDGDSDYNNWYQKPGPPKLLIYASNLSEGI 62

Qy 200 PARFSGSGSRDFTLTINPVEADVAITYCQSNEDPLTGTGTRLEIK 248
Db 63 PARFSGSGSGDFTLTINHPVEEADAITYCQSNEDPFTGSGTKLEIK 111

RESULT 11
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5-84 precursor.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J0505; HVM584.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 35.4%; Score 454; DB 1; Length 117;
Best Local Similarity 89.8%; Pred. No. 8.5e-30;
Matches 88; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSSTMSWVQTPKRLWVATISSGGSSTYY 60
Db 20 EVKLVEGGGLVPGGSLKLSCAASGFTFSSTMSWVQTPKRLWVATISSGGSSTYY 79

Qy 61 PDSVKGRTTISRDNKNTLYIQMSLRSEDATMYCYCTR 98
Db 80 PDTVKGRTTISRDNKNTLYIQMSLRSEDATMYCYCAR 117

RESULT 12
HV57_MOUSE
ID HV57_MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 6-96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J0501; HVM596.
DR HSSP; P01772; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.

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KW Immunoglobulin V region.
FT DOMAIN 1 >98 IG-LIKE.
FT NON TER 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F792FBF95B CRC64;

Query Match 35.3%; Score 462; DB 1; Length 98;
Best Local Similarity 90.8%; Pred. No. 9.9e-30; Indels 0; Gaps 0;
Matches 89; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTFSYMSWVRQTPKRLKLVATISGGSTYY 60
Db 1 EVQLVESGGGLVPGGSLKSCAASGFTFSYMSWVRQTPKRLKLVATISGGSTYY 60

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCYTR 98
Db 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCYTR 98

RESULT 13
KV3S_MOUSE
ID KV3S_MOUSE STANDARD; PRT; 111 AA.
AC P01671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region PC 7175.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
DR HSSP; P01679; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >97
FT NON TER 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 35.2%; Score 460.5; DB 1; Length 97;
Best Local Similarity 91.8%; Pred. No. 1.3e-29;
Matches 90; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTFSYMSWVRQTPKRLKLVATISGGSTYY 60
Db 1 EVQLVESGGGLVPGGSLKSCAASGFTFSYMSWVRQTPKRLKLVATISGGSTYY 59

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCYTR 98
Db 60 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCYTR 97

RESULT 15
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
DR HSSP; P01669; 1WTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >23
FT NON TER 23
SQ SEQUENCE 111 AA; 12010 MW; F041B89AA7858523 CRC64;

Query Match 35.3%; Score 462; DB 1; Length 111;
Best Local Similarity 80.7%; Pred. No. 1.1e-29;
Matches 88; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 140 VLTQSPASLVSLQQRATISCRASESDVSYGMHWYQIQPGPPKLLIYRASNLSEGI 199
Db 3 VLTQSPASLVSLQQRATISCRASKSVTSYGMHWYQKQPQPKLLIYLASNLSEGV 62

QY 200 PARFSGSGSRDFTLTNPVADVATYCCQSNEDPLTFTGTRLEIK 248
Db 63 PARFSGSGSGDFTLTNPVDEEDATYCCQSHRELPLTFGAGTKLEK 111

RESULT 14
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;

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DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/cJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malpietro U.V., Lebecque S.G., Geathart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019 (1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; J0504; HVMS91.
DR HSSP; P01810; 2PBJ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >97
FT NON TER 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 35.2%; Score 460.5; DB 1; Length 97;
Best Local Similarity 91.8%; Pred. No. 1.3e-29;
Matches 90; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTFSYMSWVRQTPKRLKLVATISGGSTYY 60
Db 1 EVQLVESGGGLVPGGSLKSCAASGFTFSYMSWVRQTPKRLKLVATISGGSTYY 59

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCYTR 98
Db 60 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCYTR 97

RESULT 15
KV3Q_MOUSE
ID KV3Q_MOUSE STANDARD; PRT; 111 AA.
AC P01669;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG kappa chain V-III region PC 7769.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79073152; PubMed=103003;
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;
RT "Rearrangement of genetic information may produce immunoglobulin
diversity.";
RL Nature 276:785-790 (1978).
DR HSSP; P01669; 1WTL.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 >23
FT NON TER 23
SQ SEQUENCE 111 AA; 12010 MW; F041B89AA7858523 CRC64;

Query Match 35.3%; Score 462; DB 1; Length 111;
Best Local Similarity 80.7%; Pred. No. 1.1e-29;
Matches 88; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

QY 140 VLTQSPASLVSLQQRATISCRASESDVSYGMHWYQIQPGPPKLLIYRASNLSEGI 199
Db 3 VLTQSPASLVSLQQRATISCRASKSVTSYGMHWYQKQPQPKLLIYLASNLSEGV 62

QY 200 PARFSGSGSRDFTLTNPVADVATYCCQSNEDPLTFTGTRLEIK 248
Db 63 PARFSGSGSGDFTLTNPVDEEDATYCCQSHRELPLTFGAGTKLEK 111

RESULT 14
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;

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Db 40 QVKLQSGGGLVPGGSLKLSCAASGDSFSEYMSWVRQAPGKLEWIGEPDSDSTINY 99
Qy 61 PDSVKGRTTISRDNKNTLYLQMSLSRSETAMYYCTREGGFTVWYFD---VWGAGTL 117
Db 100 TPSLKDKFIISRDNKNTLYLQMSKVRSEDALYYCARAS-----YGHSAWYQGQTT 152
Qy 118 VTVSAGGSGGGRASGGGSGGSENVLTQSPASLAVSLGORATISCRASGVDSYGNFMHWY 177
Db 153 VTVSAGGSGGGRASGGGSGGSDIELTQSPASLAVSGEVTITCRASGNI-----HNYLAWY 208
Qy 178 QQIFGQPKLLIYRASNLSEGIIPARFSGSGSRDFTLTINPVDADVATYVQCSNEDPL 237
Db 209 QQKQKSPQLLVNNAKTLADVPFRSGSGGTQYSLKINSLOPDPFGSYCQHFHTTTPY 268
Qy 238 TFGTGTRELEIKR 249
Db 269 TFGGGTKLEIKR 280

RESULT 2
Q7TQM2 PRELIMINARY; PRT; 243 AA.
AC Q7TQM2;
DT 01-DEC-2001 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DN SCFV 6H8 protein (Fragment).
GN SCFV 6H8
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Peter J.C., Ztekhari P., Billiald P., Wallukat G.;
RT "scrV single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ574851; CAB00495.1; -.
FT NON TER
SQ SEQUENCE 243 AA; 25976 MW; BEFFP64D2DCP4P76 CRC64;

Query Match 52.0%; Score 680.5; DB 11; Length 243;
Best Local Similarity 53.6%; Pred. No. 4.7e-49;
Matches 133; Conservative 42; Mismatches 62; Indels 11; Gaps 3;

Qy 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYMSWVRQTPKRLVWVAITSSGGSSTYY 60
Db 1 QVQLQSGSELVRFASVSKLSCKASGYFTTYMHWVKQRHGGGLEWIGNIYFGSGITNY 60
Qy 61 PDSVKGRTTISRDNKNTLYLQMSLSRSETAMYYCTREGGFTVWYFDVWGAGTLTV 120
Db 61 DEKFNKGLITVDTSSSTAYMHLSSLASEDSAVYCARGGG-----LDVWGAGTLTV 114
Qy 121 SAGGSGGGRASGGGSGGSENVLTQSPASLAVSLGORATISCRASGVDSYGNFMHWYQOI 180
Db 115 SGGGSGGSGGSGGSDIQNTQSSSFVSLGDRVTITCKASEDI-----YNYLAWYQOK 170
Qy 181 PQGPPKLLIYRASNLSEGIIPARFSGSGSRDFTLTINPVDADVATYVQCSNEDPLTFG 240
Db 171 PGNAPRLISGATSLGTGVPFRSGSGGKDYLTLSITSLQTDVATYVQCC-YWSTRTFG 229
Qy 241 TGTRELEIKR 248
Db 230 GGTRELEIKR 237

RESULT 3
Q925S1 PRELIMINARY; PRT; 218 AA.
ID Q925S1;
AC Q925S1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MRPS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C.;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice."
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c;
RA Cui D., Zeng G., Yan X., Li X., Su C.;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain."
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR InterPro; IPR007110; IG-Like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER
SQ SEQUENCE 218 AA; 23013 MW; 527B4FA8F7982817 CRC64;

Query Match 48.7%; Score 637; DB 11; Length 218;
Best Local Similarity 56.5%; Pred. No. 1.8e-45;
Matches 126; Conservative 35; Mismatches 52; Indels 10; Gaps 2;

Qy 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYMSWVRQTPKRLVWVAITSSGGSSTYY 60
Db 3 QVKLQSGSELKPKGTETVIRISCKASGYFTTAGMQWQVQKMPGKLGKLGWINTHSGVPKY 62
Qy 61 PDSVKGRTTISRDNKNTLYLQMSLSRSEDATMYCTR---EGGGFTVWYFDVWGAGTL 117
Db 63 AEEFKGRFAFSLETASATYLIQISLNKEDATYFCRWDYDGG-----FAYWGQTT 115
Qy 118 VTVSAGGSGGGRASGGGSGGSENVLTQSPASLAVSLGORATISCRASGVDSYGNFMHWY 177
Db 116 VTVSAGGSGGSGGSGGSDIVLTQSPASLAVSLGORATISCRASGVDSYGNFMHWY 175
Qy 178 QQIPQPPKLLIYRASNLSEGIIPARFSGSGSRDFTLTINPVE 220
Db 176 QQKQPPKLLIYASKQSGVFPAGLLASGSGTDFSLNIYPME 218

RESULT 4
Q921A6 PRELIMINARY; PRT; 241 AA.
ID Q921A6;
AC Q921A6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-CEA 79 single chain Fv fragment (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98170165; PubMed=9509426;
RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
RA Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;
RT "Cloning and characterization of cDNAs encoding VH and VL of a
RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and

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RT generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819 (1997).
DR EMBL; U88067; AAB4804.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 47.6%; Score 623.5; DB 11; Length 241;
Best Local Similarity 49.2%; Pred. No. 2.7e-44;
Matches 125; Conservative 51; Mismatches 59; Indels 19; Gaps 6;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTFSYTWVRQTPPKRLEWVAITISGGSSTYY 60
Db 1 QVQLQQSGPELTKRGETVTKSCASGFTFDYGNWVYQAPGKGLKRWGINTISGEPTY 60

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMVYCTREGGFTVNMVYFDVWGAGTLTV 120
Db 61 ADDPKGRFAFSLSTASTAYLIQNLKNEATATYFCARK----DLLRYFDYWGQGTITV 116

QY 121 SAGGGSGGRASGGGSENVLTQSPASLAVSLGORATISCRASESDSYGYNFMHWYQOI 180
Db 117 SSGGGSGGGSGGGSDIELTQSPSLASLGKGVITTCASQDINKY----IAYQHK 172

QY 181 PGPPK----LLIYRASNLGSIPIARFSGSGRTDFTLTINPVEADDAVATYVYCCQSNEDP 236
Db 173 PGKGRSAHTLHY----IQGIPRFGSGSGRDYFSINLEPEDIAIYIC--LHYDN 226

QY 237 LTFGTGTRLEIKR 249
Db 227 LHTFGGKLEIKR 240

RESULT 5
Q99XA4 PRELIMINARY; PRT; 487 AA.
AC Q99XA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC004786; AAB04786.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 40.1%; Score 525; DB 11; Length 487;
Best Local Similarity 43.0%; Pred. No. 1.2e-35;
Matches 128; Conservative 21; Mismatches 65; Indels 84; Gaps 7;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTFSYTWVRQTPPKRLEWVAITISGGSSTYY 60
Db 20 EVQLVESGGGLVPGGSLKSCAASGFTFSYANMSVRQTPPKRLEWVAITISGGSTYY 79

generation of a single-chain Fv molecule (scFv).";
RL Mol. Cells 7:816-819 (1997).
DR EMBL; U88067; AAB4804.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 241
SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 47.6%; Score 623.5; DB 11; Length 241;
Best Local Similarity 49.2%; Pred. No. 2.7e-44;
Matches 125; Conservative 51; Mismatches 59; Indels 19; Gaps 6;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTFSYTWVRQTPPKRLEWVAITISGGSSTYY 60
Db 1 QVQLQQSGPELTKRGETVTKSCASGFTFDYGNWVYQAPGKGLKRWGINTISGEPTY 60

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMVYCTREGGFTVNMVYFDVWGAGTLTV 120
Db 61 ADDPKGRFAFSLSTASTAYLIQNLKNEATATYFCARK----DLLRYFDYWGQGTITV 116

QY 121 SAGGGSGGRASGGGSENVLTQSPASLAVSLGORATISCRASESDSYGYNFMHWYQOI 180
Db 117 SSGGGSGGGSGGGSDIELTQSPSLASLGKGVITTCASQDINKY----IAYQHK 172

QY 181 PGPPK----LLIYRASNLGSIPIARFSGSGRTDFTLTINPVEADDAVATYVYCCQSNEDP 236
Db 173 PGKGRSAHTLHY----IQGIPRFGSGSGRDYFSINLEPEDIAIYIC--LHYDN 226

QY 237 LTFGTGTRLEIKR 249
Db 227 LHTFGGKLEIKR 240

RESULT 5
Q99XA4 PRELIMINARY; PRT; 487 AA.
AC Q99XA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC004786; AAB04786.1; -.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 40.1%; Score 525; DB 11; Length 487;
Best Local Similarity 43.0%; Pred. No. 1.2e-35;
Matches 128; Conservative 21; Mismatches 65; Indels 84; Gaps 7;

QY 1 EVQLQESGGGLVPGGSLKSCAASGFTFSYTWVRQTPPKRLEWVAITISGGSSTYY 60
Db 20 EVQLVESGGGLVPGGSLKSCAASGFTFSYANMSVRQTPPKRLEWVAITISGGSTYY 79
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 FN SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC013656; AAH13656.1; -
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 479 AA; ECB2D087748584F CRC64;

 Query Match 37.8%; Score 495; DB 11; Length 479;
 Best Local Similarity 42.7%; Pred. No. 3.8e-33;
 Matches 123; Conservative 25; Mismatches 88; Indels 72; Gaps 7;

 QY 1 EVQLQESGGGLVPGGSLKLSKAASGFTFSYMSWVRQTPPEKLEWVAITSSGGSSTYY 60
 DB 20 EVQLVESGGGLVPGGSLKLSKAASGLTFSNYSWVRQTPPEKLEWVAITSSGGSSTYY 79
 QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMVCTREGGFTVNNYEDVWGAGTLVTV 120
 DB 80 SDTWKGRFTISRDNKNTLYLQMSLSRSEDYAFYCVRGG-----YFDVWGAGTAVTV 132
 QY 121 SAG-----GGSGGRASGGGSENVLTPQSPASLA 149
 DB 133 SSEPAEPTIYPLTFPQALSSDPVIGLIHDYFPSTGMVNTWKGSKDITTVNFPFALA 192
 QY 150 VSLGORATIS-----CRASESDSYGYNFMHWYQOI-----PGQP 184
 DB 193 --SGGRYTMSSQLTLPVAVECEPESVKSCVQHDSPVQELNVNCPGICSPPTTPPPSCQ 250
 QY 185 PKLIYRASNLSEGIPTAFSGSGSRTDFTLTINPVEADDVATYYCOOS 232
 DB 251 PSLSLQRPAL-LEDLL-----LGSASITCTLNGLRDPEGAVFTWPS 291

 RESULT 8
 QY1XE1
 ID QY1XE1 PRELIMINARY; PRT; 480 AA.
 AC QY1XE1
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, last annotation update)
 DE Hypothetical protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 FN SEQUENCE FROM N.A.
 RC TISSUE=Colon;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010798; AAH10798.1; -
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 480 AA; 51936 MW; 20B9234BEF2B41ED CRC64;

Query Match 37.0%; Score 484; DB 11; Length 480;
 Best Local Similarity 42.0%; Pred. No. 3.2e-32;
 Matches 121; Conservative 30; Mismatches 67; Indels 70; Gaps 8;

 QY 1 EVQLQESGGGLVPGGSLKLSKAASGFTFSYMSWVRQTPPEKLEWVAITSSGGSSTYY 60
 DB 19 DVKLVESGGGLVPGGSLKLSKAASGFTFSNYSWVRQTPPEKLEWVAITSSGGSSTYY 78
 QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMVCTREGGFTVNNYEDVWGAGTLVTV 120
 DB 79 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMVCTREGGFTVNNYEDVWGAGTLVTV 133
 QY 121 SAG-----GGSGGRASGGGSENVLTPQSPASLA 149
 DB 134 SSEPAEPTIYPLTFPQALSSDPVIGLIHDYFPSTGMVNTWKGSKDITTVNFPFALA 193
 QY 150 VSLGORATIS-----CRASESDSYGYNFMHWYQOI-----PGQP 184
 DB 194 --SGGRYTMSSQLTLPVAVECEPESVKSCVQHDSPVQELNVNCPGICSPPTTPPPSCQ 251
 QY 185 PKLIYRASNLSEGIPTAFSGSGSRTDFTLTINPVEADDVATYYCOOS 232
 DB 252 PSLSLQRPAL-LEDLL-----LGSASITCTLNGLRDPEGAVFTWPS 292

 RESULT 9
 QY1Z07
 ID QY1Z07 PRELIMINARY; PRT; 486 AA.
 AC QY1Z07
 DT 01-DEC-2001 (TRENBLrel. 19, Created)
 DT 01-DEC-2001 (TRENBLrel. 19, last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 FN SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010324; AAH10324.1; -
 DR InterPro; IPR007110; IG_LIKE.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF00047; IG_4.
 DR SMART; SM00406; IGv; 1.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 2.
 KW Hypothetical protein.
 SQ SEQUENCE 486 AA; 52692 MW; 4FEF935125DA870B CRC64;

 Query Match 35.9%; Score 470.5; DB 11; Length 486;
 Best Local Similarity 39.3%; Pred. No. 4.3e-31;
 Matches 119; Conservative 26; Mismatches 63; Indels 95; Gaps 9;

 QY 1 EVQLQESGGGLVPGGSLKLSKAASGFTFSYMSWVRQTPPEKLEWVAITSSGGSSTYY 60
 DB 20 EVHLVESGGGLVPGGSLKLSKAASGFTFSYMSWVRQTPPEKLEWVAITSSGGSSTYY 78
 QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMVCTREGGFTVNNYEDVWGAGTLVTV 113
 DB 79 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMVCTREGGFTVNNYEDVWGAGTLVTV 133
 QY 114 AGTLTVTSAGG-----GSGGR-----130
 DB 134 QCTTITVTSSEARNPTIYPLTLPRALSDPVIIGLIHDYFPSTGMVNTWKGSKDITTV 193
 QY 131 -----ASGGGSENVLTPQSPASLAISLQGRATISCRASESDSYGYNFMHWYQOI-----180
 DB 194 NFPPLASGGGYTMSQLTLP-----VECEPESVKSCVQHDSPVQELNVNCPGICSPPTTPPPSCQ 242
 QY 181 -----PGQPPKLIYRASNLSEGIPTAFSGSGSRTDFTLTINPVEADDVATYYC 229

```
Db 243 SGPPPPCPPCPPSPSLQORPA-LEDLL-----LGSDASLTCTINGLRNPEGAFTW 295
QY 230 QQS 232
Db 296 EPS 298

RESULT 10
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-cell;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAHL5760.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4PCA3AD8ECE263D9 CRC64;

Query Match 35.3%; Score 462.5; DB 4; Length 597;
Best Local Similarity 66.9%; Pred. No. 2.6e-30;
Matches 87; Conservative 19; Mismatches 21; Indels 3; Gaps 1;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTMSWVRQTPKRLKLEWVATISSGGSTYY 60
Db 20 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTMSWVRQAPGKLEWVSAISGGSTYY 79

QY 61 PDSVKGRFTISRDNKNTLYLQMSLRSEDATMYICTREGGGTVNWF---DVWGAGTL 117
Db 80 ADSVKGRFTISRDNKNTLYLQMSLRSEDATMYICTREGGGTVNWF---DVWGAGTL 139

QY 118 VTVSAGGGGS 127
Db 140 VTVSAGGSASA 149

RESULT 11
Q811U6 PRELIMINARY; PRT; 111 AA.
AC Q811U6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Anti-human Fc gamma receptor III 368 kappa light chain variable region
DE (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Bruenke J., Valerius T., Repp R., Fey G.H.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY173024; AA018226.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
```

```
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Receptor.
FT NON_TER 1
FT NON_TER 111
SQ SEQUENCE 111 AA; 12101 MW; CEDECEE157F2C94A CRC64;

Query Match 35.1%; Score 459; DB 11; Length 111;
Best Local Similarity 80.9%; Pred. No. 6.1e-31;
Matches 89; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 140 VLTQSPASLAIVSLGQRATISCRASVSVDYGVNFMHTYQIIPGQPPKLLIYRASNLSCI 199
Db 2 VLTQSPASLAIVSLGQRATISCRASQSVDFDGSFNNYQQKPGQPPKLLIYTTNLSGI 61

QY 200 PARFSGSGSRDTFTLTINPVEADDVATYCCQSNEDPLTFGTGTRLEIKR 249
Db 62 PARFASGSGDTFTLTINHPVEEDATYCCQSNEDPYTFGGTQKLEIKR 111

RESULT 12
Q80Z17 PRELIMINARY; PRT; 487 AA.
AC Q80Z17;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Colon;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049143; AAH49143.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 487 AA; 53019 MW; 31F2C893900A4D80 CRC64;

Query Match 35.0%; Score 458; DB 11; Length 487;
Best Local Similarity 39.3%; Pred. No. 4.8e-30;
Matches 114; Conservative 37; Mismatches 71; Indels 68; Gaps 8;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSSTMSWVRQTPKRLKLEWVATI--SSGGST 58
Db 20 EVKLEAGGGLVQPGGSKLSCAASGFTFSSTMSWVRQTPKRLKLEWVATIRLNNTAT 79

QY 59 YYPDSVKGRFTISRDNKNTLYLQMSLRSEDATMYICTREGGGFTVNNYFDVWGAGTLV 118
Db 80 HYAESVKGRFTISRDDSKSVYLQNNLRAEDTGIYYCTRGYG-DPNWYFDVWGAGTTV 138

QY 119 TVSAG-----GGSGGRASGGGSGENVLITQSPAS 147
Db 139 TVSSPAREPTIPLTFFQALSDPVIIGLIHDFPSGTNNVTWGKSGDKDITTNFFPA 198
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QY 148 LAVSLGORATIS-----CRASESVDSYGVNFMHWYQOI-----PG 182
DB 199 LA--SGGRYTMSSQLTLPAVECEGSVKCSVQHDNSPVOELNVNCPGICSPPTTPPPPS 256
QY 183 QPKLLIYRASNLSPGIPARFSGSGRTDTLTINPVADVDVATYCCQS 232
DB 257 QPSSLQLQRA-LBDLL-----LGS DASITCLNGLRDPEGAVFTWPS 299

RESULT 13
Q920E9 PRELIMINARY; PRT; 111 AA.
AC Q920E9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Pterin-mimicking anti-idiotope kappa chain variable region
  (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.;
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed
  in Mammalian Cells."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307935; AAL09419.1; -.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON-TER 1
FT NON-TER 111
SQ SEQUENCE 111 AA; 12046 MW; 1B469898AA6958526 CRC64;

Query Match 34.9%; Score 457; DB 11; Length 111;
Best Local Similarity 80.7%; Pred. No. 9e-31;
Matches 88; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 140 VLTQSPASVLSQGRATISCRASESVDSYGVNFMHWYQIQQPKLLIYRASNLSEGI 199
DB 3 VLTQSPASVLSQGRATISCRASKSVSTGYSYMWYQKQPGQPKLLIYLASNLSEGV 62
QY 200 PARFSGSGSRDFTLTINPVADVDVATYCCQSNEDPLTGTGTLEIK 248
DB 53 PARFSGSGSGTDTLTINHPVEEDAAATYQCQHSRELPTTGGGTKLEIK 111

RESULT 14
Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
DR MGI; MGI:2144967; AU044919.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
```

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DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 34.6%; Score 453; DB 11; Length 473;
Best Local Similarity 72.6%; Pred. No. 1.2e-29;
Matches 90; Conservative 8; Mismatches 18; Indels 8; Gaps 2;

QY 1 EVQLQESGGGLVKPGGSLKLSCAASGFTFSYTWVSRQTPEKLEWVATISSGSGSTYY 60
DB 20 EVQLVESGGGLVKPGGSKLSCAASGFTFSYDGMHWVRQAEKLEWVATINSSTIYY 79
QY 61 PDSVKGRFTISRDNKNTLYLQMSLRSEDPTAMYYCTREGGFTVNVY--PDVWGAGTLV 118
DB 80 ADTVKGRFTISRDNKNTLFLQMTSLRSEDPTAMYYCARE-----LWLRIDYWGQGTII 133
QY 119 TVSA 122
DB 134 TVSS 137

RESULT 15
Q9RIA4 PRELIMINARY; PRT; 437 AA.
AC Q9RIA4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Gamma1 heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
  antibody (Mab 7, its light and heavy chains) and construction of a
  single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR PIR; B45837; B45837.
DR PDB; 1CQK; 11-SEP-99.
DR PDB; 1I9I; 25-DEC-02.
DR PDB; 1KCU; 11-MAY-02.
DR MGI; MGI:96446; Igh-4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
FT NON-TER 1
FT NON-TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3EE7D697C CRC64;

Query Match 34.5%; Score 451.5; DB 11; Length 437;
Best Local Similarity 53.5%; Pred. No. 1.5e-29;
Matches 106; Conservative 11; Mismatches 46; Indels 35; Gaps 7;

QY 2 VOQLQESGGGLVKPGGSLKLSCAASGFTFSYTWVSRQTPEKLEWVATISSGSGSTYY 61
DB 1 VOQLQESGGGLVKPGGSLKLSCAASGFTFSYAMSWVRQTPEKLEWVASFSGG-IIYTT 59
```

Qy	62	DSVKGRFTISRDNKNTILYLQMSLSRSED	TAMYCTREGGFTVNWYFDVWGAGTLVTS	121
Db	60	DSVKGRFTIYZKDRNLSLQMSLSRSED	TAMYICARGD-----YSAYWGPGLVTS	112
Qy	122	AGGGSGGRASGGGSENVL	TQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQQIP	181
Db	113	A-----AKTTPPSVYPLAPGS-AAQTNSMVLGCLVK-----GY-----	FP	147
Qy	182	GPPKLLIYRASNL	ESGI	199
Db	148	--EPVTWNSGSL	SSGV	163

Search completed: July 29, 2004, 08:50:23
Job time : 50.3851 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 76.7154 Seconds
(without alignments)
917.082 Million cell updates/sec

Title: US-09-661-992B-86

Perfect score: 1309
Sequence: 1 EVQLQESGGGLVFRPGSLKL.....QQSNEDPLATFGTGRLEIKR 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq.29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1309	100.0	249	4 AAB20435	Aab20435 Anti-FIX/
2	1277	97.6	294	4 AAB20442	Aab20442 Anti-FIX/
3	1277	97.6	732	4 AAB20437	Aab20437 Anti-FIX/
4	1273	97.2	325	4 AAB20438	Aab20438 Anti-FIX/
5	1230	94.0	249	4 AAB20436	Aab20436 Anti-FIX/
6	1082.5	82.7	252	4 AAU07497	Aau07497 Synthetic
7	968.5	74.0	269	4 AAB61541	Aab61541 3DX sFv p
8	963	73.6	249	4 AAB20434	Aab20434 Anti-FIX/
9	941.5	71.9	239	2 AAR79866	Aar79866 Anti-EGFR
10	909	69.4	237	7 AAE38657	Aae38657 Mouse G1
11	906.5	69.3	240	4 AAB46040	Aab46040 Human TF
12	901.5	68.9	240	2 AAY02472	Aay02472 A single
13	901.5	68.9	240	6 ABP95997	Abp95997 Human ser
14	901	68.8	293	4 AAG65715	Aag65715 Amino aci
15	896	68.4	239	5 ABP45871	Abp45871 Human Bly
16	895.5	68.4	248	5 ABP45865	Abp45865 Human Bly
17	893.5	68.3	240	4 AAB45993	Aab45993 Human MUC
18	893.5	68.3	248	5 ABP45410	Abp45410 Human Bly
19	892	68.1	243	5 ABP45934	Abp45934 Human Bly
20	892	68.1	247	5 ABP45912	Abp45912 Human Bly
21	890.5	68.0	240	4 AAB46018	Aab46018 Human MUC
22	890	68.0	241	5 ABP45878	Abp45878 Human Bly
23	889.5	68.0	240	4 AAB46038	Aab46038 Human TF
24	889	67.9	239	5 ABP45911	Abp45911 Human Bly
25	888.5	67.9	240	4 AAB45999	Aab45999 Human MUC

26	888	67.8	245	2 AAY06714	Aay06714 Antibody
27	887.5	67.8	240	4 AAB46006	Aab46006 Human MUC
28	886.5	67.7	240	4 AAB46010	Aab46010 Human MUC
29	886	67.7	237	5 ABP45895	Abp45895 Human Bly
30	885	67.6	239	4 AAU07498	Aau07498 Synthetic
31	884.5	67.6	240	4 AAB46047	Aab46047 Human TF
32	884.5	67.6	240	4 AAB46005	Aab46005 Human MUC
33	883	67.5	237	5 ABP46009	Abp46009 Human Bly
34	883	67.5	245	2 AAY06717	Aay06717 Antibody
35	882	67.4	247	5 ABP45166	Abp45166 Human Bly
36	881.5	67.3	543	7 ADD12876	Add12876 CD28/mela
37	880.5	67.3	240	4 AAB46007	Aab46007 Human MUC
38	880.5	67.3	240	4 AAB46042	Aab46042 Human TF
39	880.5	67.3	240	4 AAB46039	Aab46039 Human TF
40	880.5	67.3	240	4 AAB46048	Aab46048 Human TF
41	880	67.2	237	5 ABP45992	Abp45992 Human Bly
42	880	67.2	237	5 ABP45994	Abp45994 Human Bly
43	880	67.2	239	2 AAR64812	Aar64812 ScFv anti
44	879.5	67.2	240	4 AAB46013	Aab46013 Human MUC
45	879.5	67.2	240	4 AAB46009	Aab46009 Human MUC

ALIGNMENTS

RESULT 1
AAB20435
ID AAB20435 standard; protein; 249 AA.
XX
AC AAB20435;
XX
DT 21-JUN-2001 (first entry)
XX
DE Anti-FIX/FIXa antibody 198/AB2 scFv.
XX
Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amolytic; therapy; mouse.
XX
OS Mus musculus.
OS Synthetic.
OS Chimeric.
XX

Key Location/Qualifiers
FT Protein 1..122
FT Region 98..102
FT Peptide 123..136
FT Protein 137..249
FT Region 230..238
FT Peptide 230..238
XX WO200119992-A2.
XX 22-MAR-2001.
XX
PF 13-SEP-2000; 2000WO-BP008936.
XX
PR 14-SEP-1999; 99AT-00001576.
XX (BAXT) BAXTER AG.
XX
PI Scheiflinger F, Kerschbaumer R, Falkner F, Dornier F;
DR WPI; 2001-290358/30.
XX N-PSDB; AAF30725.
XX
PT New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.

```

XX PS Claim 12; Fig 16; 138pp; English.
XX CC
XX CC The present sequence is that of a single chain Fv (scFv) derivative of
XX CC antibody 198/AB2, comprising the heavy (VH) and light (VL) chain variable
XX CC regions of 198/AB2 joined by an artificial, flexible linker peptide. The
XX CC scFv was obtained by PCR amplification of cDNAs for 198/AB2 VH and VL
XX CC regions and cloning in vector pDAP2. 198/AB2 is an example of anti-human
XX CC Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.
XX CC Anti-FIX/FIXa and their derivatives, including scFv and CDR3 fragments,
XX CC have Factor VIIa (FVIIa) cofactor activity or FIXa activating activity.
XX CC Administration leads to an increase in the procoagulant activity of FIXa,
XX CC even in the presence of FVIIa inhibitors. This allows for rapid blood
XX CC coagulation even in the absence of FVII or FVIIa, and in the case of
XX CC FVII inhibitor patients. The antibodies and derivatives are used in a
XX CC claimed pharmaceutical composition for treating patients with blood
XX CC coagulation disorders, especially haemophilia A and haemorrhagic
XX CC diathesis.
XX CC
XX PS Sequence 249 AA;
XX CC
XX CC Query Match 100.0%; Score 1309; DB 4; Length 249;
XX CC Best Local Similarity 100.0%; Pred. No. 1e-87;
XX CC Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX CC
XX QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLVWVATISSGGSSTYY 60
XX DB 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLVWVATISSGGSSTYY 60
XX QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCTREGGFTVNNYFDVWGAGTLTV 120
XX DB 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCTREGGFTVNNYFDVWGAGTLTV 120
XX QY 121 SAGGGSGGRASGGGSGENVLTSQPSLAVSLGORATISCRASESDSYGNFMHWYQOI 180
XX DB 121 SAGGGSGGRASGGGSGENVLTSQPSLAVSLGORATISCRASESDSYGNFMHWYQOI 180
XX QY 181 PGQPPKLLIYRASNLSEGIIPARFSGSGSRDFTLTINPVEADDVATYCCQSNEDPLTFG 240
XX DB 181 PGQPPKLLIYRASNLSEGIIPARFSGSGSRDFTLTINPVEADDVATYCCQSNEDPLTFG 240
XX QY 241 TGTREIKR 249
XX DB 241 TGTREIKR 249
XX
XX RESULT 2
XX ID AAE20442 standard; protein; 294 AA.
XX AC AAE20442;
XX DT 21-JUN-2001 (first entry)
XX DE Anti-FIX/FIXa antibody 198/B1-myc-tag fusion.
XX KW Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
XX KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
XX KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse; myc-tag.
XX
XX OS Mus musculus.
XX OS Escherichia coli.
XX OS Chimeric.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..22
XX FT Protein 23..294
XX FT Protein /label= Mature_protein
XX FT Protein 23..271
XX FT Protein /label= scFv
XX FT Region 23..144

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FT FT Misc-difference 76 /label= VH
FT FT Peptide /note= "encoded by GGN"
FT FT 145..159 /label= Linker
FT FT 160..271 /label= VL
FT FT 272..274 /label= VL
FT FT /label= Spacer
FT FT 275..286 /label= Myc tag
FT FT 287..288 /label= Spacer
FT FT 289..294 /label= His_tag
FT FT
XX PN WO200119992-A2.
XX XX
XX PD 22-MAR-2001.
XX PF 13-SEP-2000; 2000WO-EP008936.
XX PR 14-SEP-1999; 99AT-00001576.
XX XX (BAXT ) BAXTER AG.
XX XX Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX PI WPI; 2001-290358/30.
XX DR N-PSDB; AAF30732.
XX XX
XX PT New factor IX/factor IXa antibodies and their derivatives useful for
XX PT increasing amidolytic activity of factor IXa, and for treating blood
XX PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX PS Example 18; Fig 34; 138pp; English.
XX CC
XX CC The present sequence is that of a fusion protein comprising: a PelB
XX CC leader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising
XX CC the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by
XX CC an artificial, flexible linker peptide; a spacer; a Myc-tag peptide; a
XX CC spacer; and a C-terminal 6His affinity tail. 198/B1 is an example of anti
XX CC human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the
XX CC invention. Anti-FIX/FIXa antibodies and their derivatives, including scFv
XX CC fragments, have FVIIa cofactor activity or FIXa activating activity.
XX CC Administration leads to an increase in the procoagulant activity of FIXa,
XX CC even in the presence of FVIIa inhibitors. This allows for rapid blood
XX CC coagulation even in the absence of FVII or FVIIa, and in the case of
XX CC FVII inhibitor patients. The antibodies and derivatives are used in a
XX CC claimed pharmaceutical composition for treating patients with blood
XX CC coagulation disorders, especially haemophilia A and haemorrhagic
XX CC diathesis. The scFv-myc-tag fusion was expressed in E. coli. It exhibited
XX CC FVII-like activity
XX CC
XX PS Sequence 294 AA;
XX CC
XX CC Query Match 97.6%; Score 1277; DB 4; Length 294;
XX CC Best Local Similarity 97.6%; Pred. No. 2.6e-85;
XX CC Matches 243; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
XX CC
XX QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLVWVATISSGGSSTYY 60
XX DB 23 EVKLVEGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLVWVATISSGGSSTYY 82
XX QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCTREGGFTVNNYFDVWGAGTLTV 120
XX DB 83 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCTREGGFTVNNYFDVWGAGTLTV 142
XX QY 121 SAGGGSGGRASGGGSGENVLTSQPSLAVSLGORATISCRASESDSYGNFMHWYQOI 180
XX DB 143 SGGGGSGGRASGGGSGDIVLTQSPASLAVSLGORATISCRASESDSYGNFMHWYQOI 202
XX QY 181 PGQPPKLLIYRASNLSEGIIPARFSGSGSRDFTLTINPVEADDVATYCCQSNEDPLTFG 240

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||||| 203 PGQPKLLIYRASNLSEGIPIRFGSGSRDFTLTINPVEADDVATYCCQSNEDPLTFG 262
||||| 241 TGTLEIKR 249
||||| 263 TGTLEIKR 271

RESULT 3
AAB20437
ID AAB20437 standard; protein; 732 AA.
XX AC AAB20437;
XX DT 21-JUN-2001 (first entry)
XX DE Anti-FIX/FIXa antibody 198/B1-alkaline phosphatase fusion.
XX KW Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
XX KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
XX KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
XX KW alkaline phosphatase.
XX OS Mus musculus.
XX OS Synthetic.
XX OS Escherichia coli.
XX OS Chimeric.
XX FH Key Location/Qualifiers
FT Peptide 1..22 /label= Signal_peptide
FT Protein 23..732 /label= Mature_protein
FT Protein 23..271 /label= scFv
FT Region 23..144 /label= VH
FT Misc-difference 76 /note= "encoded by GGN"
FT Peptide 145..159 /label= Linker
FT Region 160..271 /label= VL
FT Peptide 272..275 /label= Spacer
FT Protein 276..725 /label= Alkaline_phosphatase
FT Peptide 726..732 /label= His_tag
XX WO200119992-A2.
XX PD 22-MAR-2001.
XX PF 13-SEP-2000; 2000WO-EP008936.
XX PR 14-SEP-1999; 99AT-00001576.
XX PA (BAXT) BAXTER AG.
XX PI Scheifflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX DR WFI; 2001-290358/30.
XX DR N-PSDB; AAB30727.
XX PT New factor IX/factor IXa antibodies and their derivatives useful for
XX PT increasing amidolytic activity of factor IXa, and for treating blood
XX PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX PS Example 16; Fig 26; 138pp; English.
XX CC The present sequence is that of a fusion protein comprising: a PeIB
XX CC leader; a single chain Fv (scFv) derivative of antibody 198/B1 comprising

CC the heavy (VH) and light (VL) chain variable regions of 198/B1 joined by
CC an artificial, flexible linker peptide; a spacer; Escherichia coli
CC alkaline phosphatase; and a C-terminal 6His affinity tail. 198/B1 is an
CC example of anti-human Factor IX (FIX)/activated Factor IX (FIXa)
CC antibodies of the invention. Anti-FIX/FIXa antibodies and their
CC derivatives, including scFv fragments, have FVIIa cofactor activity or
CC FIXa activating activity. Administration leads to an increase in the
CC procoagulant activity of FIXa, even in the presence of FVIIa inhibitors.
CC This allows for rapid blood coagulation even in the absence of FVII or
CC FVIIa, and in the case of FVII inhibitor patients. The antibodies and
CC derivatives are used in a claimed pharmaceutical composition for treating
CC patients with blood coagulation disorders, especially haemophilia A and
CC haemorrhagic diathesis. The scFv-alkaline phosphatase was expressed in E.
CC coli. It exhibited FVII-like activity
XX
SQ Sequence 732 AA;

Query Match 97.6%; Score 1277; DB 4; Length 732;
Best Local Similarity 97.6%; Pred. No. 6.9e-85;
Matches 243; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSSTYMSWVRQTPEKRLIEWATISSGGSSTYY 60
DB 23 EVKLVESGGGLVPGGSLKLSCAASGFTFSSTYMSWVRQTPEKRLIEWATISSGGSSTYY 82

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSDTAMYCTREGGFTVNYFDVWGAGTLYTV 120
DB 83 PDSVKGRFTISRDNKNTLYLQMSLSRSDTAMYCTREGGFTVNYFDVWGAGTLYTV 142

QY 121 SAGGGSGGRASGGGSENVLTSQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQOI 180
DB 143 SSGGGSGGRASGGGSDIVLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQOI 202

QY 181 PGQPKLLIYRASNLSEGIPIRFGSGSRDFTLTINPVEADDVATYCCQSNEDPLTFG 240
DB 203 PGQPKLLIYRASNLSEGIPIRFGSGSRDFTLTINPVEADDVATYCCQSNEDPLTFG 262

QY 241 TGTLEIKR 249
DB 263 TGTLEIKR 271

RESULT 4
AAB20438
ID AAB20438 standard; protein; 325 AA.
XX AC AAB20438;
XX DT 21-JUN-2001 (first entry)
XX DE Anti-FIX/FIXa antibody 198/B1 bivalent miniantibody.
XX KW Factor IX; FIX; Factor IXa; FIXa; miniantibody; procoagulant;
XX KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
XX KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
XX KW bivalent antibody; plasmid pZip-198AB2#102.
XX OS Mus musculus.
XX OS Synthetic.
XX OS Escherichia coli.
XX OS Chimeric.
XX FH Key Location/Qualifiers
FT Peptide 1..22 /label= Signal_peptide
FT Protein 23..325 /note= "PeIB leader"
FT Protein 23..271 /label= Mature_protein
FT Region 23..144 /label= scFv
FT Misc-difference 76 /label= VH

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FT Peptide /note= "encoded by GGN"
FT 145..159 /label= Linker
FT 160..271 /label= VL
FT Misc-difference 166 /note= "encoded by TNT"
FT Misc-difference 181 /note= "encoded by TCN"
FT Peptide 272..274 /label= Spacer
FT Protein 275..284 /label= Hinge
FT Protein 285..319 /label= Helix
FT Peptide 320..325 /label= His_tag
XX WO200119992-A2.
PN 22-MAR-2001.
XX PD
XX PF 13-SEP-2000; 2000WO-EP008936.
XX PR 14-SEP-1999; 99AT-00001576.
XX PA (BAXT ) BAXTER AG.
XX Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
PI WPI; 2001-290358/30.
XX N-PSDB; AAF30728.
XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX Example 16; Fig 28; 138pp; English.
XX The present sequence is that of a bivalent miniantibody comprising a PelB
CC leader peptide, the single chain Fv (scFv) fragment of antibody 198/B1
CC (subclone AB2), an amphipathic helical structure and a C-terminal 6His
CC tag. The protein was expressed in Escherichia coli from plasmid
CC pZip198AB2#102 (see AAF30728). Antibody 198/B1 is an example of anti-
CC human Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the
CC invention. Anti-FIX/FIXa antibodies and their derivatives have FIXIIa
CC cofactor activity or FIXa activating activity. Administration leads to an
CC increase in the procoagulant activity of FIXa, even in the presence of
CC FVIIa inhibitors. This allows for rapid blood coagulation even in the
CC absence of FVIII or FVIIa, and in the case of FVIII inhibitor patients.
CC The antibodies and derivatives are used in a claimed pharmaceutical
CC composition for treating patients with blood coagulation disorders,
CC especially haemophilia A and haemorrhagic diathesis. The bivalent
CC miniantibody exhibited FVIII-like activity
XX Sequence 325 AA;
Query Match 97.2%; Score 1273; DB 4; Length 325;
Best Local Similarity 97.2%; Pred. No. 5.7e-85;
Matches 242; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 EVQLQESGGGLVPGGSLKSCAASGFTFSYNTMSWVRQTPKRLKLEWVAITISGGSTYY 60
DB 23 EVKLVEGGGLVPGGSLKSCAASGFTFSYNTMSWVRQTPKRLKLEWVAITISGGSTYY 82
QY 61 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGSGFTVWYFDWGAGTLATV 120
DB 83 PDSVKGRTISRDNKNTLYLQMSLSRSEDYAMYCTREGSGFTVWYFDWGAGTSVTV 142
QY 121 SAGGSGGGRASGGGGSENVLTQSPASVLSLQGRATISCRASESDSYGNFMHWYQOI 180
DB 143 SSGGGGGRASGGGGSDIVLTQSPASVLSLQGRATISCRASESDSYGNFMHWYQOI 202
QY 181 FGQPPKLLIYRASNLGSIIPARFSGSGSRDTFTLTINPVEADDDVATYYCQSNEDPLTFG 240
DB 203 PGQPPKLLIYRASNLGSIIPARFSGSGSRDTFTLTINPVEADDDVATYYCQSNEDPLTFG 262
QY 241 TGTRLEIKR 249
DB 263 TGTRLEIKR 271
RESULT 5
AAB20436
ID AAB20436 standard; protein; 249 AA.
XX AC AAB20436;
XX 21-JUN-2001 (first entry)
DE Anti-FIX/FIXa antibody 198/A1 scFv.
XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
XX Mus musculus.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FT 1..122 /label= VH
FT 99..111 /label= CDR3
FT 123..136 /label= Linker
FT 137..249 /label= VL
FT Misc-difference 142 /note= "encoded by ACN"
FT Misc-difference 224 /note= "encoded by GCN"
FT 230..238 /label= CDR3
XX WO200119992-A2.
XX 22-MAR-2001.
XX 13-SEP-2000; 2000WO-EP008936.
XX 14-SEP-1999; 99AT-00001576.
XX (BAXT ) BAXTER AG.
XX Scheiflinger F, Kerschbaumer R, Falkner F, Dorner F;
XX WPI; 2001-290358/30.
XX N-PSDB; AAF30726.
XX New factor IX/factor IXa antibodies and their derivatives useful for
PT increasing amidolytic activity of factor IXa, and for treating blood
PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX Example 10; Fig 17; 138pp; English.
XX The present sequence is that of a single chain Fv (scFv) derivative of
CC antibody 198/A1, comprising the heavy (VH) and light (VL) chain variable
CC regions of 198/A1 joined by an artificial, flexible linker peptide. The
CC scFv was obtained by PCR amplification of cDNAs for 198/A1 VH and VL
CC regions and cloning in vector pDAP2. 198/A1 is an example of anti-human
CC Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.
CC Anti-FIX/FIXa and their derivatives, including scFv and CDR3 fragments,
CC have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity.
CC Administration leads to an increase in the procoagulant activity of FIXa,

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even in the presence of FVIIa inhibitors. This allows for rapid blood coagulation even in the absence of FVIII or FVIIa, and in the case of FVII inhibitor patients. The antibodies and derivatives are used in a claimed pharmaceutical composition for treating patients with blood coagulation disorders, especially haemophilia A and haemorrhagic diathesis

Sequence 249 AA;
Query Match 94.0%; Score 1230; DB 4; Length 249;
Best Local Similarity 94.0%; Pred. No. 5.9e-82;
Matches 234; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYMSWVRQTPKRLWVAITSSGSSSTYY 60
DB 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYMSWVRQTPKRLWVAITSSGSSSTYY 60
QY 61 PDSVKGRFTISRDNKNTLYLQSSLRSEDYAMVCTREGGTVNMFYFVWAGTLTV 120
DB 61 PDSVKGRFTISRDNKNTLYLQSSLRSEDYAMVCTREGGTVNMFYFVWAGTLTV 120
QY 121 SAGGGSGGRASGGGSENVLQSPASLAVSLGQRATISCRASESDVSYGYNFMHWYQOI 180
DB 121 SAGGGSGGRASGGGSENVLQSPASLAVSLGQRATISCRASESDVSYGYNFMHWYQOI 180
QY 181 PGQPPKLLIYRASNLGSGIPARFSGSGSRDFTLTINPVEADDVATYYCQSNEDPLTFG 240
DB 181 PGQPPKLLIYRASNLGSGIPARFSGSGSRDFTLTINPVEADDVATYYCQSNEDPLTFG 240
QY 241 TGTGLEIKR 249
DB 241 AGTRLEIKR 249

RESULT 6
AAU07497
ID AAU07497 standard; protein; 252 AA.
AC AAU07497;
DT 24-OCT-2001 (first entry)
DE Synthetic antibody scFv(F8).

Antimicrobial; antiviral; cytostatic; immunomodulatory; antibody;
Gene therapy; HIV; light chain; human immunodeficiency virus; tumour;
metabolic disorder; immune disorder; auto-immune disorder; scFv(F8);
cucumber mosaic virus.

Synthetic.
Key Location/Qualifiers
FT Protein 1..125
FT /label= VH
FT /note= "Heavy chain variable region"
FT Peptide 126..140
FT /label= Linker peptide
FT /note= "This peptide is specifically claimed in claim 17"
FT Protein 141..252
FT /label= VL
FT /note= "Light chain variable region"

WO200149713-A2.
12-JUL-2001.
29-DEC-2000; 2000WO-IT000554.
30-DEC-1999; 99IT-RM000803.
(CNEA) ENEA ENTE NUOVE TECNOLOGIE ENERGIA.
(CONS-) SOC CONSORTILE METAPONTUM AGROBIOS SRL.

PI Benvenuto E, Franconi R, Desiderio A, Tavladoraki P;
XX WPI: 2001-502555/55.
DR N-PSDB; AAS11887.
XX Peptides which are able to confer stability and solubility to an antibody comprising these peptides, useful for treating pathologies (e.g. tumor) associated with accumulation of a molecule inside or outside a human, or animal cell.
PT
PT
XX Example 1; Page 81; 109pp; English.

The invention relates to peptides which are able to confer stability and solubility to an antibody comprising these peptides. The peptides are especially H-FR1, H-FR2, H-FR3, HFR4, L-FR1, L-FR2, L-FR3 or L-FR4 present within a variable region of an antibody which makes the antibody soluble and stable in cytoplasm. Peptides having the sequences of HFR1 to H-FR4 are present within the variable region of the heavy chain of an antibody, covalently linked to the H-CDR1, H-CDR2, H-CDR3 in the order (H-FR1)-(H-CDR1)-(H-FR2)-(H-CDR2)-(H-FR3)-(H-CDR3)-(H-CDR4) and the peptides having the sequences of L-FR1 to L-FR4 are present within the variable region of the light chain of an antibody, covalently linked to the L-CDR1, L-CDR2, L-CDR3 in the order (L-FR1)-(L-CDR1)-(L-FR2)-(L-CDR2)-(L-FR3)-(L-CDR3)-(L-CDR4). The antibodies and polynucleotides (e.g. by gene therapy) are useful for the manufacture of a medicament for the treatment of pathologies associated with accumulation of a molecule inside or outside a human, animal cell or plant cell. The pathologies are infectious (e.g. viral infections such as HIV, human immunodeficiency virus, infections), tumour, metabolic and immune (especially auto-immune) pathologies. The present sequence represents the synthetic antibody scFv(F8) which is used as a basis for constructing synthetic antibodies incorporating the peptides of the invention

XX Sequence 252 AA;

Query Match 82.7%; Score 1082.5; DB 4; Length 252;
Best Local Similarity 84.1%; Pred. No. 3.4e-71;
Matches 212; Conservative 11; Mismatches 26; Indels 3; Gaps 1;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYMSWVRQTPKRLWVAITSSGSSSTYY 60
DB 1 QVQLQESGGDLVQPGGSLKLSCAASGFTFSYMSWVRQTPKRLWVAITNSGGSTFY 60
QY 61 PDSVKGRFTISRDNKNTLYLQSSLRSEDYAMVCTREGG--GFTVNWYFDVWGAGTL 117
DB 61 PDSVKGRFTISRDNKNTLYLQSSLRSEDYAMVCTREGG--GFTVNWYFDVWGAGTL 120
QY 118 VTVSAGGGSGGRASGGGSENVLQSPASLAVSLGQRATISCRASESDVSYGYNFMHWY 177
DB 121 VTVSAGGGSGGGSGGGSDIELTQSPASLAVSLGQRATISCRASESDVSYGNSFMHWY 180
QY 178 QQIPGQPPKLLIYRASNLGSGIPARFSGSGSRDFTLTINPVEADDVATYYCQSNEDPL 237
DB 181 QQQPQPPKLLIYRALNLESGIPARFSGSGSRDFTLTINPVEADDVATYYCQSNEDPW 240
QY 238 TFGTGTGLEIKR 249
DB 241 TFGGTTGLEIKR 252

RESULT 7
AAB61541
ID AAB61541 standard; protein; 269 AA.
XX AAB61541;
AC AAB61541;
XX 03-APR-2001 (first entry)
DT 3DX sfv protein sequence.
DE 3DX; single chain antibody; scFv; modular protein binding domain; MPBD;
KW protein-protein interaction.
XX

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OS Unidentified.
XX WO200101137-A1.
XX
XX PD 04-JAN-2001.
XX
XX PF 29-JUN-2000; 2000WO-US017929.
XX
XX PR 30-JUN-1999; 99US-0141896P.
XX
XX PA (CHIL-) CHILDRENS MEDICAL CENT.
XX (BLOO-) CENT BLOOD RES.
XX
XX PI Mayer BJ, Saksela K, Kirchausen T;
XX WPI; 2001-123027/13.
XX DR N-PSDB; AAF28599.
XX
XX PT New fusion proteins, useful for validating protein-protein interaction
XX PT causing a specific biological activity, comprises a single chain antibody
XX PT instead of a modular protein binding domain.
XX
XX PS Example 1; Fig 1; 34pp; English.
XX
XX CC The present invention relates to fusion proteins containing a single
XX CC chain antibody (scFv) in place of a modular protein binding domain (MPBD),
XX CC or an antibody epitope in place of the linear binding epitope for a MPBD.
XX CC The fusion proteins can be used in assays to identify protein-protein
XX CC interactions. The present sequence is the protein sequence for 3DX
XX CC antibody. 3DX is derived from 9E10. 3DX was used in the method of the
XX CC present invention
XX
XX SQ Sequence 269 AA;
XX
XX Query Match 74.0%; Score 368.5; DB 4; Length 269;
XX Best Local Similarity 74.8%; Pred. No. 7.5e-63;
XX Matches 190; Conservative 22; Mismatches 37; Indels 5; Gaps 2;
XX
XX QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLVWATISSGGSSTYY 60
XX DB 6 EVQLVESGGDLVPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLVWATIGSRGYTHY 65
XX
XX QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDNTAMYYCTREGGQTV-NWYF----DWGAG 115
XX DB 66 PDSVKGRFTISRDNKNTLYLQMSLSRSEDNTAMYYCTREGGQTV-NWYF----DWGAG 125
XX
XX QY 116 TLVTVSAGGGGGSGRASGGGSENVLTQSPASLAVSLGQRATISCRASESDVSGYNFMH 175
XX DB 126 ASVTVSSGGGGSGGGSDGSDIVLTQSPASLAVSLGQRATISCRASESDVSGYFMN 185
XX
XX QY 176 WYQIPGPPKLLIYRASNLVSGIPARFSGSGRTDFTLTINPVEADVDVATYYCQSNED 235
XX DB 186 WFOQKPGQPPKLLIYATSRNGSGVPAFSGSGGTDPSLNHPVEEDSDAMVFCQQTKEV 245
XX
XX QY 236 PLTFTGTGRLIKR 249
XX DB 246 FWTFGGGTKLEIKR 259
XX
XX RESULT 8
XX ID AAB20434 standard; protein; 249 AA.
XX
XX AC AAB20434;
XX
XX XX 21-JUN-2001 (first entry)
XX
XX DE Anti-FIX/FIXa antibody 193/K2 scFv.
XX
XX KW Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
XX KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
XX KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.
XX

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OS Mus musculus.
OS Synthetic.
OS Chimeric.
XX
XX FH Key
XX FT Protein
XX FT 1.121
XX FT /label= VH
XX FT 98.110
XX FT Region
XX FT /label= CDR3
XX FT 122.135
XX FT Peptide
XX FT /label= Linker
XX FT 136.1249
XX FT Protein
XX FT /label= VL
XX FT 230.238
XX FT Region
XX FT /label= CDR3
XX
XX PN WO200119992-A2.
XX
XX XX 22-MAR-2001.
XX
XX PF 13-SEP-2000; 2000WO-EP008936.
XX
XX PR 14-SEP-1999; 99AT-00001576.
XX
XX (BAXT ) BAXTER AG.
XX
XX PA Scheiflinger P, Kerschbaumer R, Falkner F, Dorner F;
XX PI
XX XX WPI; 2001-290358/30.
XX DR N-PSDB; AAF30724.
XX
XX PT New factor IX/factor IXa antibodies and their derivatives useful for
XX PT increasing amidolytic activity of factor IXa, and for treating blood
XX PT coagulation disorders such as hemophilia A and hemorrhagic diathesis.
XX
XX PS Claim 10; Fig 15; 138pp; English.
XX
XX CC The present sequence is that of a single chain Fv (scFv) derivative of
XX CC antibody 193/K2, comprising the heavy (VH) and light (VL) chain variable
XX CC regions of 193/K2 joined by an artificial, flexible linker peptide. The
XX CC scFv was obtained by PCR amplification of cDNAs for 193/K2 VH and VL
XX CC regions and cloning in vector pDAP2. 193/K2 is an example of anti-human
XX CC Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.
XX CC Anti-FIX/FIXa and their derivatives, including scFv and CDR3 fragments,
XX CC have Factor VIIIa (FVIIIa) cofactor activity or FIXa activating activity.
XX CC Administration leads to an increase in the procoagulant activity of FIXa,
XX CC even in the presence of FVIIIa inhibitors. This allows for rapid blood
XX CC coagulation even in the absence of FVIII or FVIIIa, and in the case of
XX CC FVIII inhibitor patients. The antibodies and derivatives are used in a
XX CC claimed pharmaceutical composition for treating patients with blood
XX CC coagulation disorders, especially haemophilia A and haemorrhagic
XX CC diathesis
XX
XX SQ Sequence 249 AA;
XX
XX Query Match 73.6%; Score 963; DB 4; Length 249;
XX Best Local Similarity 75.7%; Pred. No. 1.7e-62;
XX Matches 190; Conservative 23; Mismatches 34; Indels 4; Gaps 3;
XX
XX QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLVWATISSGGSSTYY 60
XX DB 1 EVQLVESGGGLVPGGSLKLSCAASGFTFSYTMWVRQTPKRLVWATISSGGSSTYY 60
XX
XX QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDNTAMYYCTREGG-GFTVWVYFDVWAGTLVT 119
XX DB 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDNTAMYYCTRDGGHGYGSS--FDYWGQGTTLT 118
XX
XX QY 120 VSAGGGGGSGRASGGGSENVLTQSPASLAVSLGQRATISCRASES-VDSYGYNFMHWY 178
XX DB 119 VSSGGGGSGRASGGGSGQIVLTQSPSLPVSLSGQASISCRSSQSVHSGNTYLEWYL 178
XX
XX QY 179 QIPGPPKLLIYRASNLVSGIPARFSGSGRTDFTLTINPVEADVDVATYYCQSNEDPLT 238
XX DB 179 QIPGPPKLLIYRASNLVSGIPARFSGSGRTDFTLTINPVEADVDVATYYCQSNEDPLT 238
XX

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Db	179	QKFGQSKLLIYKVNRRSGVPDKFSGSGSGTDFTLKISRVEADLGVIYCFQGSHPWMT	238
Qy	239	FGTGRLEIKR	249
		:	
Db	239	FGGKLEIKR	249
RESULT 9			
ID	AAAR79866	standard; protein; 239 AA.	
AC	AAAR79866;		
CC	XX		
DT	02-JUL-1996	(first entry)	
DE	XX	Anti-EGFR single chain antibody (Clone 4 B 2).	
EW	XX	Single chain antibody; antibody; epidermal growth factor receptor; EGFR;	
KW	XX	tumour; cancer; glioma; melanoma; carcinoma; diagnosis; assessment;	
KW	XX	phage antibody library.	
OS	XX	Mus musculus.	
PN	XX	WO9525167-A1.	
PD	XX	21-SEP-1995.	
PF	XX	16-MAR-1995; 95WO-EP000978.	
PR	XX	17-MAR-1994; 94EP-00104160.	
PR	XX	02-DEC-1994; 94EP-00118970.	
PA	XX	(MERE) MERCK PATENT GMBH.	
PI	XX	Kettleborough AC, Bendig MM, Ansell KH, Guessow D, Adan J;	
PI	XX	Mitjans F, Rosell E, Biasco F, Pluats J;	
DR	XX	WPI; 1995-336972/43.	
DR	XX	N-PSDB; AAT04019.	
PT	XX	Anti-EGFR antibodies and single chain Fv antibody fragments - obtained	
PT	XX	from phage-antibody libraries, useful for diagnosis and therapy of	
PS	XX	tumours.	
PS	XX	Claim 4; Page 58; 93pp; English.	
CC	XX	Anti-epidermal growth factor receptor (EGFR) single chain antibodies and	
CC	XX	antibodies constructed from anti-EGFR antibody fragments can be used for	
CC	XX	diagnosis of tumours and assessment of tumour growth in vitro and in	
CC	XX	vivo. They may also be used in a pharmaceutical composition for the	
CC	XX	therapy of e.g. melanomas, gliomas and carcinomas. The antibodies and	
CC	XX	fragments are derived from mice but are humanised so as to cause minimum	
CC	XX	reaction against them. They are produced using the phage antibody	
CC	XX	library. They are produced using the phage antibody library. (See	
CC	XX	AAT04011-T04026 and AAR79858-R79873)	
SQ	XX	Sequence 239 AA;	

Qy	180	IFGQPPKLLIYRASNLGGSI	PARGSGSGSTDTFLINPV	EADVATYYCQOSNEDPLTF	239
Db	177	KFGQPPKLLIYARSNLGGSI	VPARGSGSGDTFLNIHP	VEEDDIAMFYCQOSRKVPSF	236
Qy	240	GTG 242			
Db	237	GGG 239			
RESULT 10					
AAE38657	ID	AAE38657	standard; protein;	237 AA.	
XX	AC	AAE38657;			
XX	XX				
DT	04-DEC-2003	(first entry)			
XX	XX	Mouse GI single chain Fv-recombinant antibody.			
XX	XX	Major histocompatibility complex; MHC; HLA-restricted antigen; cancer;			
KW	KW	viral infection; autoimmune disease; gene therapy; cytostatic; virucide;			
KW	KW	immunomodulator; mouse.			
XX	XX				
OS	Mus sp.				
XX	XX				
FH	Key	Location/Qualifiers			
FT	Domain	1. .118			
FT	FT	/note= "VH domain"			
FT	Region	31. .35			
FT	FT	/note= "Complementarity determining region"			
FT	Region	50. .66			
FT	FT	/note= "Complementarity determining region"			
FT	Region	99. .108			
FT	FT	/note= "Complementarity determining region"			
FT	Region	119. .234			
FT	FT	/note= "Peptide linker"			
FT	Domain	135. .237			
FT	FT	/note= "VL domain"			
FT	Region	158. .167			
FT	FT	/note= "Complementarity determining region"			
FT	Region	182. .189			
FT	FT	/note= "Complementarity determining region"			
FT	Region	222. .230			
FT	FT	/note= "Complementarity determining region"			

CC The invention is useful in gene therapy. The present sequence is mouse G1
 CC single chain Fv-recombinant antibody
 QQ Sequence 237 AA;
 XX
 YY
 ZZ
 Query Match 69.4%; Score 909; DB 7; Length 237;
 Best Local Similarity 71.4%; Pred. No. 1.4e-58;
 Matches 175; Conservative 24; Mismatches 38; Indels 8; Gaps 2;
 QY 1 EVQLQESGGGLVFPGGSLKLSCAASGFTFSSYMSWVRQTPKRLLEWATISSGGSTYY 60
 DB 1 QVKLQESGGGLVFPGGSLKLSCAASGFTFSSYMSWVRQTPKRLLEWATISSGGSTYY 60
 QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMTYCTREGGGTVNWFVWAGTLVTV 120
 DB 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMTYCTREGGGTVNWFVWAGTLVTV 120
 QY 121 SAGGGSGGRASGGGSENVLTQSPASLAVSLGORATISCRASESDVSYGNFMHWYQQ 180
 DB 118 SGGGGSGGRASGGGSENVLTQSPALMSASPERVMTCSASSI-----RVIYVQK 172
 QY 181 PGQPKLLIYRASNLESGIPARESGSGSRDFTLTINPVEADDVATYCCQSNEDPLTF 240
 DB 173 PGSPRLIYDTSNVAPGVPRFSGSGSTSYSLTINRMEADDAATYCCQMSGYPTFG 232
 QY 241 TGTPL 245
 DB 233 GGTKL 237
 RESULT 11
 AAB46040
 ID AAB46040 standard; peptide; 240 AA.
 XX
 AC AAB46040;
 XX
 XX
 DT 23-MAR-2001 (first entry)
 DE Human TF anti-idiotype antibody fragment P8.
 XX
 XX MUC1; human; vaccine; conformation-dependent antigen; antibody; cancer;
 KW antidiotopic antibody; cytostatic; virucidal; antibacterial; TF antigen;
 KW antiparasitic; infectious disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200073430-A2.
 XX
 PD 07-DEC-2000.
 XX
 XX 29-MAY-2000; 2000WO-DE001809.
 XX
 XX 27-MAY-1999; 99DE-01024405.
 PR 09-SEP-1999; 99DE-01043016.
 XX
 XX (DELB-) DELBUECK CENT MOLEKULARE MEDIZIN MAX.
 XX
 XX Goletz S, Karsten U;
 XX
 XX WPI; 2001-049937/06.
 XX
 XX Vaccines against conformation-dependent or non-peptide antigens, based on
 FT DNA encoding peptide which mimics the antigen, useful e.g. as antitumor
 FT vaccines.
 XX
 PS Disclosure; Page 11; 36pp; German.
 XX
 CC This invention describes a novel vaccine (V1) against conformation-
 CC dependent antigens (CDA) comprising DNA (I) and/or an antibody, or
 CC peptide which immunologically imitates CDA, is new. (I) encodes a region
 CC of an antidiotopic antibody (Ab2) or another peptide which: (a)
 CC specifically binds to the binding site of an antibody (Ab1) or an antigen
 CC binding molecule; and (b) immunologically mimics the initial antigen. The

CC epitope is partially or completely conformation-dependent, and has an
 CC immunogenic structure defined by a specific spatial conformation of amino
 CC acids. (I) is used in the form of linear or circular naked DNA and/or
 CC with a viral vector and/or adjuvants. The products of the invention have
 CC cytostatic, virucidal, antibacterial and antiparasitic. The invention
 CC also describes (1) a corresponding vaccine (V2) against antigens which
 CC are not proteins or peptides, as defined above but which have epitopes
 CC which show an immunogenic structure; (2) preparing (V1) and (V2); (3)
 CC human antidiotopic antibody fragments against the MUC1-conformation
 CC epitope having one of 31 approximately 60 residue amino acids sequences,
 CC all fully defined in the specification; (4) MUC1-conformation epitope
 CC mimics having one of 16 9-17 residue amino acid sequences, all fully in
 CC the specification; (5) antidiotopic antibody fragments against the TF
 CC antigen having one of 24 approximately 200 residue amino acid sequences,
 CC fully defined in the specification; (6) TF carbohydrate epitope mimetics
 CC having one of 25 7-13 residue amino acid sequences, all fully defined in
 CC the specification; and (7) DNA sequences encoding the fragments and
 CC derivatives defined in (3, 4, 5, or 6). (V1) and (V2) are used to treat
 CC cancer, and infectious diseases, e.g. caused by prions, viruses, bacteria
 CC and parasites. The vaccines are effective in cases where vaccination has
 CC previously not been possible
 XX
 XX Sequence 240 AA;
 Query Match 69.3%; Score 906.5; DB 4; Length 240;
 Best Local Similarity 69.2%; Pred. No. 2.2e-58;
 Matches 173; Conservative 33; Mismatches 33; Indels 11; Gaps 3;
 QY 1 EVQLQESGGGLVFPGGSLKLSCAASGFTFSSYMSWVRQTPKRLLEWATISSGGSTYY 60
 DB 1 EVQLLESGGLVFPGGSLRLSCAASGFTFSSYMSWVRQAPGKLEWVSTISATGSGTYY 60
 QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMTYCTREGGGTVNWFVWAGTLVTV 120
 DB 61 ADSVKGRFTISRDNKNTLYLQMSLSRAVDATVYCAKSSDG-----FDYWGGLVTV 114
 QY 121 SAGGGSGGRASGGGSENV-LTQSPASLAVSLGORATISCRASESDVSYGNFMHWYQQ 179
 DB 115 SGGGGSGGGSGGGGSDIQMTQSPSLASVGDRTVITCRASQSISSY----LNNYQQ 170
 QY 180 IPGQPKLLIYRASNLESGIPARESGSGSRDFTLTINPVEADDVATYCCQSNEDPLTF 239
 DB 171 KPGKAPKLLIYRASNLOSGVPSRFGSGSGGDFTLTISLQPEDFATYCCQASSAPATF 230
 QY 240 GTGTRLEIKR 249
 DB 231 GQGIKVEIKR 240
 RESULT 12
 AAY02472
 ID AAY02472 standard; protein; 240 AA.
 XX
 AC AAY02472;
 XX
 DT 15-JUL-1999 (first entry)
 DE A single chain antibody (ScFv).
 XX
 XX Screening; functional polypeptide; ligand; non-functional; enrichment;
 KW single chain antibody; ScFv.
 XX
 OS Unidentified.
 XX
 XX WO9920749-A1.
 XX
 XX 29-APR-1999.
 PD
 XX 20-OCT-1998; 98WO-GB003135.
 PF
 XX 20-OCT-1997; 97GB-00022131.
 PR 13-NOV-1997; 97US-0065428P.
 PR 21-NOV-1997; 97US-0066729P.

XX PA (MEDI-) MEDICAL RES COUNCIL.
 XX FI Tomlinson I, Winter G;
 XX DR WPI; 1999-288302/24.
 XX DR N-PSDB; AAX36070.
 XX PT Screening for functional polypeptides which bind a ligand.
 XX PS Disclosure; Fig 2; 67pp; English.
 XX CC The specification describes a method for screening for functional
 CC polypeptides which bind a ligand. The method comprises contacting a
 CC repertoire of polypeptides with a generic ligand, and then screening
 CC selected functional polypeptides with a target ligand. The method permits
 CC the removal from a chosen repertoire of polypeptides, those which are non
 CC - functional, e.g. as a result of the introduction of frame-shift
 CC mutations, stop codons, folding mutants or expression mutants which would
 CC be or are incapable of binding to any target ligand. The method also
 CC permits the enrichment of a chosen repertoire of polypeptides for those
 CC polypeptides which are functional, well folded and highly expressed. The
 CC polypeptides obtained can be used in diagnostic, prophylactic and
 CC therapeutic procedures. The present sequence represents the single chain
 CC antibody (ScFv) that forms the basis of a library according to the
 CC invention
 XX CC
 XX SQ Sequence 240 AA;
 Query Match 68.9%; Score 901.5; DB 2; Length 240;
 Best Local Similarity 69.2%; Pred. No. 5.1e-56;
 Matches 173; Conservative 31; Mismatches 35; Indels 11; Gaps 3;
 QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYNTMSWVRQTPKRLWVATISSGGSSTYY 60
 Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSAISGGSSTYY 60
 QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCTREGGFTVNWYFDVWAGTLTVV 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYCAKSYG-----FDYWGQGTLLTV 114
 QY 121 SAGGGSGGRASGGGSENV-LTQSPASLAVSLGQRATISCRASESVDSYGNFMHWYQQ 179
 Db 115 SSGGGSGGGSGGGGSTDIDQMTQSPSLASVGDRTVITCRASQSISSY----LHWYQQ 170
 QY 180 IPQPPKLLIYRASNLSEGIAPRFGSGSRTDFTLTINPVEADVATYYCQSNEDPLTF 239
 Db 171 KPGKAPKLLIYAASLSQGVPSRFGSGSGCTDFTLTISLQPEDFATYYCQSYSTPNTF 230
 QY 240 GTGTLEIKR 249
 Db 231 GGGTKVEIKR 240
 RESULT 13
 ABP95997
 ID ABP95997 standard; protein; 240 AA.
 XX AC ABP95997;
 XX DT 01-MAY-2003 (first entry)
 XX DE Human serum albumin antibody related protein #1.
 XX KW Ligand; human serum albumin; HSA; antibody; cytostatic; anti-HIV;
 KW antiinflammatory; antianaemic; immunosuppressive; neuroprotective;
 KW dual-specific ligand; cancer; HIV infection; hepatitis; rubella; anaemia;
 KW inflammation; autoimmune disorder; multiple sclerosis; Crohn's disease;
 KW myasthenia gravis.
 XX OS Homo sapiens.
 XX OS Synthetic.
 XX

PN WO2003002609-A2.
 XX PD 09-JAN-2003.
 XX PF 28-JUN-2002; 2002WO-GB003014.
 XX PR 28-JUN-2001; 2001GB-00015841.
 XX PA (MEDI-) MEDICAL RES COUNCIL.
 XX PI Winter G, Ignatovich O, Tomlinson I;
 XX WPI; 2003-210246/20.
 XX DR N-PSDB; ABZ76706.
 XX PT Dual-specific ligand having immunoglobulins with binding specificity to
 PT different antigens or epitopes, useful for treating, preventing or
 PT diagnosing diseases, e.g. cancer, HIV infection, inflammations, or
 PT myasthenia gravis.
 XX PS Example 1; Fig 1; 84pp; English.
 XX CC The present invention describes a dual-specific ligand (I) comprising:
 CC (a) a first single immunoglobulin variable domain with a binding
 CC specificity to a first antigen or epitope; and (b) a second complementary
 CC immunoglobulin single variable domain with a binding activity to a second
 CC antigen or epitope. The binding domains are mutually complementary, and
 CC the first and second domains lack mutually complementary domains that
 CC share the same specificity. (I) has cytostatic, anti-HIV, antianaemic,
 CC antiinflammatory, immunosuppressive and neuroprotective activities. The
 CC dual-specific ligand is useful for treating, preventing or diagnosing
 CC diseases, e.g. cancer, HIV infection, hepatitis, rubella, anaemia,
 CC inflammations or autoimmune disorders (e.g. multiple sclerosis, Crohn's
 CC disease or myasthenia gravis). The dual-specific ligand may be used to
 CC recruit cytotoxic T-cells to a cancer cell. The dual-specific ligand is
 CC also useful for monitoring the efficacy of drugs, as well as for
 CC monitoring toxicity. The present sequence represents a human serum
 CC albumin (HSA) related antibody sequence, which is used in an example from
 CC the present invention
 XX CC
 XX SQ Sequence 240 AA;
 Query Match 68.9%; Score 901.5; DB 6; Length 240;
 Best Local Similarity 69.2%; Pred. No. 5.1e-58;
 Matches 173; Conservative 31; Mismatches 35; Indels 11; Gaps 3;
 QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYNTMSWVRQTPKRLWVATISSGGSSTYY 60
 Db 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSAISGGSSTYY 60
 QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDAMYCTREGGFTVNWYFDVWAGTLTVV 120
 Db 61 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYCAKSYG-----FDYWGQGTLLTV 114
 QY 121 SAGGGSGGRASGGGSENV-LTQSPASLAVSLGQRATISCRASESVDSYGNFMHWYQQ 179
 Db 115 SSGGGSGGGSGGGGSTDIDQMTQSPSLASVGDRTVITCRASQSISSY----LHWYQQ 170
 QY 180 IPQPPKLLIYRASNLSEGIAPRFGSGSRTDFTLTINPVEADVATYYCQSNEDPLTF 239
 Db 171 KPGKAPKLLIYAASLSQGVPSRFGSGSGCTDFTLTISLQPEDFATYYCQSYSTPNTF 230
 QY 240 GTGTLEIKR 249
 Db 231 GGGTKVEIKR 240
 RESULT 14
 AAG65715
 ID AAG65715 standard; protein; 293 AA.
 XX AC AAG65715;
 XX

DT 07-JAN-2002 (first entry)
 XX Amino acid sequence of secreted form of scFv 4A.
 XX Polymorphic immunoglobulin receptor; pIgR; ligand; therapeutic;
 KW carcinoma diagnosis; veterinary; scFv 4A.
 XX Synthetic.
 XX FH Key Location/Qualifiers
 FT Peptide 1..22
 FT /note= "PelB leader"
 FT Peptide 23..27
 FT /note= "FLAG epitope"
 FT Region 28..58
 FT /note= "Heavy chain framework 1"
 FT Region 59..62
 FT /note= "CDR1"
 FT Region 63..76
 FT /note= "Heavy chain framework 2"
 FT Region 77..93
 FT /note= "CDR2"
 FT Region 94..125
 FT /note= "Heavy chain framework 3"
 FT Region 126..139
 FT /note= "CDR3"
 FT Region 140..147
 FT /note= "Heavy chain framework 4"
 FT Region 148..162
 FT /note= "linker"
 FT Region 163..185
 FT /note= "light chain framework 1"
 FT Region 186..196
 FT /note= "CDR1"
 FT Region 197..211
 FT /note= "light chain framework 2"
 FT Region 212..218
 FT /note= "CDR2"
 FT Region 219..250
 FT /note= "light chain framework 3"
 FT Region 251..259
 FT /note= "CDR3"
 FT Region 260..270
 FT /note= "light chain framework 4"
 FT Peptide 274..283
 FT /note= "myc epitope tag"
 FT Peptide 288..293
 FT /note= "6 His tag"
 XX WO200172846-A2.
 XX 04-OCT-2001.
 XX 26-MAR-2001; 2001WO-US009699.
 XX 27-MAR-2000; 2000US-0192197P.
 XX 27-MAR-2000; 2000US-0192198P.
 XX (REGC) UNIV CALIFORNIA.
 XX Mostov KE, Chapin SJ, Richman-Eisenstat J;
 XX WPI; 2001-611619/70.
 XX New ligands binding to a specific region of a polymorphic immunoglobulin
 PT receptor, useful for transporting therapeutic or diagnostic compositions
 PT into or across cells expressing pIgR e.g. in drug delivery.
 XX Disclosure; Fig 5; 102pp; English.
 XX The invention provides ligands that bind specifically to a region of an
 CC animal cell polymorphic immunoglobulin receptor (pIgR). The pIgR cleaves to
 CC produce a stalk region remaining attached to the cell and a secretory

CC component existing in the organ of interest in several forms. The ligands
 CC do not bind to the stalk or the most abundant form of the secretory
 CC component present in the organ under physiological conditions. The
 CC ligands are useful for transporting therapeutic or diagnostic
 CC compositions into or across cells expressing pIgR, useful to introduce or
 CC transport ligands such as antibodies and/or to deliver biologically
 CC active components such as proteins, nucleic acids or detectable labels.
 CC They are used to deliver therapeutic compositions to mucosal surfaces
 CC such as the gastro-intestinal tract, respiratory system etc. in humans.
 CC They are also useful to label cells expressing pIgR, e.g. to distinguish
 CC epithelial cells from a mixed cell population in pathology studies or to
 CC aid in carcinoma diagnosis (since pIgR expression is reduced in
 CC carcinomas relative to normal epithelium). They can also be used to
 CC deliver veterinary compositions, especially in mammals such as farm,
 CC domestic or wild mammals or birds e.g. birds reared for human
 CC consumption. The present sequence represents the amino acid sequence of
 CC secreted form of scFv 4A
 XX
 SQ Sequence 293 AA;
 Query Match 68.8%; Score 901; DB 4; Length 293;
 Best Local Similarity 69.2%; Pred. NO. 6.8e-58;
 Matches 173; Conservative 32; Mismatches 37; Indels 8; Gaps 3;
 QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYTHSWVRQTPKRWLVATISSGSSSTYY 60
 DB 28 QVQLVQSGGGLVPGGSLRLSCAASGFTFSYAVSWVRQAPGKGLVWVAISGGSTYY 87
 QY 61 PDSVKGRFTISRDNKNTLYLQMSLRSEDATMYCTREGGFTVN--WYFDVWGAGTLVT 119
 DB 88 ADSVKGRFTISRDNKNTLYLQMSLRSEDATMYCTREGGFTVN--WYFDVWGAGTLVT 144
 QY 120 VSAGGGSGGRASGGGSENVLTQSPASLAVSLQCRATISCRASEVDSYGYNFMHYQQ 179
 DB 145 VSSGGSGGGGGGGGGSEIVLTQSPSTLSASIGDRVITTCRASEGI---YHMLAWYQQ 200
 QY 180 IPGPPKLLIYRASNLESGIPARFSGSGSRDFTLTINPVEADDAVATYYCQSNEDPLTF 239
 DB 201 KPGKAPKLLIYRASNLESGIPARFSGSGSRDFTLTINPVEADDAVATYYCQSNEDPLTF 260
 QY 240 GTGTRLEIKR 249
 DB 261 GQGTKVDIKR 270
 RESULT 15
 ABP45871
 ID ABP45871 standard; protein; 239 AA.
 XX AC ABP45871;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human BlyS binding scFv SEQ ID 1882.
 XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX OS Homo sapiens.
 XX WO200202641-A1.
 XX 10-JAN-2002.
 XX 15-JUN-2001; 2001WO-US019110.
 XX 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.

Search completed: July 29, 2004, 08:46:38
Job time : 77.7154 secs

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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:50:28 ; Search time 61.1123 Seconds
(without alignments)
1278.091 Million cell updates/sec

Title: US-09-661-992B-86
Perfect score: 1309
Sequence: 1 EVQLQESGGGLVPRGGSGLK.....QQSNEDELFTGTTRLEIKR 249

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1082.5	82.7	252	14	US-10-169-351-49
2	968.5	74.0	269	13	US-10-027-770-2
3	968.5	74.0	269	13	US-10-027-770-5
4	951.5	72.7	291	12	US-10-406-830-10
5	904.5	69.1	291	12	US-10-406-830-9
6	901.5	68.9	240	9	US-09-192-854-2
7	901.5	68.9	240	9	US-09-968-561A-2
8	901.5	68.9	240	10	US-09-968-744A-2
9	901.5	68.9	240	12	US-09-968-561A-2
10	901	68.8	288	9	US-09-818-247-22
11	896	68.4	239	10	US-09-880-748-1882
12	896	68.4	239	12	US-10-293-418-1882
13	895.5	68.4	248	10	US-09-880-748-1876
14	895.5	68.4	248	12	US-10-293-418-1876
15	893.5	68.3	248	10	US-09-880-748-1421

16	893.5	68.3	248	12	US-10-293-418-1421
17	892	68.1	243	10	US-09-880-748-1945
18	892	68.1	243	12	US-10-293-418-1945
19	892	68.1	247	10	US-09-880-748-1923
20	892	68.1	247	12	US-10-293-418-1923
21	890	68.0	241	10	US-09-880-748-1889
22	890	68.0	241	12	US-10-293-418-1889
23	889	67.9	239	10	US-09-880-748-1922
24	889	67.9	239	12	US-10-293-418-1922
25	886	67.7	237	10	US-09-880-748-1906
26	886	67.7	237	12	US-10-293-418-1906
27	885	67.6	239	14	US-10-169-351-50
28	883	67.5	237	10	US-09-880-748-2020
29	883	67.5	237	12	US-10-293-418-2020
30	882	67.4	247	10	US-09-880-748-1177
31	882	67.4	247	12	US-10-293-418-1177
32	880	67.2	237	10	US-09-880-748-2003
33	880	67.2	237	12	US-10-293-418-2003
34	880	67.2	237	10	US-09-880-748-2005
35	880	67.2	237	12	US-10-293-418-2005
36	879	67.2	237	10	US-09-880-748-2118
37	879	67.2	237	12	US-10-293-418-2118
38	878	67.1	237	10	US-09-880-748-2019
39	878	67.1	237	12	US-09-880-748-2019
40	878	67.1	237	10	US-09-880-748-2110
41	878	67.1	237	10	US-09-880-748-2114
42	878	67.1	237	10	US-09-880-748-2115
43	878	67.1	237	12	US-10-293-418-2019
44	878	67.1	237	12	US-10-293-418-2040
45	878	67.1	237	12	US-10-293-418-2110

ALIGNMENTS

RESULT 1

US-10-169-351-49
; Sequence 49, Application US/10169351
; Publication No. US20030157090A1
; GENERAL INFORMATION:
; APPLICANT: BENVENUTO, EUGENIO
; APPLICANT: FRANCONI, ROSELLA
; APPLICANT: DESIDERIO, ANGIOLA
; APPLICANT: TAVLADORAKI, PARASKEVI
; TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
; TITLE OF INVENTION: WHICH INCLUDE THEM
; FILE REFERENCE: 4161-4
; CURRENT APPLICATION NUMBER: US/10/169,351
; CURRENT FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: PCT/IT00/00554
; PRIOR FILING DATE: 2000-12-29
; PRIOR APPLICATION NUMBER: IT RM99A000803
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: scFv(F8)
; OTHER INFORMATION: amino acid sequence

US-10-169-351-49

Query Match 82.7%; Score 1082.5; DB 14; Length 252;
Best Local Similarity 84.1%; Pred. No. 1.4e-75;
Matches 212; Conservative 11; Mismatches 26; Indels 3; Gaps 1;

QY 1 EVQLQESGGGLVPRGGSGLKSCAASGFTFSYTHSWVQTEKRLWVATISSGSSSTYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QVQLQESGGDLVQPGGSLKSCAASGFTFSYTHSWVQTEKRLWVATINSNGSTFY 60

QY 61 PDSVKGRFTISRDNAKNTLYIQMSSLRSEDATMYCYCTREGG---GFTVNVFDVKGAGTGL 117

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Db 61 PDSVKGRFTISRDNKNTLYLQMSLSKSEDTAMYYCARRRNPYYIGSRGYPDYWGCGTT 120
Qy 118 VTVSAGGGGGGRASGGGGSENVLTQSPASLAVSLGQRATISCRASESDSYGYNFMH 177
Db 121 VTVSAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 180
Qy 178 QQLPGQPPKLLIYRASNLGSDIPARFSGSGSRDFTLTINPVEADDVATYCCQSNEDPL 237
Db 181 QQRPGQPPKLLIYALNLESGIPARFSGSGSRDFTLTINPVEADDVATYCCQSNEDPW 240
Qy 238 TFGTGTRLEIKR 249
Db 241 TFGGTGKLEIKR 252

RESULT 2
US-10-027-770-2
; Sequence 2, Application US/10027770
; Publication No. US20020151684A1
; GENERAL INFORMATION:
; APPLICANT: MAYER, BRUCE
; APPLICANT: SAKSELA, KALLE
; APPLICANT: KIRCHAUSEN, TOMAS
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10
US-10-027-770-2

Query Match 74.0%; Score 968.5; DB 13; Length 269;
Best Local Similarity 74.8%; Pred. No. 9.2e-67;
Matches 190; Conservative 22; Mismatches 37; Indels 5; Gaps 2;

Qy 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYTMVSRQTPDKRLEWVAITSGGSSTYY 60
Db 6 EVKLVESGDLVQPGGSLKLSCAASGFTFSHYGMSWRQTPDKRLEWVAITSGRTYTHY 65
Qy 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDTAMYYCTREGGFTV-NWYF-----DVGAG 115
Db 66 PDSVKGRFTISRDNKNTLYLQMSLSRSEDTAMYYCARRSEFYNGNTTYSAMDYWGQG 125
Qy 116 TLVTVSAGGGGGGRASGGGGSENVLTQSPASLAVSLGQRATISCRASESDSYGYNFMH 175
Db 126 ASVTSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 185
Qy 176 WYQIIPGQPPKLLIYRASNLGSDIPARFSGSGSRDFTLTINPVEADDVATYCCQSNED 235
Db 186 WFQKPGQPPKLLIYASNRGSGVPAFSGSGSGTDFSLNHPVEEDDSAMYFCQQTKEV 245
Qy 236 PLTTGTGTRLEIKR 249
Db 246 PWTFGGTGKLEIKR 259

RESULT 3
US-10-027-770-5
; Sequence 5, Application US/10027770
; Publication No. US20020151684A1
; GENERAL INFORMATION:
; APPLICANT: MAYER, BRUCE
; APPLICANT: SAKSELA, KALLE
; APPLICANT: KIRCHAUSEN, TOMAS
; TITLE OF INVENTION: FUSION PROTEIN AND USES THEREOF
; FILE REFERENCE: 701039-050001-C
; CURRENT APPLICATION NUMBER: US/10/027,770
; PRIOR FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: PCT/US00/17929
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 60/141,896
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 269
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: 3DX, a
; OTHER INFORMATION: second-generation ScFv derived from monoclonal
; OTHER INFORMATION: antibody 9E10
US-10-027-770-5

Query Match 74.0%; Score 968.5; DB 13; Length 269;
Best Local Similarity 74.8%; Pred. No. 9.2e-67;
Matches 190; Conservative 22; Mismatches 37; Indels 5; Gaps 2;

Qy 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYTMVSRQTPDKRLEWVAITSGGSSTYY 60
Db 6 EVKLVESGDLVQPGGSLKLSCAASGFTFSHYGMSWRQTPDKRLEWVAITSGRTYTHY 65
Qy 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDTAMYYCTREGGFTV-NWYF-----DVGAG 115
Db 66 PDSVKGRFTISRDNKNTLYLQMSLSRSEDTAMYYCARRSEFYNGNTTYSAMDYWGQG 125
Qy 116 TLVTVSAGGGGGGRASGGGGSENVLTQSPASLAVSLGQRATISCRASESDSYGYNFMH 175
Db 126 ASVTSSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG 185
Qy 176 WYQIIPGQPPKLLIYRASNLGSDIPARFSGSGSRDFTLTINPVEADDVATYCCQSNED 235
Db 186 WFQKPGQPPKLLIYASNRGSGVPAFSGSGSGTDFSLNHPVEEDDSAMYFCQQTKEV 245
Qy 236 PLTTGTGTRLEIKR 249
Db 246 PWTFGGTGKLEIKR 259

RESULT 4
US-10-406-830-10
; Sequence 10, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000410US
; CURRENT APPLICATION NUMBER: US/10/406,830
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 10
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic antibody.
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match 68.9%; Score 901.5; DB 9; Length 240;
Best Local Similarity 69.2%; Pred. No. 1.2e-61;
Matches 173; Conservative 31; Mismatches 35; Indels 11; Gaps 3;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYMSWVRQTPKEKLEWVATISSGGSSTYY 60
DB 1 EVQLLESQGGGLVQPGGSLRLSRAEDTAIVYCAKSYG-----FDYWGQGLTLTV 60

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDATMYCTREGGFTVNWYFDVWGAGTLTV 120
DB 61 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAIVYCAKSYG-----FDYWGQGLTLTV 114

QY 121 SAGGGGSGRASGGGSENV-LTQSPASLAVSLGQRATISCRASESDSYGNFMHWYQQ 179
DB 115 SSGGGGSGGSGGGGSDTIQMTQSPSLASVGDRTVITCRASQSISSY----LNWYQQ 170

QY 180 IPGQPPKLLIYRASNLESGIPARESGSGSRDFTLTINPVEADDVATYYCOQSNEDPLTF 239
DB 171 KPGKAPKLLIYAASLSQSGVPSRFSGSGGDTFTLTISLQPEDFATYYCQSYSTPNTF 230

QY 240 GTGTRLEIKR 249
DB 231 GQGTKVEIKR 240

RESULT 8

US-09-968-744A-2
; Sequence 2, Application US/09968744A
; Publication No. US20030148372A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phase Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073
; CURRENT APPLICATION NUMBER: US/09/968,744A
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-744A-2

Query Match 68.9%; Score 901.5; DB 10; Length 240;
Best Local Similarity 69.2%; Pred. No. 1.2e-61;
Matches 173; Conservative 31; Mismatches 35; Indels 11; Gaps 3;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYMSWVRQTPKEKLEWVATISSGGSSTYY 60
DB 1 EVQLLESQGGGLVQPGGSLRLSRAEDTAIVYCAKSYG-----FDYWGQGLTLTV 60

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDATMYCTREGGFTVNWYFDVWGAGTLTV 120
DB 61 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAIVYCAKSYG-----FDYWGQGLTLTV 114

QY 121 SAGGGGSGRASGGGSENV-LTQSPASLAVSLGQRATISCRASESDSYGNFMHWYQQ 179
DB 115 SSGGGGSGGSGGGGSDTIQMTQSPSLASVGDRTVITCRASQSISSY----LNWYQQ 170

QY 180 IPGQPPKLLIYRASNLESGIPARESGSGSRDFTLTINPVEADDVATYYCOQSNEDPLTF 239
DB 171 KPGKAPKLLIYAASLSQSGVPSRFSGSGGDTFTLTISLQPEDFATYYCQSYSTPNTF 230

QY 240 GTGTRLEIKR 249
DB 231 GQGTKVEIKR 240

RESULT 9

US-09-968-561A-2
; Sequence 2, Application US/09968561A
; Publication No. US20040038291A2
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phase Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073B
; CURRENT APPLICATION NUMBER: US/09/968,561A
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-561A-2

Query Match 68.9%; Score 901.5; DB 12; Length 240;
Best Local Similarity 69.2%; Pred. No. 1.2e-61;
Matches 173; Conservative 31; Mismatches 35; Indels 11; Gaps 3;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYMSWVRQTPKEKLEWVATISSGGSSTYY 60
DB 1 EVQLLESQGGGLVQPGGSLRLSRAEDTAIVYCAKSYG-----FDYWGQGLTLTV 60

QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDATMYCTREGGFTVNWYFDVWGAGTLTV 120
DB 61 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAIVYCAKSYG-----FDYWGQGLTLTV 114

QY 121 SAGGGGSGRASGGGSENV-LTQSPASLAVSLGQRATISCRASESDSYGNFMHWYQQ 179
DB 115 SSGGGGSGGSGGGGSDTIQMTQSPSLASVGDRTVITCRASQSISSY----LNWYQQ 170

QY 180 IPGQPPKLLIYRASNLESGIPARESGSGSRDFTLTINPVEADDVATYYCOQSNEDPLTF 239
DB 171 KPGKAPKLLIYAASLSQSGVPSRFSGSGGDTFTLTISLQPEDFATYYCQSYSTPNTF 230

QY 240 GTGTRLEIKR 249
DB 231 GQGTKVEIKR 240

RESULT 10

US-09-818-247-22
; Sequence 22, Application US/09818247
; Patent No. US20020102657A1
; GENERAL INFORMATION:
; APPLICANT: Mostov, Keith E.


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; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1421
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1421

Query Match      68.3%; Score 893.5; DB 10; Length 248;
Best Local Similarity 68.1%; Pred. No. Se-61;
Matches 173; Conservative 32; Mismatches 38; Indels 11; Gaps 3;

Qy      1 EVQLQESGGGLVAPGQGIKLSCAASGFTFSYTHSWYRQTPKXLEWVAISSGGSSTYY 60
Db      1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAHWYRQAPGKGLEWVAISYDGSNKYY 60

Qy      61 PDSVKGRFTISRDNKNTLYLQMSLRSEDTAMYICTREGG-----GFTVNWYFDVMGAG 115
Db      61 ADSVKGRFTISRDNKNTLYLQMSLRSEDTAVYICARAYDYDILTGY--SYIFDYWGKG 118

Qy      116 TLVTVSAGGGGGGGRASGGGSENVLTQSPASLAVSLGQRATISCRASESDSYGYNFMH 175
Db      119 TLVTVSSGGGGGGGGGGGSDIQMTQSPSTMSASIGDRVITICRASEGI---YHWLA 174

Qy      176 WYQIQGPQPKLLIYRASNLSEGIAPRFGSGGSRDFTLTINPVEADVDVATYYCQOSNED 235
Db      175 WYQQKPGKAPKLLIYKASSLASGAPSRFGSGGSGTDFLTILSSLPDDPATYYCQQYSNY 234

Qy      236 PLTFTGTTRLEIKR 249
Db      235 PLTFGGGKLEIKR 248
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Search completed: July 29, 2004, 09:12:27
Job time : 62.1123 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:27 ; Search time 22.4295 Seconds
(without alignments)
573.123 Million cell updates/sec

Title: US-09-661-992B-86

Perfect score: 1309

Sequence: 1 EVQIQESGGGLVPGGSLKL.....QQSNEDPLFTGTRLEIKR 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	941.5	71.9	239	2	US-08-553-497A-18
2	888	67.8	245	4	US-08-918-148-75
3	882	67.4	245	4	US-08-918-148-78
4	878	67.1	281	4	US-09-025-769B-178
5	862	65.9	282	2	US-08-860-174A-10
6	854	65.2	277	2	US-08-256-790-2
7	853	65.2	245	4	US-08-918-148-76
8	847.5	64.7	236	2	US-08-150-199A-65
9	845.5	64.6	248	2	US-08-887-352B-22
10	845.5	64.6	248	3	US-09-109-207C-22
11	845.5	64.6	248	3	US-09-296-005-22
12	845.5	64.6	248	4	US-09-920-171-22
13	841.5	64.3	244	4	US-08-918-148-77
14	841	64.2	247	3	US-09-227-693-34
15	841	64.2	248	1	US-08-331-398A-34
16	841	64.2	248	2	US-08-331-397B-34
17	841	64.2	248	2	US-08-759-804A-34
18	840.5	64.2	248	2	US-08-887-352B-23
19	840.5	64.2	248	3	US-09-109-207C-23
20	840.5	64.2	248	3	US-09-296-005-23
21	840.5	64.2	248	4	US-09-920-171-23
22	839.5	64.1	255	4	US-09-553-498-8
23	839.5	64.1	255	4	US-09-618-869-8
24	830	63.4	284	3	US-08-564-164A-2
25	827.5	63.2	240	2	US-08-956-047-25
26	823	62.9	482	4	US-09-509-031-16
27	822	62.8	268	4	US-09-554-765-2

28	822	62.8	408	4	US-09-554-765-15	Sequence 15, Appl
29	822	62.8	409	4	US-09-554-765-14	Sequence 14, Appl
30	821	62.7	240	1	US-08-488-113B-148	Sequence 148, App
31	821	62.7	240	1	US-08-477-484B-148	Sequence 148, App
32	821	62.7	240	2	US-08-646-360-148	Sequence 148, App
33	821	62.7	240	3	US-08-839-765-148	Sequence 148, App
34	821	62.7	240	3	US-09-136-389-148	Sequence 148, App
35	821	62.7	240	4	US-09-610-838-148	Sequence 148, App
36	821	62.7	240	4	US-09-711-485-148	Sequence 148, App
37	804.5	61.5	301	2	US-08-661-052-14	Sequence 14, Appl
38	804.5	61.5	301	3	US-09-188-082-14	Sequence 14, Appl
39	804.5	61.5	301	4	US-09-364-088-14	Sequence 14, Appl
40	804.5	61.5	301	4	US-09-102-716-14	Sequence 14, Appl
41	804.5	61.5	553	3	US-08-661-052-16	Sequence 16, Appl
42	804.5	61.5	553	3	US-09-188-082-16	Sequence 16, Appl
43	804.5	61.5	553	4	US-09-364-088-16	Sequence 16, Appl
44	804.5	61.5	553	4	US-09-102-716-16	Sequence 16, Appl
45	802	61.3	289	3	US-09-184-658-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1

US-08-553-497A-18
; Sequence 18, Application US/08553497A
; Patent No. 5844033
; GENERAL INFORMATION:
; APPLICANT: KETTESBOROUGH, C. A.
; APPLICANT: BENDIG, MARY M.
; APPLICANT: ANSELL, KEITH H.
; APPLICANT: GUSSOW, DETLEF
; APPLICANT: ADAN, JAUME
; APPLICANT: MITJANS, FRANCES
; APPLICANT: ROSELL, ELISABET
; APPLICANT: BLASCO, FRANCES
; APPLICANT: PULATS, JAUME
; TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FVS AND ANTI-EGFR
; TITLE OF INVENTION: ANTIBODIES
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
; STREET: 2200 CLARENDON BLVD. SUITE 1400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: US
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/553.497A
; FILING DATE: 17-NOV-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP95/00978
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94104160.0
; FILING DATE: 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94118970.6
; FILING DATE: 02-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1726
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 18:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-553-497A-18

Query Match      71.9%; Score 941.5; DB 2; Length 239;
Best Local Similarity 76.5%; Pred. No. 3.5e-74;
Matches 186; Conservative 20; Mismatches 32; Indels 5; Gaps 2;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYTWMSWVRQTPPEKLEWVAITSSGGSSTYY 60
DB 1 EVKLQESGGDLVQPGGSLKLSCAASGFTFSYTWMSWVRQTPPEKLEWVAITSSGGSSTYY 60
QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDVTAMYYCTRT-EGGQFTVNNVFDVWGAGTLVT 119
DB 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDVTAMYYCARLETGYAL----DYWGQGTIVT 116
QY 120 VSAGGGSGGRASGGGSENVLTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQQ 179
DB 117 VSSGGSGGGGGGGGSDIELTQSPASLAVSLGQRTATIFCKDSQSDYDGDSDYNNWYQQ 176
QY 180 IPGQPPKLLIYRASNLSEGIPTARESGSGSRDFTLTINPVEADDVATYYCQSNEDPLTF 239
DB 177 KPGQPPKLLIYRASNLSEGPAREFSGSGSDTFLNHPVEEDDIAMVFCQSRKVPWSF 236
QY 240 GTG 242
DB 237 GGG 239

RESULT 2
US-08-918-148-75
; Sequence 75, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W. Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918.148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 75
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
; US-08-918-148-78

Query Match      67.4%; Score 888; DB 4; Length 245;
Best Local Similarity 67.9%; Pred. No. 1.6e-69;
Matches 169; Conservative 33; Mismatches 39; Indels 8; Gaps 2;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYTWMSWVRQTPPEKLEWVAITSSGGSSTYY 60
DB 3 EVQLVQSGGGVLVQPGGSLRLSCLASGFTFSYTWMSWVRQAPGKLEWVSISSGGSSTYY 62
QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDVTAMYYCTREGGFTVNNVFDVWGAGTLVT 120
DB 63 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVVYCARDRGTCM---DVGGRGLTVT 118
QY 121 SAGGGSGGRASGGGSENVLTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQQI 180
DB 119 SSGGGSGGGGGGGSDIVMTQSPSLASIGDRVITTCRASEGI----YHVLAWYQQK 174
QY 181 PQQPPKLLIYRASNLSEGIPTAREFSGSGSRDFTLTINPVEADDVATYYCQSNEDPLTF 240
DB 175 PGKAPKLLIYKASSLASGAPRFSGSGSDFTLTISLQPDPTATYYCQYSNYPLTF 234
QY 241 TGTRELEIKR 249
DB 235 GGTGLEIKR 243

RESULT 4
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
```

```
QY 241 TGTRELEIKR 249
DB 235 GGTGLEIKR 243

RESULT 3
US-08-918-148-78
; Sequence 78, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W. Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918.148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 78
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: unknown
; LOCATION: 208
; OTHER INFORMATION: unknown amino acid
; US-08-918-148-78

Query Match      67.4%; Score 882; DB 4; Length 245;
Best Local Similarity 68.3%; Pred. No. 5.3e-69;
Matches 170; Conservative 33; Mismatches 38; Indels 8; Gaps 2;

QY 1 EVQLQESGGGLVQPGGSLKLSCAASGFTFSYTWMSWVRQTPPEKLEWVAITSSGGSSTYY 60
DB 3 QVQLVESGGGLVQPGGSLRLSCLASGFTFSYSHNNMNVVRQAPGKLEWVSISSGGSSTYY 62
QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDVTAMYYCTREGGFTVNNVFDVWGAGTLVT 120
DB 63 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVVYCARDRGTCM---DVGGRGLTVT 118
QY 121 SAGGGSGGRASGGGSENVLTQSPASLAVSLGQRTATISCRASESVDSYGNFMHWYQQI 180
DB 119 SSGGGSGGGGGGGGSKIQTQSPSLASIGDRVITTCRASEGI----YHVLAWYQQK 174
QY 181 PQQPPKLLIYRASNLSEGIPTAREFSGSGSRDFTLTINPVEADDVATYYCQSNEDPLTF 240
DB 175 PGKAPKLLIYKASSLASGAPRFSGSGSDFTLTISLQPDPTATYYCQYSNYPLTF 234
QY 241 TGTRELEIKR 249
DB 235 GGTGLEIKR 243

RESULT 4
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
```

COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-178

Query Match 67.1%; Score 878; DB 4; Length 281;
Best Local Similarity 68.8%; Pred. No. 1.4e-68;
Matches 176; Conservative 25; Mismatches 45; Indels 10; Gaps 4;

QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYMSWVRQTPKRLKLEWATISSGGSTYY 60
Db 26 EVQLVGGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGGSGSTYY 85
QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMVYCTREGG-GFTVMVYFDVAGAGTLVT 119
Db 86 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYICARWGDDF---YANDYWGQGLT 142
QY 120 VS-----AGGGSGGGRAGSGGSENVLTPSPASLAVSLGORATISCRASES-VDSYGYNF 173
Db 143 VSSAGGSGGGGGGGGGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLHLSNGYNY 202
QY 174 MHWYQIQPGPPKLLIYRANLSESGIPARESGGSRDFTLTINPVEADVAVYVYCCQSN 233
Db 203 LDWTLQRPQSPQLLIYLGNRASGVPDRFSGSGGDFDTLKISRVEADVGVYVYCCQHY 262
QY 234 EDPLTFGTGRLEIKR 249
Db 263 TTPPTFGGQTKVEIKR 278

RESULT 5
US-08-860-174A-10
Sequence 10, Application US/08860174A
Patent No. 5989830
GENERAL INFORMATION:
APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOOT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisea
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: 9th Floor, East Tower
STATE: WASHINGTON, D.C.
COUNTRY: UNITED STATES
ZIP: 20005-3918

COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-178

Query Match 67.1%; Score 878; DB 4; Length 281;
Best Local Similarity 68.8%; Pred. No. 1.4e-68;
Matches 176; Conservative 25; Mismatches 45; Indels 10; Gaps 4;

QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYMSWVRQTPKRLKLEWATISSGGSTYY 60
Db 26 EVQLVGGGGLVPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVAISGGSGSTYY 85
QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMVYCTREGG-GFTVMVYFDVAGAGTLVT 119
Db 86 ADSVKGRFTISRDNKNTLYLQMSLSRAEDTAVYICARWGDDF---YANDYWGQGLT 142
QY 120 VS-----AGGGSGGGRAGSGGSENVLTPSPASLAVSLGORATISCRASES-VDSYGYNF 173
Db 143 VSSAGGSGGGGGGGGGGGGSDIVMTQSPLSLPVTPGEPASISCRSSQSLHLSNGYNY 202
QY 174 MHWYQIQPGPPKLLIYRANLSESGIPARESGGSRDFTLTINPVEADVAVYVYCCQSN 233
Db 203 LDWTLQRPQSPQLLIYLGNRASGVPDRFSGSGGDFDTLKISRVEADVGVYVYCCQHY 262
QY 234 EDPLTFGTGRLEIKR 249
Db 263 TTPPTFGGQTKVEIKR 278

RESULT 5
US-08-860-174A-10
Sequence 10, Application US/08860174A
Patent No. 5989830
GENERAL INFORMATION:
APPLICANT: DAVIS, Paul James
APPLICANT: VAN DER LOOT, Cornelis Paul Erik
APPLICANT: VERHOEIJEN, Martine Elisea
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
CITY: 9th Floor, East Tower
STATE: WASHINGTON, D.C.
COUNTRY: UNITED STATES
ZIP: 20005-3918

COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD, WINDOWS 95, Ver. 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/860,174A
FILING DATE: June 16, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-860-174A-10

Query Match 65.9%; Score 862; DB 2; Length 282;
Best Local Similarity 67.3%; Pred. No. 3.4e-67;
Matches 169; Conservative 28; Mismatches 50; Indels 4; Gaps 3;

QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYMSWVRQTPKRLKLEWATISSGGSTYY 60
Db 23 QVQLQESGGDLVPGGSLTSLCATSGFTFSYAFSWVRQTSKSLKLEWATISSDTDTYY 82
QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYAMVYCTREGGFTVMVYFDVAGAGTLVT 120
Db 83 SDNVKGRFTISRDNKNTLYLQMSLSKSEDYAVYICARH--GYIKGKGFYWGQGTITV 140
QY 121 SAGGSGGGRAGSGGSENVLTPSPASLAVSLGORATISCRASES-VDSYGY-NFMHWYQ 178
Db 141 SSGGSGGSGGGGGGGSDIELTQSPFLTVTAGKVTNCKSGQSLLSNVQRNVLTVYQ 200
QY 179 QIQPGPPKLLIYRANLSESGIPARESGGSRDFTLTINPVEADVAVYVYCCQSNEDPLT 238
Db 201 QKPGPPKLLIYVASTRESGVDRFTASGSGDFTLTISVQAEDLAVYVYCCNDYTPFT 260
QY 239 FGTGRLEIKR 249
Db 261 FGGTKLEIKR 271

RESULT 6
US-08-256-790-2
Sequence 2, Application US/08256790
Patent No. 5910573
GENERAL INFORMATION:
APPLICANT: PLUECKTHUN, ANDREAS
APPLICANT: PACK, PETER
TITLE OF INVENTION: MONOMERIC AND DIMERIC ANTIBODY FRAGMENT
TITLE OF INVENTION: FUSION PROTEINS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,790
FILING DATE: 22-JUL-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: PCT/EP93/00082
; FILING DATE: 15-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 92101069
; FILING DATE: 23-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: HAMLET-KING, DIANA
; REGISTRATION NUMBER: 33,302
; REFERENCE/DOCKET NUMBER: MERCK 1598
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-243-6333
; TELEFAX: 703-243-6410
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-256-790-2

Query Match      65.2%; Score 854; DB 2; Length 277;
Best Local Similarity 64.8%; Pred. No. 1.6e-66;
Matches 164; Conservative 38; Mismatches 45; Indels 6; Gaps 3;

QY      1 EVQLQESGGGLVQPGGSLKLSKAASGFTFSYTMWVRQTPKRLKLEWATISSGGS--ST 58
DB      22 EVKLVEGGGLVQPGGSLRLSCATSGTFTDFYMEWVRQPPGKRLKLEWIAASRNKNGKYYT 81

QY      59 YYPDSVKGRTISRDNKNTLYLQMSLSRSEDATMYCTREGGGFTVNWTFDVGAGTLV 118
DB      82 EYSASVKGRTISRDTSQSLYLQNNALRAEDTAIYFCARNYGST--WYFDVGAGTIV 139

QY      119 TVSAGGGSGGRASGGGSENVLTQSPASLAVSLGQRATISCRASESVDSYG--YVFMHW 176
DB      140 TVSSGGGSGGGGGGGSDIVMTQSPSSLSVSAGERVTWCKSSQSLNSGNKQKFLAW 199

QY      177 YQIIPGPPKLLIYRASNLSEGIPIARFSGSGSRDFTLTINPVEADVAIYCCQSNEDP 236
DB      200 YQKPGPPKLLIYGASTRESGVDRITGSGSGDFTLTISVQAEDLAVIYCCQNDHSP 259

QY      237 LTFGTGTRLEIKR 249
DB      260 LTFGAGTKLELR 272

RESULT 7
US-08-918-148-76
; Sequence 76, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918.148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 76
; LENGTH: 245
; TYPE: PRT
; ORGANISM: artificial
; US-08-918-148-76

Query Match      65.2%; Score 853; DB 4; Length 245;
Best Local Similarity 65.9%; Pred. No. 1.7e-66;
Matches 164; Conservative 33; Mismatches 44; Indels 8; Gaps 2;

QY      1 EVQLQESGGGLVQPGGSLKLSKAASGFTFSYTMWVRQTPKRLKLEWATISSGGSSTYY 60
DB      3 EVQLVQSGGGLVQPGGSLKLSKAASGFTITRTYGMHWVRQAPGKLEWVAGISFDGRSEY 62

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QY      61 PDSVKGRTISRDNKNTLYLQMSLSRSEDATMYCTREGGGFTVNWTFDVGAGTLVTV 120
DB      63 ADSVKGRTISRDNKNTLYLQMSLSRAEDTAVIYCARDRGSGYM----DVWGRGTWTV 118

QY      121 SAGGGSGGRASGGGSENVLTQSPASLAVSLGQRATISCRASESVDSYGYNFMHWYQOI 180
DB      119 SSGGGSGGGGGGGGGDIQNTQSPSLASIGDRVITCRASEGI----YHMLAWYQOK 174

QY      181 PQPPKLLIYRASNLSEGIPIARFSGSGSRDFTLTINPVEADVAIYCCQSNEDPITFG 240
DB      175 PKAPKLLIYKASSLASGAPSRFSGSGSGDFTLTISLQPDFFATYCCQSYNYPLTFG 234

QY      241 TGTRELEIKR 249
DB      235 GGTRELEIKR 243

RESULT 8
US-08-190-199A-65
; Sequence 65, Application US/08190199A
; Patent No. 5830663
; GENERAL INFORMATION:
; APPLICANT: EMBLETON, Michael J.
; APPLICANT: GOROCHOV, Guy
; APPLICANT: JONES, Peter T.
; APPLICANT: WINTER, Gregory P.
; TITLE OF INVENTION: TREATMENT OF CELL POPULATIONS
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESS: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190.199A
; FILING DATE: 13-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/01483
; FILING DATE: 10-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9212419.7
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9117352.6
; FILING DATE: 10-AUG-1991
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-190-199A-65

Query Match      64.7%; Score 847.5; DB 2; Length 236;
Best Local Similarity 66.3%; Pred. No. 5e-66;
Matches 165; Conservative 29; Mismatches 42; Indels 13; Gaps 2;

QY      1 EVQLQESGGGLVQPGGSLKLSKAASGFTFSYTMWVRQTPKRLKLEWATISSGGSSTYY 60
DB      1 DVQLVESGGGLVQPGGSRKLSKAASGFTFSFGMHWVRQAPKLEWVAIYSSGSSSTYY 60

QY      61 PDSVKGRTISRDNKNTLYLQMSLSRSEDATMYCTREGGGFTVNWTFDVGAGTLVTV 120
DB      61 ADTVKGRFTISKDNPNPNTLFLQMTLSRSEDATMYCYCARDYGAI-----WGQGTLLTV 112

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; OTHER INFORMATION: sfv sequence derived from MAE11
US-09-296-005-22

Query Match 64.6%; Score 845.5; DB 3; Length 248;
Best Local Similarity 65.2%; Pred. No. 7.9e-66;
Matches 163; Conservative 40; Mismatches 44; Indels 3; Gaps 3;
QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFS-YTMSWVRQTPKRLWVATISGGSSY 59
DB 1 EVQLVESGGGLVPGGSLRLSCLVSGVITSGYSWIRQAPGKLEWVASITYDGSY 60
QY 60 YPDSVKGRFTISRDNKNTLYLQMSLSRSEDYCTREGGFTVNNYFVWAGTTLVT 119
DB 61 NP-SVKGRITISRDNKNTLYLQMSLSRAEDTAVYCAR-GSHYFGHWHFAVWGQTLVT 118
QY 120 VSAGGGSGGGRASGGGSENVLTQSPASLAVSLGQRATISCRASESDSYGNFMHWYQQ 179
DB 119 VSSEGSGGSEGGSGGSDIQLTQSPSLASVGDRTVITCRASKPVDGSDSYLNWYQQ 178
QY 180 IPGPAPKLLIYRASNLSGIPARFSGSGSRDFTLTINPVEADDVATYCCQSNEDPLTF 239
DB 179 KPGKAPKLLIYRASNLSGIPARFSGSGSGDFTLTISLQPEDPATYCCQSHEDPYTF 238
QY 240 GTGTRLEIKR 249
DB 239 GQGTKVEIKR 248

RESULT 12
US-09-920-171-22
; Sequence 22, Application US/0920171
; Patent No. 6682735
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Improved Anti-IgE Antibodies (as amended)
; FILE REFERENCE: P1123C2US
; CURRENT APPLICATION NUMBER: US/09/920,171
; CURRENT FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: US 08/887,352
; PRIOR FILING DATE: 1997-07-02
; PRIOR APPLICATION NUMBER: US 09/296,005
; PRIOR FILING DATE: 1999-04-21
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 22
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sfv sequence derived from MAE11
US-09-920-171-22

Query Match 64.6%; Score 845.5; DB 4; Length 248;
Best Local Similarity 65.2%; Pred. No. 7.9e-66;
Matches 163; Conservative 40; Mismatches 44; Indels 3; Gaps 3;
QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFS-YTMSWVRQTPKRLWVATISGGSSY 59
DB 1 EVQLVESGGGLVPGGSLRLSCLVSGVITSGYSWIRQAPGKLEWVASITYDGSY 60
QY 60 YPDSVKGRFTISRDNKNTLYLQMSLSRSEDYCTREGGFTVNNYFVWAGTTLVT 119
DB 61 NP-SVKGRITISRDNKNTLYLQMSLSRAEDTAVYCAR-GSHYFGHWHFAVWGQTLVT 118
QY 120 VSAGGGSGGGRASGGGSENVLTQSPASLAVSLGQRATISCRASESDSYGNFMHWYQQ 179
DB 119 VSSEGSGGSEGGSGGSDIQLTQSPSLASVGDRTVITCRASKPVDGSDSYLNWYQQ 178
QY 180 IPGPAPKLLIYRASNLSGIPARFSGSGSRDFTLTINPVEADDVATYCCQSNEDPLTF 239
DB 179 KPGKAPKLLIYRASNLSGIPARFSGSGSGDFTLTISLQPEDPATYCCQSHEDPYTF 238

QY 240 GTGTRLEIKR 249
DB 239 GQGTKVEIKR 248
RESULT 13
US-08-918-148-77
; Sequence 77, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Pendi, Brian M.
; APPLICANT: Gurney, Ausin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0379
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 77
; LENGTH: 244
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-77

Query Match 64.3%; Score 841.5; DB 4; Length 244;
Best Local Similarity 64.7%; Pred. No. 1.7e-65;
Matches 161; Conservative 35; Mismatches 44; Indels 9; Gaps 2;
QY 1 EVQLQESGGGLVPGGSLKLSCAASGFTFSYTWVRQTPKRLWVATISGGSSY 60
DB 3 QVQLVQSGGGLVPRPGGSLSLSCAVSGITLRTYGMHWVRQAPGKLEWVAGISFDGRSEY 62
QY 61 PDSVKGRFTISRDNKNTLYLQMSLSRSEDYCTREGGFTVNNYFVWAGTTLVT 120
DB 63 ADSVQGRFTISRDNKNTLYLQMSLSRAEDTAVYCAR-----GAHYGFDIWGQGTWTV 117
QY 121 SAGGGSGGGRASGGGSENVLTQSPASLAVSLGQRATISCRASESDSYGNFMHWYQQI 180
DB 118 SSGGGGTGGGGSGGGSDIQTQSPSLASIGDRVITCRASEGI----YHMLAWYQOK 173
QY 181 PGQPPKLLIYRASNLSGIPARFSGSGSRDFTLTINPVEADDVATYCCQSNEDPLTF 240
DB 174 PKGAPKLLIYRASNLSGIPARFSGSGSGDFTLTISLQPEDPATYCCQSYNYPLTF 233
QY 241 TGTREIKR 249
DB 234 GQTELEIKR 242

RESULT 14
US-09-227-693-34
; Sequence 34, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Kourie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:

This Page Blank (uspto)

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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:27 ; Search time 1.56658 Seconds
(without alignments)
982.436 Million cell updates/sec

Title: US-09-661-992B-105

Perfect score: 80
Sequence: 1 CXYGNSPKGFAYXC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR.78.*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	55.0	205	2	T19356
2	44	55.0	305	1	S59863
3	42	52.5	109	2	P30607
4	42	52.5	166	2	T39586
5	42	52.5	568	1	A55377
6	42	52.5	626	2	B70749
7	41	51.2	389	2	H90083
8	41	51.2	429	2	D70763
9	41	51.2	453	2	S75579
10	41	51.2	1866	1	GNWE2C
11	41	51.2	2515	2	A41519
12	40	50.0	107	2	AH3499
13	40	50.0	109	1	K3HUGO
14	40	50.0	359	2	T47208
15	40	50.0	382	2	S51425
16	40	50.0	382	2	T39431
17	40	50.0	384	2	A51398
18	40	50.0	395	1	S27257
19	40	50.0	395	2	A37118
20	40	50.0	395	2	S65800
21	40	50.0	404	2	T34085
22	40	50.0	404	2	T34084
23	39.5	49.4	1787	2	A22009
24	39.5	49.4	1800	2	A11918
25	39	48.8	218	2	F84170
26	39	48.8	318	2	H86342
27	39	48.8	401	2	H82175
28	39	48.8	503	1	S64019
29	36	47.5	92	2	S37519

Ig kappa chain V r
probable metalloca
Ig kappa chain V-I
Ig kappa chain V-I
Ig kappa chain V r
Ig kappa chain - h
Ig kappa chain V r
Wnt-4 protein - mo
developmental regu
hypothetical prote
conserved hypothet
probable bacteriop
protein F21D18.20
probable acyl-CoA
phosphoprotein pho
Ig kappa chain V r

ALIGNMENTS

RESULT 1

T19356

hypothetical protein C17E4.5 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T19356

R;Percy, C.

submitted to the EMBL Data Library, October 1996

A;Reference number: Z19113

A;Accession: T19356

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-205 <WIL>

A;Cross-references: EMBL:Z81037; PIDN:CA02750.1; GSPDB:GN00019; CESP:C17E4.5

A;Experimental source: clone C17E4

C;Genetics:

A;Gene: CESP:C17E4.5

A;Map position: 1

A;Introns: 22/3; 120/2

Query Match 55.0%; Score 44; DB 2; Length 205;

Best Local Similarity 53.8%; Pred. No. 2.9;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXYGNSPKGFAY 13

Db 111 CDRFGHPKGFAY 123

RESULT 2

S59863

polyA binding protein II - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Nov-1999

C;Accession: S59863

R;Nemeth, A.; Krause, S.; Blank, D.; Jenny, A.; Jenoe, P.; Lustig, A.; Wahle, E.

Nucleic Acids Res. 23, 4034-4041, 1995

A;Title: Isolation of genomic and cDNA clones encoding bovine poly(A) binding protein II

A;Reference number: S59863; MUID:96071160; PMID:7479061

A;Accession: S59863

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: mRNA

A;Residues: 1-306 <NEM>

A;Cross-references: EMBL:X89969; NID:g1065677; PIDN:CAAG2006.1; PID:g1051125

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1995

C;Superfamily: bovine polyA binding protein II; ribonucleoprotein repeat homology

F;173-239/Domain: ribonucleoprotein repeat homology <RM2>

Query Match 55.0%; Score 44; DB 1; Length 306;

Best Local Similarity 53.8%; Pred. No. 4.3;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
 Db 205 CDKFSGHPKGFAY 217

RESULT 3

IG kappa chain V-III region (Bor) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 21-Jan-2000
 C:Accession: F30607
 R:Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Soldo
 J. Immunol. 142, 3158-3163, 1989
 A:Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies
 A:Reference number: A30601; MUID:89215279; PMID:2496160
 A:Accession: F30607
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-109 <GON>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 52.5%; Score 42; DB 2; Length 109;
 Best Local Similarity 63.6%; Pred. No. 3.5; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 3

QY 1 CXXYGNSPKGF 11
 Db 89 CQYGNSPQTF 99

RESULT 4

rna binding protein - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T39586
 R:Voickaert, G.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z21865
 A:Accession: T39586
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-166 <VOI>
 A:Cross-references: ENBL:Z99759; PIDN:CA16904.1; GSPDB:GN00067; SPDB:SPBC16E9.12c
 A:Experimental source: strain 972h-; cosmid c16E9
 C:Genetics:
 A:Gene: SPDB:SPBC16E9.12c
 A:Map position: 2
 A:Introns: 12/3; 97/2; 126/3

Query Match 52.5%; Score 42; DB 2; Length 166;
 Best Local Similarity 53.8%; Pred. No. 5.2; Indels 0; Gaps 0;
 Matches 7; Conservative 1; Mismatches 5

QY 1 CXXYGNSPKGFAY 13
 Db 88 CDKFTGHPKGFAY 100

RESULT 5

CPE-binding protein - African clawed frog
 N:Alternate names: cytoplasmic polyadenylation element-binding protein
 C:Species: Xenopus laevis (African clawed frog)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
 C:Accession: A55377
 R:Hake, L.E.; Richter, J.D.
 Cell 79, 617-627, 1994
 A:Title: CPEB is a specificity factor that mediates cytoplasmic polyadenylation during X
 A:Reference number: A55377; MUID:95042759; PMID:7954828
 A:Accession: A55377

A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-568 <HAK>
 A:Cross-references: GB:U14169; NID:9987224; PIDN:AAA80483.1; PID:g624634
 C:Superfamily: African clawed frog CPE-binding protein; ribonucleoprotein repeat homology
 F:314-388/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match 52.5%; Score 42; DB 1; Length 568;
 Best Local Similarity 53.8%; Pred. No. 17;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
 Db 353 CPPKGNMPKGYV 365

RESULT 6

probable Acyl-CoA Synthetase - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: B70749
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
 Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987; PMID:9634230
 A:Accession: B70749
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-626 <COL>

A:Cross-references: GB:T74697; GB:AL123456; NID:g3261602; PIDN:CAA98985.1; PID:g1405966
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: fadD26

C:Superfamily: 4-coumarate-CoA ligase; acetate-CoA ligase homology
 F:103-610/Domain: acetate-CoA ligase homology <ACL>

Query Match 52.5%; Score 42; DB 2; Length 626;
 Best Local Similarity 77.8%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNSPKGF 12
 Db 73 YGSDPKGF 81

RESULT 7

polyadenylate-binding protein [imported] - Giardia theta nucleomorph
 C:Species: nucleomorph Giardia theta
 A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
 C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
 C:Accession: H90083
 R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
 Nature 410, 1091-1096, 2001
 A:Title: The highly reduced genome of an enslaved algal nucleus.
 A:Reference number: A99082; MUID:11323671; PMID:11323671
 A:Accession: H90083
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-389 <DOU>
 A:Cross-references: GB:AF165818; NID:gi3794428; PIDN:AAK39803.1; GSPDB:GN00150
 C:Genetics:
 A:Gene: Eabl

A:Map position: 1

A:Genome: nucleomorph

C:Keywords: nucleomorph

Query Match 51.2%; Score 41; DB 2; Length 389;
 Best Local Similarity 70.0%; Pred. No. 18;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 13
| : |||||
Db 222 YNSIPKGFAY 231

RESULT 8
D70763
threonine ammonia-lyase (EC 4.3.1.19) ilvA [similarity] - Mycobacterium tuberculosis (sb
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 21-Jun-2002
C;Accession: D70763
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holtroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70763
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-429 <COL>
A;Cross-references: GB:274020; GB:AL123456; NID:g3261584; PIDN:CAA99332.1; PID:g1403483
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: ilvA
C;Superfamily: threonine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; phos
P;66/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 51.2%; Score 41; DB 2; Length 429;
Best Local Similarity 53.8%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
| : |||||
Db 88 CSSAGNHAQGFAY 100

RESULT 9
S75579
hypothetical protein sll0804 - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 02-Feb-2001
C;Accession: S75579
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A;Reference number: S74322; MUID:97061201; PMID:8905231
A;Accession: S75579
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-453 <KAN>
A;Cross-references: EMBL:D90911; GB:AB001339; NID:gl653083; PIDN:BAAL18140.1; PID:g165322
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: hypothetical protein sll0804; translation elongation factor Tu homology
C;Keywords: GTP binding; nucleoside binding; P-loop
F;62-176/Domain: translation elongation factor Tu homology <ETU>
F;68-75/Region: nucleotide-binding motif A (P-loop)
F;173-176/Region: GTP-binding NKXD motif
F;367-369/Region: GTP-binding SAK/L motif

Query Match 51.2%; Score 41; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YGNSPKG 10
| : |||||

Db 224 YGNSPKG 230

RESULT 10
GNWE2C
genome polyprotein B - cowpea aphid-borne mosaic virus
N;Contains: 24K viral proteinase (EC 3.4.22.-); 32K proteinase cofactor; 58K membrane-b
C;Species: cowpea aphid-borne mosaic virus CABMV
C;Date: 18-Apr-1984 #sequence_revision 18-Apr-1984 #text_change 31-Mar-2000
C;Accession: A04211
R;Lomonosoff, G.P.; Shanks, M.
EMBO J. 2, 2253-2259, 1983
A;Title: The nucleotide sequence of cowpea mosaic virus B RNA.
A;Reference number: A04211
A;Accession: A04211
A;Molecule type: genomic RNA
A;Residues: 1-1866 <LOW>
A;Note: the polyprotein is cleaved to give at least eight mature proteins; however, the
A;Note: the authors translated the codon AAU for residue 630 as Asp, GAG for 844 as Gly,
C;Superfamily: cowpea aphid-borne mosaic virus genome polyprotein B
C;Keywords: cysteine proteinase; genome-linked protein; hydrolase; membrane protein; nu
F;2-326/Product: 32K proteinase cofactor #status predicted <PCF>
F;327-919/Product: 58K membrane-binding protein #status predicted <MBP>
F;920-947/Product: genome-linked protein VPg #status predicted <VPG>
F;948-1155/Product: 24K viral proteinase #status predicted <VPT>
F;1156-1866/Product: RNA-directed RNA polymerase #status predicted <RRP>

Query Match 51.2%; Score 41; DB 1; Length 1866;
Best Local Similarity 58.3%; Pred. No. 84;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 12
| : |||||
Db 285 CYNYGTSKGFAY 296

RESULT 11
A41519
posterior-group protein tudor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 24-Sep-1999
C;Accession: A41519; S19019
R;Golumbeski, G.S.; Bardsley, A.; Tax, F.; Boswell, R.E.
Genes Dev. 5, 2060-2070, 1991
A;Title: tudor, a posterior-group gene of Drosophila melanogaster, encodes a novel prote
A;Reference number: A41519; MUID:92038995; PMID:1936993
A;Accession: A41519
A;Molecule type: mRNA
A;Residues: 1-2515 <GOL>
A;Cross-references: GB:X62420; NID:98753; PIDN:CAA44286.1; PID:g98754
C;Genetics:
A;Gene: tud
A;Cross-references: FlyBase:FBgn0003891
C;Superfamily: posterior-group protein tudor

Query Match 51.2%; Score 41; DB 2; Length 2515;
Best Local Similarity 87.5%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNSPKGF 11
| : |||||
Db 2171 YGNSPKSF 2178

RESULT 12
AH3499
hypothetical exported protein BMEI1982 [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AH3499
R;DeIvecchio, V.G.; Kapratl, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova,
; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen *Brucella melitens*
A:Reference number: A03252; PMID:11756688
A:Accession: AH3499
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-107 <KUR>
A:Cross-references: GB:AE008917; PIDN:AALS163.1; PID:gl7984034; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1982
A:Map position: 1

Query Match 50.0%; Score 40; DB 2; Length 107;
Best Local Similarity 43.8%; Pred. No. 7.6;
Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAYXXC 16
DB 50 CRSYGFKPTDPAFC 65

RESULT 13
K3HUGO
IG kappa chain V-III region (Gol) - human
N/Alternate names: rheumatoid factor
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 21-Jan-2000
C:Accession: A01893
Mol. Immunol. 23, 239-244, 1986
A:Title: Amino acid sequence of a light chain variable region of a human rheumatoid factor
A:Reference number: A01893; MUID:86230578; PMID:3086710
A:Accession: A01893
A:Molecule type: protein
A:Residues: 1-109 <NEW>
C:Genetics:
A:Gene: GDB:IGKV3
A:Cross-references: GDB:136266
A:Map position: 2p12-2p11
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into larger complexes.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>
F:23-89/Disulfide bonds: #status predicted

Query Match 50.0%; Score 40; DB 1; Length 109;
Best Local Similarity 54.5%; Pred. No. 7.7;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGF 11
DB 89 CQYGGSPRSP 99

RESULT 14
T47208
methionine adenosyltransferase (EC 2.5.1.6) [imported] - *Neurospora crassa* (fragment)
C:Species: *Neurospora crassa*
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: T47208
R:Barra, J.L.; Mautino, M.R.; Rosa, A.L.
A:Description: Eth-1r, a mutant allele of *Neurospora crassa* S-adenosylmethionine synthetase submitted to the EMBL Data Library, September 1995
A:Reference number: 224392
A:Accession: T47208
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-359 <BAR>
A:Cross-references: EMBL:U036761; PIDN:AAA83756.1
C:Genetics:
A:Gene: eth-1r
A>Note: Intron positions not resolved (incomplete sequence)

C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Query Match 50.0%; Score 40; DB 2; Length 359;
Best Local Similarity 53.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
DB 62 YDDSSKGFYKTC 74

RESULT 15
S51425

methionine adenosyltransferase (EC 2.5.1.6) 1 - yeast (*Saccharomyces cerevisiae*)
N/Alternate names: protein L9470.9; protein YLR180w; S-adenosylmethionine synthetase 1
C:Species: *Saccharomyces cerevisiae*
C:Date: 23-Feb-1995 #sequence_revision 11-Aug-1995 #text_change 05-May-2000
C:Accession: S51425; A28480
R:Wohldmann, P.

submitted to the EMBL Data Library, November 1994
A:Description: The sequence of *S. cerevisiae* cosmid 9470.

A:Reference number: S51414
A:Accession: S51425
A:Molecule type: DNA
A:Residues: 1-382 <WOH>
A:Cross-references: EMBL:U17246; NID:G577192; PIDN:AAB67461.1; PID:G577201; MIPS:YLR180w
R:Thomas, D.; Surdin-Kerjan, Y.
J. Biol. Chem. 262, 16704-16709, 1987
A:Title: SAM1, the structural gene for one of the S-adenosylmethionine synthetases in *S. cerevisiae*
A:Reference number: A92621; MUID:88059059; PMID:3316224
A:Accession: A28480
A:Molecule type: DNA
A:Residues: 1-245, 'T', 247-356, 'F', 358-382 <THO>
A:Cross-references: EMBL:J03477; NID:G172533; PIDN:AAA66932.1; PID:G172534
C:Genetics:
A:Gene: SGD:SAM1; ETH10
A:Cross-references: SGD:S0004170; MIPS:YLR180w
A:Map position: 12R
C:Function:
A:Description: transferase
C:Superfamily: methionine adenosyltransferase
C:Keywords: S-adenosylmethionine; transferase

Query Match 50.0%; Score 40; DB 2; Length 382;
Best Local Similarity 53.8%; Pred. No. 27;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
DB 79 YDDSAKGFYKTC 91

Search completed: July 29, 2004, 08:51:49
Job time : 2.56658 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 1.06527 Seconds
(without alignments)
782.073 Million cell updates/sec

Title: US-09-661-992B-105
Perfect score: 80
Sequence: 1 CXXYGNPKGFAYXXC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	53.8	723	1 S21C MOUSE	Q8K078 mus musculus
2	43	53.8	723	1 S21C RAT	Q99N01 rattus norv
3	42	52.5	332	1 NDP2 VIBVY	P60056 vibrio vuln
4	42	52.5	583	1 FD26 MYCTU	Q10976 mycobacteri
5	41	51.2	429	1 THD1 MYCTU	Q10766 mycobacteri
6	41	51.2	1866	1 VGNB CPWV	P03600 cowpea mcsa
7	41	51.2	2515	1 TUD DROME	P25823 drosophila
8	40	50.0	109	1 KV3G HUMAN	P04206 homo sapien
9	40	50.0	382	1 METK SCHPO	Q60198 schizosacch
10	40	50.0	382	1 METK YEAST	P10659 saccharomyc
11	40	50.0	383	1 METL YEAST	P19358 saccharomyc
12	40	50.0	393	1 METK ASCIM	P50304 ascobolus i
13	40	50.0	395	1 METK HUMAN	P31153 homo sapien
14	40	50.0	395	1 METK NEUCR	P48466 neurospora
15	40	50.0	395	1 METK RAT	P18298 rattus norv
16	40	50.0	404	1 METK CAEEL	P50305 caenorhabdi
17	40	50.0	404	1 METL CAEEL	P50306 caenorhabdi
18	40	50.0	404	1 METN CAEEL	Q27522 caenorhabdi
19	39	48.8	351	1 WNT4 CHICK	P49337 gallus gall
20	39	48.8	503	1 ATE1 YEAST	P16639 saccharomyc
21	39	48.8	589	1 CH60 LEIMA	Q94596 leishmania
22	38	47.5	351	1 WNT4 HUMAN	P56705 homo sapien
23	38	47.5	351	1 WNT4 MOUSE	P22724 mus musculu
24	38	47.5	351	1 WNT4 RAT	Q9gxd5 rattus norv
25	38	47.5	351	1 WNT4 XENLA	P49338 xenopus lae
26	38	47.5	352	1 WN4A BRASE	P47793 brachydanio
27	37	46.2	109	1 KV3B HUMAN	P01620 homo sapien
28	37	46.2	129	1 KV3L HUMAN	P18135 homo sapien
29	37	46.2	223	1 FLGA AQUAE	O57005 aquifex aeo
30	37	46.2	394	1 PHFY PSBAE	P20586 pseudomonas
31	37	46.2	394	1 PHFY PSBAE	P00438 pseudomonas
32	37	46.2	476	1 VTDB MOUSE	P21614 mus musculu
33	37	46.2	476	1 VTDB RAT	P04276 rattus norv

```

34 37 46.2 512 1 V233 FOMPV
35 37 46.2 572 1 LAC3 THACU
36 37 46.2 1180 1 RNT1 DROME
37 36 45.0 109 1 KV3D HUMAN
38 36 45.0 314 1 P2A5 TOBAC
39 36 45.0 395 1 METL HUMAN
40 36 45.0 397 1 METL RAT
41 36 45.0 408 1 METK DROME
42 36 45.0 452 1 HOS2 YEAST
43 36 45.0 609 1 RPSD BUCBP
44 36 45.0 611 1 LYP1 YEAST
45 36 45.0 722 1 S21C HUMAN

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ALIGNMENTS

```

RESULT 1
S21C_MOUSE
ID S21C_MOUSE STANDARD; PRT; 723 AA.
AC Q8K078;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Solute carrier family 21 member 12 (Sodium-independent organic anion
DE transporter E) (Organic anion transporting polypeptide E) (OATP-E).
GN SLC21A12 OR OATPE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RP SEQUENCE=Q57BL/6; TISSUE=Retina;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rosa S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA Villalon D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Mediates the Na(+)-independent transport of organic
CC anions such as the thyroid hormone T3 (triiodo-L-thyronine) and of
CC taurocholate (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q8K078-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q8K078-2; Sequence=VSP_006157, VSP_006158;
CC Note=No experimental confirmation available;
CC Note=SIMILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPORTERS.
CC -!- SIMILARITY: BELONGS TO THE SLC21 FAMILY OF TRANSPORTERS.
CC -----
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DR EMBL; AP005347; BAC96903.1; --
DR HAWAP; MF 00730; -- 1.
KW Complete proteome.
SQ SEQUENCE 332 AA; 38241 MW; 9272959A747674B0 CRC64;

Query Match 52.5%; Score 42; DB 1; Length 332;
Best Local Similarity 77.8%; Pred. No. 3.2;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNSPKGPA 12
||: |||||
DB 48 YGDKPKGPA 56

RESULT 4
FD26 MYCTU STANDARD; PRT; 583 AA.
ID FD26 MYCTU STANDARD; PRT; 583 AA.
AC Q10976;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative fatty-acid--CoA ligase fadD26 (EC 6.2.1.-) (Acyl-CoA
DE synthetase).
GN FAD26 OR RV2930 OR MT2999 OR MTCY338.19.
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Davlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
RN [2]

RP SEQUENCE FROM N.A.
RC STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Dutboy S., Grondin S., Lacroix C., Monsepe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).
CC -!- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC threonine in a two-step reaction. The first step is a dehydration
CC of threonine, followed by rehydration and liberation of ammonia.

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DR EMBL; Z74697; CAA98985.1; ALT INIT.
DR EMBL; AE007122; AAK47327.1; --

DR TIGR; MT2999; --
DR TubercuList; RV2930; --
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PROSITE; PS00455; AMP BINDING; FALSE_NEG.
KW Hypothetical protein; Ligase; Fatty acid metabolism;
KW complete proteome.
SQ SEQUENCE 583 AA; 63043 MW; F97CD6E19E217435 CRC64;

Query Match 52.5%; Score 42; DB 1; Length 583;
Best Local Similarity 77.8%; Pred. No. 5.8;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNSPKGPA 12
||: |||||
DB 30 YGSDPKGPA 38

RESULT 5
THD1 MYCTU STANDARD; PRT; 429 AA.
ID THD1 MYCTU STANDARD; PRT; 429 AA.
AC Q10766;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable threonine dehydratase biosynthetic (EC 4.3.1.19) (Threonine
DE deaminase).
GN ILVA OR RV1559 OR MT1610 OR MTCY48.06C OR MB1585.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765,
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
RN [2]

RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490 (2002).
RN [3]

RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;
RA Garnier T., Eiglmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Dutboy S., Grondin S., Lacroix C., Monsepe C., Simon S.,
RA Harris B., Atkin R., Doggett J., Mayes R., Keating L., Wheeler P.R.,
RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

CC -!- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC threonine in a two-step reaction. The first step is a dehydration
CC of threonine, followed by rehydration and liberation of ammonia.

CC -!- CATALYTIC ACTIVITY: L-threonine = 2-oxobutanoate + NH(3).
 CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -!- PATHWAY: Isoleucine biosynthesis; first step.
 CC -!- SIMILARITY: Belongs to the serine/threonine dehydratase family.
 CC -----
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 CC -----
 CC EMBL; 274020; CAA98332.1; -.
 CC EMBL; AE007027; AAK45877.1; -.
 CC EMBL; BX248339; CAD96252.1; -.
 CC PIR; D70763; D70763.
 CC HSP; P04968; ITD1.
 CC TIGR; M1610; -.
 CC Tuberculin; Rv1559; -.
 CC InterPro; IPR001926; B6 enzyme beta.
 CC InterPro; IPR00634; S/T dehydratase BS.
 CC InterPro; IPR001721; ThrD_C.
 CC Pfam; PF00291; PALP; 1.
 CC Pfam; PF00585; Thr_dehydrat_C; 1.
 CC PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
 CC Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
 CC Complete proteome.
 CC BINDING 66 66 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC DOMAIN 145 149 POLY-ALA.
 CC DOMAIN 196 199 POLY-GLY.
 CC SEQUENCE 429 AA; 45041 MW; DDC761EC258AC51 CRC64;
 CC -----
 CC Query Match 51.2%; Score 41; DB 1; Length 429;
 CC Best Local Similarity 53.8%; Pred. No. 6.4;
 CC Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 CC -----
 CC QY 1 CXXYGNSPKGFAY 13
 CC 88 CSSAGNHQGFAY 100
 CC -----
 CC RESULT 6
 CC VGNB_CPMV STANDARD; PRT; 1866 AA.
 CC ID VGNB_CPMV STANDARD; PRT; 1866 AA.
 CC AC P03600;
 CC DT 21-JUL-1986 (Rel. 01, Created)
 CC DT 21-JUL-1986 (Rel. 01, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Genome polypeptide B [Contains: Protease cofactor; Membrane binding
 CC protein; VEG; Protease (EC 3.4.22.-); RNA polymerase (EC 2.7.7.48)].
 CC OS Cowpea mosaic virus (CPMV).
 CC OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
 CC Comovirus.
 CC NCBI_TaxID=12264;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC RA Lomonosoff G.P.; Shanks M.;
 CC RT "The nucleotide sequence of cowpea mosaic virus B RNA."
 CC EMBO J. 2:2253-2258(1983).
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC [RNA](N).
 CC -!- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
 CC -!- SIMILARITY: TO OTHER COMOVIRUSES GENOME POLYPEPTIDE B.
 CC -----
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DR EMBL; X00206; CAA25029.1; -.
 DR PIR; A04211; GNWE2C.
 DR MEROPS; C03.003; -.
 DR InterPro; IPR004004; Calici_pol_hel.
 DR InterPro; IPR009003; Cys_Ser_trypsin.
 DR InterPro; IPR000605; RNA_helicase.
 DR InterPro; IPR007095; RNA_pol_PS.
 DR InterPro; IPR001205; RNA_pol_PSD.
 DR InterPro; IPR007094; RNA_pol_PSVir.
 DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
 DR Pfam; PF00910; RNA_helicase; 1.
 DR PRINTS; PR00918; CALICIVIRUS.
 KW Polyprotein; transmembrane; Hydrolase; Protease; Transferase;
 KW RNA-directed RNA polymerase; ATP-binding.
 FT CHAIN 1 326 PROTEASE COFACTOR (POTENTIAL).
 FT CHAIN 327 919 MEMBRANE-BINDING PROTEIN (POTENTIAL).
 FT CHAIN 920 947 VEG PROTEIN (POTENTIAL).
 FT CHAIN 948 1155 PROTEASE (POTENTIAL).
 FT CHAIN 1156 1866 RNA-DIRECTED RNA POLYMERASE (POTENTIAL).
 FT NP_BIND 434 501 ATP (POTENTIAL).
 FT ACT_SITE 987 987 THIOL PROTEASE (POTENTIAL).
 FT ACT_SITE 1023 1023 THIOL PROTEASE (POTENTIAL).
 FT ACT_SITE 1113 1113 THIOL PROTEASE (POTENTIAL).
 SQ SEQUENCE 1866 AA; 209809 MW; 0D4CD8A11C0B2976 CRC64;
 CC -----
 CC Query Match 51.2%; Score 41; DB 1; Length 1866;
 CC Best Local Similarity 58.3%; Pred. No. 30;
 CC Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 CC -----
 CC QY 1 CXXYGNSPKGFAY 12
 CC 285 CXXYGNKGFAY 296
 CC -----
 CC RESULT 7
 CC TUD_DROME STANDARD; PRT; 2515 AA.
 CC ID TUD_DROME STANDARD; PRT; 2515 AA.
 CC AC P25823;
 CC DT 01-MAY-1992 (Rel. 22, Created)
 CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Maternal tudor protein.
 CC GN TUD.
 CC OS Drosophila melanogaster (Fruit fly).
 CC OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephydroidea; Drosophilidae; Drosophila.
 CC NCBI_TaxID=7227;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC RX MEDLINE-92038995; PubMed-1936993;
 CC RA Golumbeski G.S.; Bardsley A.; Tax F.; Boswell R.E.;
 CC RT "Tudor, a posterior-group gene of Drosophila melanogaster, encodes a
 CC novel protein and an mRNA localized during mid-oogenesis."
 CC RL Genes Dev. 5:2060-2070(1991).
 CC -!- FUNCTION: REQUIRED DURING OOGENESIS FOR THE FORMATION OF
 CC PRIMORDIAL GERM CELLS AND FOR NORMAL ABDOMINAL SEGMENTATION.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE.
 CC -!- MISCELLANEOUS: THE TUD MRNA ACCUMULATES WITHIN THE POSTERIOR
 CC REGION OF THE DEVELOPING OOCYTE DURING THE EARLY TO MIDDLE STAGES
 CC OF OOGENESIS.
 CC -!- SIMILARITY: Contains 9 Tudor domains.
 CC -----
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 CC -----
 CC EMBL; X62420; CAA44286.1; -.
 CC PIR; A41519; A41519.

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DR HSP; Q16637; IG5V.
DR FlyBase; Fgn0003891; tud.
DR GO; GO:0019090; P:mitochondrial rRNA, mitochondrial export; IMP.
DR GO; GO:0007315; P:pole plasm assembly; IMP.
DR InterPro; IPR008191; Maternal_tudor.
DR InterPro; IPR002999; Tudor.
DR Pfam; PF00567; Tudor; 10.
DR SMART; SM00333; Tudor; 10.
DR PROSITE; PS0304; Tudor; 9.
KW Developmental protein; Repeat.
FT DOMAIN 455 513
FT DOMAIN 513 513
FT DOMAIN 641 696
FT DOMAIN 1062 1122
FT DOMAIN 1355 1414
FT DOMAIN 1662 1718
FT DOMAIN 1839 1898
FT DOMAIN 2023 2082
FT DOMAIN 2211 2269
FT DOMAIN 2392 2451
SQ SEQUENCE 2515 AA; 285236 MW; 683C100AD308BADA CRC64;

Query Match 51.2%; Score 41; DB 1; Length 2515;
Best Local Similarity 87.5%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGN5PKGF 11
DB 2171 YGN5PKSF 2178

RESULT 8
KV3G HUMAN
ID KV3G HUMAN STANDARD; PRT; 109 AA.
AC P04206;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region GOL (Rheumatoid factor).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86230578; PubMed=3086710;
RA Newkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
RA "Amino acid sequence of a light chain variable region of a human
RT rheumatoid factor of the Wa idiotype group, in part predicted by its
RT reactivity with anti-peptide antibodies.";
KL Mol. Immunol. 23:239-244(1986).
DR PIR; A01893; K3HUGO.
DR HSP; P80362; 1WTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11830 MW; 9349A5B1D93588B6 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 109;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGN5PKGF 11
DB 89 CQYGN5PKSF 99

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RESULT 9
METX SCHPO
ID METX SCHPO STANDARD; PRT; 382 AA.
AC O00138;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
  adenosyltransferase) (AdoMet synthetase).
GN SAM1 OR SPBC14F5.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A. AND FUNCTION.
RX MEDLINE=20089020; PubMed=10620770;
RA Hilti N., Graub R., Jorg M., Arnold P., Schweingruber A.M.,
RA Schweingruber M.E.;
RA "Gene sam1 encoding adenosylmethionine synthetase: effects of its
RT expression in the fission yeast Schizosaccharomycetes pombe.";
RL Yeast 16:1-10(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feitelwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
RA Rutherford K., Rutter S., Saunders R., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkart G., Aert R., Robben J., Grymoprez B.,
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Calbert F., Aves S.U., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomycetes pombe.";
RT Nature 415:871-880(2002).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
  methionine and ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
  diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
  1 potassium ion per subunit (by similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
CC -----
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  or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AJ001705; CAA04941.1; -
CC EMBL; AL023780; CAA19323.1; -

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DR PIR: T39451; T39451.
DR HSSP: P04384; 1MXB.
DR GeneDB SPombe; SPBC14F5, 05c; -.
DR InterPro; IPR002133; S-AdoMet_synth.
DR Pfam; PF00438; S-AdoMet_synth; 1.
DR Pfam; PF02772; S-AdoMet_synthD2; 1.
DR Pfam; PF02773; S-AdoMet_synthD3; 1.
DR TIGRfams; TIGR01034; metK; 1.
DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.
DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
DR Transferase; One-carbon metabolism; ATP-binding; Magnesium; Potassium;
KW Metal-binding.
FT NP_BIND 118 123 ATP (POTENTIAL).
FT METAL 18 18 MAGNESIUM (BY SIMILARITY).
FT METAL 44 44 POTASSIUM (BY SIMILARITY).
FT METAL 270 270 POTASSIUM (BY SIMILARITY).
FT METAL 278 278 MAGNESIUM (BY SIMILARITY).
FT BINDING 146 146 ATP (POTENTIAL).
SQ SEQUENCE 382 AA; 41831 MW; 9970A9D1195C5738 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 382;
Best Local Similarity 53.8%; Pred. No. 8.6;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
DB 79 YDSKGFYKTC 91

RESULT 10
METK_YEAST STANDARD; PRT; 382 AA.
AC P10659;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE S-adenosylmethionine synthetase 1 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 1) (AdoMet synthetase 1).
GN SAM1 OR ETH10 OR YLR180W OR L9470.9.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A. PubMed=3316224;
RX MEDLINE=86059059; PubMed=3316224;
RA Thomas D., Surdin-Kerjan Y.;
RT "SAM1, the structural gene for one of the S-adenosylmethionine
RT synthetases in Saccharomyces cerevisiae. Sequence and expression."
RL J. Biol. Chem. 262:16704-16709(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L., Riles L., Albermann K., Andre B., Anserge W.,
RA Benes V., Bruckner M., Delius H., Dubois E., Duesterhoft A.,
RA Entian K.-D., Floeth M., Goffeau A., Hebling U., Heumann K.,
RA Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P.,
RA Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D.,
RA Mueller-Auer S., Netwisch U., Obermaier B., Piravandi E., Pohl T.M.,
RA Portetelle D., Purnelle B., Reckmann S., Rieger M., Rinke M., Rose M.,
RA Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S.,
RA Underwood A.P., Urrestarazu L.A., Vandenbol M., Verhasselt P.,
RA Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E.,
RA Wedler H., Zimmermann F.K., Zollner A., Hani J., Hohseil J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII."
RL Nature 387:87-90(1997).
RN [3]
RP SEQUENCE OF 157-162; 187-196 AND 253-258.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE=97089742; PubMed=8935650;
RA Norbeck J., Blomberg A.;
RT "protein expression during exponential growth in 0.7 M NaCl medium of

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RT RT
RL RT
CC FEMS Microbiol. Lett. 137:1-8(1996).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SUBUNIT: Heterotetramer.
CC -!- MISCELLANEOUS: In yeast, there are two genes coding for AdoMet
CC synthetase.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
CC
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CC
CC -----
CC EMBL; J03477; AAA66932.1; -.
CC EMBL; U17246; AAB67461.1; -.
CC FIR; S51425; S51425.
CC HSSP; P04384; 1MXB.
CC GerMOnline; 142242; -.
CC SGD; S0004170; SAM1.
CC GO; GO:0005737; Cytoplasm; IDA.
CC GO; GO:0004478; F-methionine adenosyltransferase activity; IGI.
CC InterPro; IPR002133; S-AdoMet_synth.
CC Pfam; PF00438; S-AdoMet_synth; 1.
CC Pfam; PF02772; S-AdoMet_synthD2; 1.
CC Pfam; PF02773; S-AdoMet_synthD3; 1.
CC TIGRfams; TIGR01034; metK; 1.
CC PROSITE; PS00376; ADOMET SYNTHETASE_1; 1.
CC PROSITE; PS00377; ADOMET SYNTHETASE_2; 1.
CC Transferase; One-carbon metabolism; Multigene family; ATP-binding;
KW Magnesium; Potassium; Metal-binding.
FT NP_BIND 118 123 ATP (POTENTIAL).
FT METAL 18 18 MAGNESIUM (BY SIMILARITY).
FT METAL 44 44 POTASSIUM (BY SIMILARITY).
FT METAL 270 270 POTASSIUM (BY SIMILARITY).
FT METAL 278 278 MAGNESIUM (BY SIMILARITY).
FT BINDING 146 146 ATP (POTENTIAL).
FT CONFLICT 246 246 A -> T (IN REF. 1).
FT CONFLICT 357 357 I -> F (IN REF. 1).
SQ SEQUENCE 382 AA; 41818 MW; 18F82FC809EE4706 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 382;
Best Local Similarity 53.8%; Pred. No. 8.6;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
DB 79 YDSKGFYKTC 91

RESULT 11
METL_YEAST STANDARD; PRT; 383 AA.
AC P19356;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase 2 (EC 2.5.1.6) (Methionine
DE adenosyltransferase 2) (AdoMet synthetase 2).
GN SAM2 OR ETH2 OR YDR502C OR D9719.8.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=89218973; PubMed=3072475;
RA Thomas D., Rothstein R., Rosenberg N., Surdin-Kerlan Y.;
RT "SAM2 encodes the second methionine S-adenosyl transferase in
RT Saccharomyces cerevisiae: physiology and regulation of both
RT enzymes.";
RL Mol. Cell. Biol. 8:5132-5139(1988).
RN [2].

RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
RA Benito A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunnicke-Smith S., Hyman R., Kemp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yelton M., Botstein D., Davis R.W.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3].

RP ACETYLATION.
RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RL Submitted (SEP-1994) to Swiss-Prot.
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SUBUNIT: Heterotetramer.
CC -!- MISCELLANEOUS: In yeast, there are two genes coding for AdoMet
CC synthetase.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.

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CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL; M23368; AAA35017.1; -;
CC EMBL; U33057; AAB64944.1; -;
CC DR PIR; A31398;
CC DR HSP; P04384; 1MXB.
CC DR Germline; 140994; -;
CC DR SGD; S0002910; SAM2.
CC DR InterPro; IPR002133; S-AdoMet_synt.
CC DR Pfam; PF00438; S-AdoMet_synt; 1.
CC DR Pfam; PF02772; S-AdoMet_syntD2; 1.
CC DR Pfam; PF02773; S-AdoMet_syntD3; 1.
CC DR TIGRfams; TIGR01034; metK; 1.
CC DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.
CC DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
CC DR Pfam; PF02773; S-AdoMet_syntD3; 1.
CC DR TIGRfams; TIGR01034; metK; 1.
CC DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.
CC DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
CC DR Transferase; One-carbon metabolism; Multigene family; ATP-binding;
CC Acetylation; Magnesium; Potassium; Metal-binding.
CC INIT_MET 0 0
CC METAL 19 19 MAGNESIUM (BY SIMILARITY).
CC FT METAL 45 45 POTASSIUM (BY SIMILARITY).
CC FT METAL 271 271 POTASSIUM (BY SIMILARITY).
CC FT METAL 279 279 MAGNESIUM (BY SIMILARITY).
CC FT MOD_RES 1 1 ACETYLATION.
CC FT NP_BIND 119 124 ATP (POTENTIAL).
CC FT NP_BIND 147 147 ATP (POTENTIAL).
CC SQ SEQUENCE 383 AA; 42124 MW; 466879A2797E80B1 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 383;
Best Local Similarity 53.8%; Pred. No. 8.6;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXKC 16
Db 80 YDPSAKGFDYKTC 92

RESULT 12
METK_ASCIM STANDARD; PRT; 393 AA.
ID METK_ASCIM
AC P50304;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (SC 2.5.1.6) (Methionine
DE adenosyltransferase) (AdoMet synthetase).
OS Ascombolus immersus.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
OC Pezizales; Ascombolaceae; Ascombolus.
OX NCBI_TaxID=5191;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EM42;
RX MEDLINE=96200878; PubMed=8621082;
RA Mautino M.R., Goyon C., Rosa A.L.;
RT "Cloning and sequence of the Ascombolus immersus S-adenosyl-L-
RT methionine synthetase-encoding gene.";
RL Gene 170:155-156(1996).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
CC methionine and ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
CC diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
CC 1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.

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CC -----
CC EMBL; U21548; AAB03805.1; -;
CC DR HSP; P04384; 1MXB.
CC DR InterPro; IPR002133; S-AdoMet_synt.
CC DR Pfam; PF00438; S-AdoMet_synt; 1.
CC DR Pfam; PF02772; S-AdoMet_syntD2; 1.
CC DR Pfam; PF02773; S-AdoMet_syntD3; 1.
CC DR TIGRfams; TIGR01034; metK; 1.
CC DR PROSITE; PS00376; ADOMET SYNTHETASE 1; 1.
CC DR PROSITE; PS00377; ADOMET SYNTHETASE 2; 1.
CC DR Transferase; One-carbon metabolism; ATP-binding; Magnesium; Potassium;
CC Metal-binding
CC NP_BIND 127 132 ATP (POTENTIAL).
CC FT METAL 27 27 MAGNESIUM (BY SIMILARITY).
CC FT METAL 53 53 POTASSIUM (BY SIMILARITY).
CC FT METAL 279 279 POTASSIUM (BY SIMILARITY).
CC FT METAL 287 287 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 393 AA; 43010 MW; 88FB2F2F14B751C3 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 393;
Best Local Similarity 53.8%; Pred. No. 8.8;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXKC 16
Db 88 YDPSAKGFDYKTC 100

RESULT 13
METK_HUMAN STANDARD; PRT; 395 AA.
ID METK_HUMAN
AC P31153;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)

10-OCT-2003 (Rel. 42, Last annotation update)
S-adenosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine
adenosyltransferase) (AdoMet synthetase) (MAT-II).
MAT2A OR MAT2A2 OR AMS2.
Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA MEDLINE=93050159; PubMed=1426236;
RA Horikawa S., Tsukada K.;
RT "Molecular cloning and developmental expression of a human kidney S-
adenosylmethionine synthetase.";
RL FEBS Lett. 312:37-41(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max J., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.J., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Fulyk S.W.,
RA Villalón D.K., Muzly D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faray J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonifard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
methionine and ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: In mammalian tissues, there are three distinct
forms of AdoMet synthase designated as alpha, beta, and gamma.
CC Alpha and beta are expressed only in adult liver, while gamma is
widely distributed in extrahepatic tissues.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
CC
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CC
CC -----
CC EMBL; X68836; CAA48726.1; -.
CC EMBL; BC001686; AAH01686.1; -.
CC EMBL; BC001854; AAH01854.1; -.
CC PIR; S27257; S27257.
CC HSSP; P04384; 1MXB.
CC Genew; HGNC:6904; MAT2A.
CC MIM; 601468; -.
CC GO; GO:0004478; P:methionine adenosyltransferase activity; TAS.
CC InterPro; IPR002133; S-AdoMet_synt.
CC Pfam; PF00438; S-AdoMet_synt; 1.
CC Pfam; PF02772; S-AdoMet_syntD2; 1.
CC

Pfam; PF02773; S-AdoMet_syntD3; 1.
DR TIGRFAMS; TIGR01034; meck; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase; One-carbon metabolism; Magnesium; Potassium;
KW Metal-binding; Multigene family; ATP-binding.
FT NP_BIND 131 136 ATP (POTENTIAL).
FT METAL 31 31 MAGNESIUM (BY SIMILARITY).
FT METAL 57 57 POTASSIUM (BY SIMILARITY).
FT METAL 283 283 POTASSIUM (BY SIMILARITY).
FT METAL 291 291 MAGNESIUM (BY SIMILARITY).
FT BINDING 159 159 ATP (POTENTIAL).
SQ SEQUENCE 395 AA; 43660 MW; 2E7D1B91CC4F7BDD CRC64;

Query Match 50.0%; Score 40; DB 1; Length 395;
Best Local Similarity 53.8%; Pred. No. 8.9; Indels 0; Gaps 0;
Matches 7; Conservative 1; Mismatches 5;

OY 4 YGNPKGFAYXXC 16
DB 92 YDSSKGFYKTC 104

RESULT 14
METK NEUCR STANDARD; PRT; 395 AA.
AC P48466;
DT 01-PEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE S-adenosylmethionine synthetase (EC 2.5.1.6) (Methionine
adenosyltransferase) (AdoMet synthetase).
GN ETH-1.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Micelial;
RX MEDLINE=97002541; PubMed=8849888;
RA Nautino M.R., Barra J.L., Rosa A.L.;
RT "eth-1, the Neurospora crassa locus encoding S-adenosylmethionine
synthetase: molecular cloning, sequence analysis and in vivo
overexpression.";
RL Genetics 142:789-800(1996).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
methionine and ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.
CC
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or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; U21547; AAC49260.1; -.
CC PIR; S65800; S65800.
CC HSSP; P04384; 1MXB.
CC InterPro; IPR002133; S-AdoMet_synt.
CC Pfam; PF00438; S-AdoMet_synt; 1.
CC Pfam; PF02772; S-AdoMet_syntD2; 1.
CC Pfam; PF02773; S-AdoMet_syntD3; 1.
CC TIGRFAMS; TIGR01034; meck; 1.
CC PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
CC PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
CC

KW Transferase; One-carbon metabolism; ATP-binding; Magnesium; Potassium;
KW Metal-binding.
FT NP BIND 130 135 ATP (POTENTIAL).
FT METAL 30 30 MAGNESIUM (BY SIMILARITY).
FT METAL 56 56 POTASSIUM (BY SIMILARITY).
FT METAL 282 282 POTASSIUM (BY SIMILARITY).
FT METAL 290 290 MAGNESIUM (BY SIMILARITY).
FT BINDING 158 158 ATP (POTENTIAL).
SQ SEQUENCE 395 AA; 42986 MW; 8CF95CED9831AFOF CRC64;

Query Match 50.0%; Score 40; DB 1; Length 395;
Best Local Similarity 53.8%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
| : | | | | |
Db 91 YDSSKGFDFYKTC 103

RESULT 15
METK_RAT
ID METK_RAT STANDARD; PRT; 395 AA.
AC P18298;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE S-adenosylmethionine synthetase gamma form (EC 2.5.1.6) (Methionine
adenosyltransferase) (AdoMet synthetase) (MAT-II).
GN MAT2A OR AMS2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Kidney;
RX MEDLINE=90337579; PubMed=1696256;
RA Horikawa S.; Sasuga J.; Shimizu K.; Ozasa H.; Tsukada K.;
RT "Molecular cloning and nucleotide sequence of cDNA encoding the rat
kidney S-adenosylmethionine synthetase.";
RL J. Biol. Chem. 265:13683-13686(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98121185; PubMed=9461287;
RA Hiroki T.; Horikawa S.; Tsukada K.;
RT "Structure of the rat methionine adenosyltransferase 2A gene and its
promoter.";
RL Eur. J. Biochem. 250:653-660(1997).
CC -!- FUNCTION: Catalyzes the formation of S-adenosylmethionine from
methionine and ATP.
CC -!- CATALYTIC ACTIVITY: ATP + L-methionine + H(2)O = phosphate +
diphosphate + S-adenosyl-L-methionine.
CC -!- COFACTOR: Binds 2 divalent ions, such as magnesium or cobalt, and
1 potassium ion per subunit (By similarity).
CC -!- PATHWAY: Activated methyl cycle.
CC -!- SUBUNIT: Homodimer.
CC -!- TISSUE SPECIFICITY: IN MAMMALIAN TISSUES, THERE ARE THREE DISTINCT
FORMS OF ADOMET SYNTH. DESIGNATED AS ALPHA, BETA, AND GAMMA. ALPHA
AND BETA ARE EXPRESSED ONLY IN ADULT LIVER, WHILE GAMMA IS WIDELY
DISTRIBUTED IN EXTRAHEPATIC TISSUES. IN ADDITION THE GAMMA FORM
PREDOMINANTLY EXISTS IN FETAL RAT LIVER AND IS PROGRESSIVELY
REPLACED BY THE ALPHA AND BETA FORMS DURING DEVELOPMENT.
CC -!- SIMILARITY: Belongs to the AdoMet synthetase family.

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or send an email to license@isb-sib.ch).

DR EMBL; J05571; AAA42106.1; -.

DR EMBL; AB000717; BAA19170.1; -.
DR EMBL; AB000716; BAA19170.1; JOINED.
DR PIR; A37118; A37118.
DR HSP; P04384; 1MXB.
DR InterPro: IPR002133; S-AdoMet_synt.
DR Pfam: PF00438; S-AdoMet_synt; 1.
DR Pfam: PF02772; S-AdoMet_syntD2; 1.
DR Pfam: PF02773; S-AdoMet_syntD3; 1.
DR TIGRFAMs: TIGR01034; metK; 1.
DR PROSITE: PS00376; ADO MET SYNTHETASE 1; 1.
DR PROSITE: PS00377; ADO MET SYNTHETASE 2; 1.
KW Transferase; One-carbon metabolism; Magnesium; Potassium;
KW Metal-binding; Multigene family; ATP-binding.
FT NP BIND 131 136 ATP (POTENTIAL).
FT METAL 31 31 MAGNESIUM (BY SIMILARITY).
FT METAL 57 57 POTASSIUM (BY SIMILARITY).
FT METAL 283 283 POTASSIUM (BY SIMILARITY).
FT METAL 291 291 MAGNESIUM (BY SIMILARITY).
FT BINDING 159 159 ATP (POTENTIAL).
SQ SEQUENCE 395 AA; 43715 MW; 4DA9AFABF7D09C79 CRC64;

Query Match 50.0%; Score 40; DB 1; Length 395;
Best Local Similarity 53.8%; Pred. No. 8.9;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
| : | | | | |
Db 92 YDSSKGFDFYKTC 104

Search completed: July 29, 2004, 08:47:35
Job time : 1.06527 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 3.2376 Seconds
(without alignments)
1559.271 Million cell updates/sec

Title: US-09-661-992B-105
Perfect score: 80
Sequence: 1 CXXYGNPKGFAYXXC 16

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertibrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	56.2	390	13 Q7ZW04	Q7ZW04 brachydanio
2	44	55.0	120	11 Q920E8	Q920E8 mus musculus
3	44	55.0	205	5 Q93233	Q93233 caenorhabdi
4	44	55.0	292	11 Q8CCS6	Q8CCS6 mus musculus
5	44	55.0	298	4 Q86U42	Q86U42 homo sapien
6	44	55.0	302	11 Q35335	Q35335 mus musculus
7	44	55.0	306	4 Q43484	Q43484 homo sapien
8	44	55.0	306	6 Q28165	Q28165 bos taurus
9	43	53.8	294	16 Q8XN61	Q8XN61 clostridium
10	43	53.8	723	11 Q8BZT4	Q8BZT4 mus musculus
11	42	52.5	160	3 Q9UTU1	Q9UTU1 schizosacch
12	42	52.5	166	3 Q14327	Q14327 schizosacch
13	42	52.5	295	13 Q7ZXB8	Q7ZXB8 xenopus lae
14	42	52.5	296	13 Q9DDY9	Q9DDY9 xenopus lae
15	42	52.5	491	4 Q9BZB7	Q9BZB7 homo sapien
16	42	52.5	559	13 Q9DED5	Q9DED5 carassius a

17	42	52.5	559	13 Q9YGM5	Q9YGM5 brachydanio
18	42	52.5	561	11 P70166	P70166 mus musculus
19	42	52.5	566	4 Q9BZB8	Q9BZB8 homo sapien
20	42	52.5	568	13 Q91572	Q91572 xenopus lae
21	42	52.5	583	16 Q7TXM1	Q7TXM1 mycobacteri
22	42	52.5	600	13 Q93386	Q93386 brachydanio
23	42	52.5	833	3 Q13620	Q13620 schizosacch
24	41	51.2	218	13 Q804A5	Q804A5 xenopus lae
25	41	51.2	389	8 Q98RZ7	Q98RZ7 guillardi
26	41	51.2	415	16 Q7UGL1	Q7UGL1 rhodospirill
27	41	51.2	453	16 P74064	P74064 synechocyst
28	41	51.2	467	16 Q832Q1	Q832Q1 enterococcu
29	41	51.2	1044	10 Q84UN0	Q84UN0 oryza sativ
30	41	51.2	2515	5 Q9WZJ8	Q9WZJ8 drosophila
31	40	50.0	107	16 Q8YE96	Q8YE96 bruceella me
32	40	50.0	107	16 Q8FXV1	Q8FXV1 bruceella su
33	40	50.0	203	3 Q875X7	Q875X7 saccharomyc
34	40	50.0	211	5 Q8MU02	Q8MU02 heterodera
35	40	50.0	279	13 Q7ZTW2	Q7ZTW2 brachydanio
36	40	50.0	291	5 Q9VTH9	Q9VTH9 drosophila
37	40	50.0	353	5 Q86N14	Q86N14 caenorhabdi
38	40	50.0	359	3 Q12642	Q12642 neurospora
39	40	50.0	385	3 Q9P842	Q9P842 candida alb
40	40	50.0	395	11 Q99J57	Q99J57 mus musculus
41	40	50.0	396	13 Q7ZY54	Q7ZY54 xenopus lae
42	40	50.0	865	5 Q79XV8	Q79XV8 ephydatia f
43	40	50.0	1312	16 Q98NH6	Q98NH6 rhizobium l
44	39.5	49.4	570	5 Q9NL49	Q9NL49 ciona savign
45	39.5	49.4	1787	16 Q8YWI8	Q8YWI8 anabaena sp

ALIGNMENTS

RESULT 1

Q7ZW04 ID Q7ZW04 PRELIMINARY; PRT; 390 AA.
AC Q7ZW04;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to methionine adenosyltransferase I, alpha.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]_TaxID=7955;
RP SEQUENCE FROM N.A.
RC TISSUE=Body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC045343; AAH45343.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004478; F:methionine adenosyltransferase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR002133; S-AdoMet_synth.
DR Pfam; PF00438; S-AdoMet_synthD2; 1.
DR Pfam; PF02772; S-AdoMet_synthD3; 1.
DR TIGRFAMs; TIGR01034; metX; 1.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
KW Transferase.
SQ SEQUENCE 390 AA; 43289 MW; 253AC38E7639B437 CRC64;

Query Match 56.2%; Score 45; DB 13; Length 390;

Best Local Similarity 61.5%; Fred. No. 7;

Matches 8; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16

|||||

Db 87 YDNSEKGFYKTC 99

RESULT 2

Q920E8 PRELIMINARY; PRT; 120 AA.

AC Q920E8; (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Pterin-mimicking anti-idiotope heavy chain variable region (Fragment).

DE Mus musculus (Mouse).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA Atkin J.D., Tape A., Jennings I.G., Horaitis O., Cotton R.G.H.; "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed in Mammalian Cells."

RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF307936; AAL09420.1; --

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF00047; IG; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT NON_TER 120 120

FT NON_TER 1

FT NON_TER 1

SQ SEQUENCE 120 AA; 13204 MW; DC4834AB1DE56F3C CRC64;

Query Match 55.0%; Score 44; DB 11; Length 120;

Best Local Similarity 80.0%; Pred. No. 3;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 YGNSPKGFAY 13

Db 101 YGNSPAFAAY 110

RESULT 3

Q93233 PRELIMINARY; PRT; 205 AA.

AC Q93233;

DT 01-FEB-1997 (TREMELrel. 02, Created)

DT 01-FEB-1997 (TREMELrel. 02, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE C17E4.5 protein.

GN C17E4.5

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

OX NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A.

RA Percy C.M.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=99069613; PubMed=9851916;

RT "Genome sequence of the nematode C.elegans: A platform for investigating biology."

RL Science 282:2012-2018 (1998).

DR EMBL; Z81037; CAB02750.1; --

DR PIR; T19356; T19356.

DR WormPep; C17E4.5; CE08254.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF00076; rrm; 1.

DR SMART; SM00360; RRM; 1.

DR PROSITE; PS50102; RRM; 1.

DR PROSITE; PS00030; RRM_RNP_1; 1.

SQ SEQUENCE 205 AA; 22603 MW; F6845A30DCF57746 CRC64;

Query Match 55.0%; Score 44; DB 5; Length 205;

Best Local Similarity 53.8%; Pred. No. 5.4;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13

Db 111 CDRFSGHPKGFAY 123

RESULT 4

Q8CCS6 PRELIMINARY; PRT; 292 AA.

AC Q8CCS6;

DT 01-MAR-2003 (TREMELrel. 23, Created)

DT 01-MAR-2003 (TREMELrel. 23, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Poly.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Olfactory brain;

RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium,

RA The RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."

RL Nature 420:563-573 (2002).

DR EMBL; AK032172; BAC27741.1; --

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF00076; rrm; 1.

DR SMART; SM00360; RRM; 1.

DR PROSITE; PS50102; RRM; 1.

DR PROSITE; PS00030; RRM_RNP_1; 1.

SQ SEQUENCE 292 AA; 31044 MW; 0874042BA4A60A2A CRC64;

Query Match 55.0%; Score 44; DB 11; Length 292;

Best Local Similarity 53.8%; Pred. No. 7.9;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13

Db 201 CDRFSGHPKGFAY 213

RESULT 5

Q86U42 PRELIMINARY; PRT; 298 AA.

AC Q86U42;

DT 01-JUN-2003 (TREMELrel. 24, Created)

DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Human full-length cDNA clone CS0DF018YN09 of fetal brain of Homo sapiens (Human) (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal brain;

RA Genoscope;

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Fetal brain;

RP TISSUE=Fetal brain;

RA Li W.B., Gruber C., Jesse J., Polayes D.;

RT "Full-length cDNA libraries and normalization";
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX247976; CAD233.10.1; -.
 DR PIR; PT0271; PT0271.

DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF00076; rrm; 1.
 DR SMART; SM00360; RRM; 1.
 DR PROSITE; PS50102; RRM; 1.
 DR PROSITE; PS00030; RRM_RNP_1; 1.
 KW Plasmid.

FT NON TER
 SQ SEQUENCE 298 AA; 1 31639 MW; 85C955A9A68043F8 CRC64;

Query Match 55.0%; Score 44; DB 4; Length 298;
 Best Local Similarity 53.8%; Pred. No. 8;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNPKGFAY 13
 | : |||||
 DB 207 CDKFSGHKGFAY 219

RESULT 6

C35935 ID O35935 PRELIMINARY; PRT; 302 AA.

AC C35935; DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Poly(A) binding protein II (Pabpn1 protein).
 GN PABPN1 OR MPABII.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129;

RA MEDLINE=98094238; PubMed=9434149;

RT "Genomic structure and expression of murine poly(A) binding protein II

gene.";

RL Biochim. Biophys. Acta 1395:40-46(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Colon;

RA MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Raha S.S., Iqbalano M.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska J., Schmutz J., Myers R.M., Schein J.B.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Colon;

RA Strausberg R.;

RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; U93050; AAC00210.1; -.

DR EMBL; BC055866; AAH55866.1; -.

DR MGD; MGI:1859158; Pabpn1.

DR GO; GO:0003676; F:nucleic acid binding; IEA.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF00076; rrm; 1.

DR SMART; SM00360; RRM; 1.

DR PROSITE; PS50102; RRM; 1.

DR PROSITE; PS00030; RRM_RNP_1; 1.

SQ SEQUENCE 302 AA; 32296 MW; 2F0F6F7CC19C1986 CRC64;

Query Match 55.0%; Score 44; DB 11; Length 302;
 Best Local Similarity 53.8%; Pred. No. 8.2;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNPKGFAY 13
 | : |||||
 DB 201 CDKFSGHKGFAY 213

RESULT 7

O43484

ID O43484 PRELIMINARY; PRT; 306 AA.

AC O43484;

DT 01-JUN-1998 (TrEMBLrel. 06, Created)

DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Poly(A) binding protein II (Similar to poly(A)-binding protein,

DE nuclear 1).

GN PABP2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98122579; PubMed=9462747;

RA Brais B., Bouchard J.-P., Xie Y.-G., Rochefort D.L., Chretien N.,

RA Tome F.M.S., Lafreniere R.G., Rommens J.M., Uyama E., Nohira O.,

RA Blumen S., Korcyn A.D., Heutink P., Mathieu J., Duranceau A.,

RA Codere F., Fardeau M., Rouleau G.A.;

RT "Short CGG expansions in the PABP2 gene cause oculopharyngeal muscular

RT dystrophy.";

RL Nat. Genet. 18:164-167(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Skin;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF026029; AAC39596.1; -.

DR EMBL; BC010939; AAH10939.1; -.

DR Genew; HGNC:8565; PABPN1.

DR GK; O43484; -.

DR GO; GO:0003723; F:RNA binding; TAS.

DR GO; GO:0009336; P:muscle contraction; TAS.

DR GO; GO:0008396; P:RNA processing; TAS.

DR InterPro; IPR000504; RNA_rec_mot.

DR Pfam; PF00076; rrm; 1.

DR SMART; SM00360; RRM; 1.

DR PROSITE; PS50102; RRM; 1.

DR PROSITE; PS00030; RRM_RNP_1; 1.

SQ SEQUENCE 306 AA; 32749 MW; 2E5B0AEFEA5AFBC3 CRC64;

Query Match 55.0%; Score 44; DB 4; Length 306;
 Best Local Similarity 53.8%; Pred. No. 8.3;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNPKGFAY 13
 | : |||||
 DB 205 CDKFSGHKGFAY 217

RT fission yeast cells by the use of a GFP-fusion genomic DNA library.;"

RL Genes Cells 5:169-190(2000).
DR EMBL; AB228003; BA87307.1; -
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
KW Hypothetical protein.
FT NON_TER 160 160
SQ SEQUENCE 160 AA; 18116 MW; 168A1FD5D5A94F5 CRC64;

Query Match 52.5%; Score 42; DB 3; Length 160;
Best Local Similarity 87.5%; Pred. No. 9.6;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 NSPKGFAY 13
| : |||||
DB 58 NNPKGFAY 65

RESULT 12

ID O14327 PRELIMINARY; PRT; 166 AA.
AC O14327;
DT 01-JAN-1999 (TrEMBLrel. 09, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Pucative poly(a) binding protein.
GN SPBC169.12C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972h-;
RA Volckaert G., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z99759; CAB16904.1; -
DR PIR; T39586; T39586.
DR GeneDB; Stombs; SPBC169.12c; -
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 166 AA; 18461 MW; A602B5EFC55600E8 CRC64;

Query Match 52.5%; Score 42; DB 3; Length 166;
Best Local Similarity 53.8%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
| : |||||
DB 88 CDKFTGHPKGFAY 100

RESULT 13

ID Q7ZXB8 PRELIMINARY; PRT; 295 AA.
AC Q7ZXB8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to poly(A) binding protein, nuclear 1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;

OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC045063; AAH45063.1; -
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 295 AA; 32212 MW; 0E221DE8B503678B CRC64;

Query Match 52.5%; Score 42; DB 13; Length 295;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
| : |||||
DB 195 CDKFTGHPKGFAY 207

RESULT 14

ID Q9DDY9 PRELIMINARY; PRT; 296 AA.
AC Q9DDY9;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Poly(A) binding protein II.
GN PABP11.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC Kim J., Choi S., Han J.;
RL "Developmental expression of Poly(A) Binding Protein II in Xenopus laevis.";
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257236; AAG36902.1; -
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00076; rrm; 1.
DR SMART; SM00360; RRM; 1.
DR PROSITE; PS0102; RRM; 1.
DR PROSITE; PS00030; RRM_RNP_1; 1.
SQ SEQUENCE 296 AA; 32449 MW; 319E1235DF4B33E3 CRC64;

Query Match 52.5%; Score 42; DB 13; Length 296;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
| : |||||
DB 196 CDKFTGHPKGFAY 208

RESULT 15

ID Q9BZB7 PRELIMINARY; PRT; 491 AA.
AC Q9BZB7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cytoplasmic polyadenylation element-binding protein short form.
OS CPEB1.
GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary, and Brain;
RX MEDLINE=21125222; PubMed=11223249;
RA Welk J.F., Charlesworth A., Smith G.D., MacNicol A.M.;
RT "Identification and characterization of the gene encoding human
RT cytoplasmic polyadenylation element binding protein.";
RL Gene 263:113-121(2001).
DR EMBL; AF329403; AAK01240.1; --
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR000504; RNA_rec_mot.
DR PROSITE; PS0102; RM; 2_
SQ SEQUENCE 491 AA; 54162 MW; 561A40FEBD482262 CRC64;

Query Match 52.5%; Score 42; DB 4; Length 491;
Best Local Similarity 53.8%; Pred.No. 32;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
Db 276 CPPKGNPKGYV 288

Search completed: July 29, 2004, 08:50:25
Job time : 5.2376 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:27 ; Search time 1.44125 Seconds
(without alignments)
573.123 Million cell updates/sec

Title: US-09-661-992B-105
Perfect score: 80
Sequence: 1 CXXYGNSPKGFAYXC 16

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	55.0	62	4	US-09-621-976-4459
2	44	55.0	365	4	US-08-149-476-696
3	44	55.0	365	4	US-08-010-147B-24
4	41	51.2	415	4	US-08-134-000C-6391
5	40	50.0	395	4	US-08-976-594-471
6	39	48.8	109	4	US-08-025-769B-16
7	38	47.5	107	4	US-08-635-109-7
8	38	47.5	119	1	US-08-207-996-18
9	38	47.5	119	1	US-08-207-996-19
10	38	47.5	119	1	US-08-207-996-20
11	38	47.5	119	1	US-08-207-996-21
12	38	47.5	119	1	US-08-207-996-22
13	38	47.5	119	1	US-08-207-996-27
14	38	47.5	119	2	US-08-760-840A-18
15	38	47.5	119	2	US-08-760-840A-19
16	38	47.5	119	2	US-08-760-840A-20
17	38	47.5	119	2	US-08-760-840A-21
18	38	47.5	119	2	US-08-760-840A-22
19	38	47.5	119	3	US-08-760-840A-28
20	38	47.5	119	3	US-08-266-119-18
21	38	47.5	119	3	US-08-266-119-19
22	38	47.5	119	3	US-08-266-119-20
23	38	47.5	119	3	US-08-266-119-21
24	38	47.5	119	3	US-08-266-119-22
25	38	47.5	119	3	US-08-266-119-28
26	38	47.5	119	4	US-09-602-709-18
27	38	47.5	119	4	US-09-602-709-19

28	38	47.5	119	4	US-09-602-709-20	Sequence 20, Appl
29	38	47.5	119	4	US-09-602-709-21	Sequence 21, Appl
30	38	47.5	119	4	US-09-602-709-22	Sequence 22, Appl
31	38	47.5	119	4	US-09-602-709-28	Sequence 26, Appl
32	38	47.5	351	3	US-09-067-782A-2	Sequence 21, Appl
33	37	46.2	143	4	US-09-795-926-21	Sequence 21, Appl
34	37	46.2	240	4	US-09-795-926-33	Sequence 33, Appl
35	37	46.2	263	5	PCT-US94-00844-11	Sequence 11, Appl
36	37	46.2	426	4	US-09-252-991A-32215	Sequence 32215, A
37	37	46.2	572	2	US-09-032-315-7	Sequence 7, Appl
38	37	46.2	572	2	US-08-993-318A-7	Sequence 7, Appl
39	37	46.2	572	3	US-09-399-886-7	Sequence 7, Appl
40	37	46.2	572	3	US-09-396-260-7	Sequence 7, Appl
41	37	46.2	572	3	US-09-576-281-7	Sequence 7, Appl
42	36	45.0	69	4	US-09-621-976-6307	Sequence 6307, Ap
43	36	45.0	149	4	US-09-252-991A-19973	Sequence 19973, A
44	36	45.0	396	4	US-09-325-932A-153	Sequence 153, App
45	36	45.0	484	4	US-09-134-001C-5402	Sequence 5402, Ap

ALIGNMENTS

RESULT 1
US-09-621-976-4459
; Sequence 4459, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 4459
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4459

Query Match 55.0%; Score 44; DB 4; Length 62;
Best Local Similarity 53.8%; Pred. No. 1.9;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXXYGNSPKGFAY 13
| : |||||
Db 45 CDKFSGHKGFAY 57

RESULT 2
US-09-149-476-696
; Sequence 696, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334

[illegible]

; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-08-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 55.0%; Score 44; DB 4; Length 365;
Best Local Similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNPKGPAY 13
| : |||||
Db 264 CDKFSGHPKGPAY 276

RESULT 3
US-09-010-147B-24
; Sequence 24, Application US/09010147B
; Patent No. 6653445
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: Human Proteins
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC
; compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,147B
; FILING DATE: 12-Nov. 6653445-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/034,205
; FILING DATE: 21-JAN-1997

; APPLICATION NUMBER: US 60/034,204
; FILING DATE: 21-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Jonathan L. Klein
; REGISTRATION NUMBER: 41,119
; REFERENCE/DOCKET NUMBER: PF353
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 365 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-010-147B-24

Query Match 55.0%; Score 44; DB 4; Length 365;
Best Local Similarity 53.8%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNPKGPAY 13
| : |||||
Db 264 CDKFSGHPKGPAY 276

RESULT 4
US-09-134-000C-6391
; Sequence 6391, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 6391
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6391

Query Match 51.2%; Score 41; DB 4; Length 415;
Best Local Similarity 77.8%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 YGNSPKGF 12
| : |||||
Db 353 FGTSKGF 361

RESULT 5
US-09-976-594-471
; Sequence 471, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Buchbinder, Jenny
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 471

; LENGTH: 395
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6673549 2600262CD1
 US-09-976-594-471

Query Match 50.0%; Score 40; DB 4; Length 395;
 Best Local Similarity 53.8%; Pred. No. 57;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
 Db 92 YDSSKGFYKTC 104

RESULT 6
 US-09-025-769B-16
 ; Sequence 16, Application US/09025769B
 ; Patent No. 6300064
 ; GENERAL INFORMATION:
 ; APPLICANT: Knappik, Achim
 ; APPLICANT: Pack, Peter
 ; APPLICANT: Ilag, Vic
 ; APPLICANT: Ge, Liming
 ; APPLICANT: Moroney, Simon
 ; APPLICANT: Plueckthun, Andreas
 ; TITLE OF INVENTION: Protein/(poly)peptide libraries
 ; NUMBER OF SEQUENCES: 373
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 ; STREET: 1251 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10021

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/025.769B
 ; FILING DATE: 18-FEB-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: EP 95 11 3021.0
 ; FILING DATE: 18-AUG-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: James F. Haley, Jr., Esq.
 ; REGISTRATION NUMBER: 27,794
 ; REFERENCE/DOCKET NUMBER: MORPHO/5
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212)596-9000
 ; TELEFAX: (212)596-9090
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 109 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-09-025-769B-16

Query Match 48.8%; Score 39; DB 4; Length 109;
 Best Local Similarity 63.6%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXXYGNPKGF 11
 Db 89 CQYGNSPYTF 99

RESULT 7
 US-08-635-109-7
 ; Sequence 7, Application US/08635109
 ; Patent No. 6538114
 ; GENERAL INFORMATION:
 ; APPLICANT: Persson, Mats A. A.
 ; APPLICANT: Allander, Tobias E.
 ; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR
 ; TITLE OF INVENTION: HEPATITIS C VIRUS (HCV) E2 ANTIGEN
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: REED & ROBINS
 ; STREET: 285 Hamilton Avenue, Suite 200
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94301
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/635,109
 ; FILING DATE: 19-APR-1996
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McCracken, Thomas P
 ; REGISTRATION NUMBER: 38,548
 ; REFERENCE/DOCKET NUMBER: 2300-6146
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 327-3400
 ; TELEFAX: (415) 327-3231
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 107 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-635-109-7

Query Match 47.5%; Score 38; DB 4; Length 107;
 Best Local Similarity 54.5%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNPKGF 11
 Db 88 CQYGNSPYTF 98

RESULT 8
 US-08-207-996-18
 ; Sequence 18, Application US/08207996
 ; Patent No. 5646253
 ; GENERAL INFORMATION:
 ; APPLICANT: Scottgen Biopharmaceuticals, Inc.
 ; APPLICANT: 1014 Hamilton Court
 ; APPLICANT: Menlo Park, California 94025
 ; APPLICANT: United States of America
 ; APPLICANT: 1345 Avenue of the Americas
 ; APPLICANT: New York, New York 10105
 ; APPLICANT: United States of America
 ; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
 ; TITLE OF INVENTION: ANTIBODIES
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Felfe & Lynch
 ; STREET: 805 Third Avenue
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-207-996-18

Query Match 47.5%; Score 38; DB 1; Length 119;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
|:|:|
Db 96 CARHGDDPAWFAY 108

RESULT 9
US-08-207-996-19
Sequence 19, Application US/08207996
Patent No. 5646253
GENERAL INFORMATION:
APPLICANT: Scotgen Biopharmaceuticals, Inc.
APPLICANT: 1014 Hamilton Court
APPLICANT: Menlo Park, California 94025
APPLICANT: United States of America
APPLICANT: 1345 Avenue of the Americas
APPLICANT: New York, New York 10105
APPLICANT: United States of America
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-207-996-20

Query Match 47.5%; Score 38; DB 1; Length 119;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
|:|:|
Db 96 CARHGDDPAWFAY 108

RESULT 10
US-08-207-996-20
Sequence 20, Application US/08207996
Patent No. 5646253
GENERAL INFORMATION:
APPLICANT: Scotgen Biopharmaceuticals, Inc.
APPLICANT: 1014 Hamilton Court
APPLICANT: Menlo Park, California 94025
APPLICANT: United States of America
APPLICANT: 1345 Avenue of the Americas
APPLICANT: New York, New York 10105
APPLICANT: United States of America
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-207-996-20

Query Match 47.5%; Score 38; DB 1; Length 119;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
|:|:|
Db 96 CARHGDDPAWFAY 108

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-207-996-19

Query Match 47.5%; Score 38; DB 1; Length 119;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
|:|:|
Db 96 CARHGDDPAWFAY 108

RESULT 10
US-08-207-996-20
Sequence 20, Application US/08207996
Patent No. 5646253
GENERAL INFORMATION:
APPLICANT: Scotgen Biopharmaceuticals, Inc.
APPLICANT: 1014 Hamilton Court
APPLICANT: Menlo Park, California 94025
APPLICANT: United States of America
APPLICANT: 1345 Avenue of the Americas
APPLICANT: New York, New York 10105
APPLICANT: United States of America
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-207-996-20

Query Match 47.5%; Score 38; DB 1; Length 119;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
|:|:|
Db 96 CARHGDDPAWFAY 108

INFORMATION FOR SEQ ID NO: 19:

RESULT 11
US-08-207-996-21
; Sequence 21, Application US/08207996
; Patent No. 5646253
; GENERAL INFORMATION:
; APPLICANT: Scotgen Biopharmaceuticals, Inc.
; APPLICANT: 1014 Hamilton Court
; APPLICANT: Menlo Park, California 94025
; APPLICANT: United States of America
; APPLICANT: 1345 Avenue of the Americas
; APPLICANT: New York, New York 10105
; APPLICANT: United States of America
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.0/ASCII standard
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,996
; FILING DATE: 08-MAR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894
; REFERENCE/DOCKET NUMBER: LUD-5363
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-688-9200
; TELEFAX: 212-838-3884
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-207-996-21
Query Match 47.5%; Score 38; DB 1; Length 119;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CXXYGNSPKPAY 13
Db 96 CARHGDDPAWFAY 108
RESULT 12
US-08-207-996-22
; Sequence 22, Application US/08207996
; Patent No. 5646253
; GENERAL INFORMATION:
; APPLICANT: Scotgen Biopharmaceuticals, Inc.
; APPLICANT: 1014 Hamilton Court
; APPLICANT: Menlo Park, California 94025
; APPLICANT: United States of America
; APPLICANT: 1345 Avenue of the Americas
; APPLICANT: New York, New York 10105
; APPLICANT: United States of America
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.0/ASCII standard
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,996
FILING DATE: 08-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD-5363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-207-996-22
Query Match 47.5%; Score 38; DB 1; Length 119;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 CXXYGNSPKPAY 13
Db 96 CARHGDDPAWFAY 108
RESULT 13
US-08-207-996-27
; Sequence 27, Application US/08207996
; Patent No. 5646253
; GENERAL INFORMATION:
; APPLICANT: Scotgen Biopharmaceuticals, Inc.
; APPLICANT: 1014 Hamilton Court
; APPLICANT: Menlo Park, California 94025
; APPLICANT: United States of America
; APPLICANT: 1345 Avenue of the Americas
; APPLICANT: New York, New York 10105
; APPLICANT: United States of America
; TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.0/ASCII standard
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,996
; FILING DATE: 08-MAR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Pasqualini, Patricia A.
; REGISTRATION NUMBER: 34,894

REFERENCE/DOCKET NUMBER: LUD-5363
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-207-996-27

Query Match 47.5%; Score 38; DB 1; Length 119;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXYGNSPKGFAY 13
Db 96 CARHGDDPAWFAY 108

RESULT 14
US-08-760-840A-18
Sequence 18, Application US/08760840A
Patent No. 5952484
GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-760-840A-18

Query Match 47.5%; Score 38; DB 2; Length 119;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXYGNSPKGFAY 13
Db 96 CARHGDDPAWFAY 108

RESULT 15
US-08-760-840A-19
Sequence 19, Application US/08760840A
Patent No. 5952484
GENERAL INFORMATION:
APPLICANT: Paul WALLACE;
APPLICANT: William J. HARRIS;
APPLICANT: Wolfgang J. RETTIG;
APPLICANT: Pilar GARIN-CHESA;
APPLICANT: Lloyd J. OLD
TITLE OF INVENTION: RECOMBINANT HUMAN ANTI-LK26 ANTIBODIES
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,840A
FILING DATE: 05-DEC-1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 95/03094
FILING DATE: 08-MAR-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 5952484man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5363.1 DIV. - JEL/NDH/SLH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-688-9200
TELEFAX: 212-838-3884
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-760-840A-19

Query Match 47.5%; Score 38; DB 2; Length 119;
Best Local Similarity 46.2%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXYGNSPKGFAY 13
Db 96 CARHGDDPAWFAY 108

Search completed: July 29, 2004, 08:53:09
Job time : 1.44125 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:42:22 ; Search time 4.9295 seconds

(without alignments)
917.082 Million cell updates/sec

Title: US-09-661-992B-105

Perfect score: 80

Sequence: 1 CXYGNPKGFAYXXC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Geneseq_29Jan04:*
2: geneseq1980s:*
3: geneseq1990s:*
4: geneseq2000s:*
5: geneseq2001s:*
6: geneseq2002s:*
7: geneseq2003s:*
8: geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72	90.0	16	4 AAB20444	Aab20444 Anti-FIX/
2	66	82.5	242	4 AAB20433	Aab20433 Anti-FIX/
3	58	72.5	10	4 AAB20388	Aab20388 Anti-FIX/
4	44	55.0	365	2 AAW59884	Aaw59884 Amino aci
5	44	55.0	365	5 ASG93556	Asg93556 Human nov
6	44	55.0	365	5 ASG934750	Asg934750 Fragment
7	42	52.5	132	5 ABP62216	Abp62216 Human imm
8	42	52.5	583	6 ABR82455	AbR82455 FACLLABE
9	42	52.5	583	7 ABR83540	AbR83540 M. tuberc
10	42	52.5	626	4 AAB66460	Aab66460 Protein e
11	41	51.2	429	6 ABM15850	Abm15850 Mycobacte
12	41	51.2	2515	4 ABB64427	Abb64427 Drosophil
13	40	50.0	107	5 ABG76564	Abg76564 HCV El an
14	40	50.0	136	5 ABP62206	Abp62206 Human imm
15	40	50.0	261	5 ABP43671	Abp43671 Methionin
16	40	50.0	291	4 ABB63366	Abb63366 Drosophil
17	40	50.0	382	6 ABR52625	AbR52625 Protein s
18	40	50.0	384	6 ABR53048	AbR53048 Protein s
19	40	50.0	385	3 AAY95075	Aay95075 Candida a
20	40	50.0	503	4 ABG22854	Abg22854 Novel hum
21	40	50.0	503	7 ADC32915	Adc32915 Human nov
22	39	48.8	116	5 ABP08836	Abp08836 Human ORF
23	39	48.8	401	6 ABU49388	Abu49388 Protein e
24	39	48.8	572	4 ABG03182	Abg03182 Novel hum
25	36	47.5	91	5 ABG7145	Abg7145 Anti-IGF-

26	38	47.5	105	5 AAO18433	Aao18433 Anti-GD2
27	38	47.5	105	7 ABO33833	Abo33833 Human ant
28	38	47.5	105	7 ABO33829	Abo33829 Human ant
29	38	47.5	106	2 AAW31724	Aaw31724 Alpha lig
30	38	47.5	108	4 AAB62780	Aab62780 Human HIV
31	38	47.5	108	6 ABP71368	Abp71368 Anti-OPGL
32	38	47.5	108	6 ABR55800	Abr55800 Kappa cha
33	38	47.5	108	6 ABR55804	Abr55804 Kappa cha
34	38	47.5	109	4 AAB62753	Aab62753 Human HIV
35	38	47.5	109	6 ADA89180	Ada89180 Human ant
36	38	47.5	109	6 ADA89220	Ada89220 Human ant
37	38	47.5	119	2 AAR82986	Aar82986 LK26 huma
38	38	47.5	119	2 AAR82980	Aar82980 LK26 huma
39	38	47.5	119	2 AAR82981	Aar82981 LK26 huma
40	38	47.5	119	2 AAR82982	Aar82982 LK26 huma
41	38	47.5	119	2 AAR82979	Aar82979 LK26 huma
42	38	47.5	119	2 AAR82977	Aar82977 LK26 heav
43	38	47.5	129	3 AAY43866	Aay43866 Heavy Cha
44	38	47.5	211	4 AAE09692	Aae09692 Human gen
45	38	47.5	211	7 ADC22070	Adc22070 Human pro

ALIGNMENTS

RESULT 1
AAB20444
ID AAB20444 standard; peptide; 16 AA.

XX AAB20444;

AC

XX 21-JUN-2001 (first entry)

DT Anti-FIX/FIXa antibody CDR3.

DE

XX Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;
XX Factor VIII cofactor; blood coagulation disorder; haemophilia A;
KW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
KW complementarity determining region; CDR.

XX Mus musculus.

XX

Key Location/Qualifiers

FT Misc-difference 2 /note= "any amino acid"

FT Misc-difference 3 /note= "any amino acid"

FT Misc-difference 14 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

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FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

FT Misc-difference 15 /note= "any amino acid"

WO200119992-A2.
22-MAR-2001.
13-SEP-2000; 2000WO-EP008936.
14-SEP-1999; 99AT-00001576.
(BAXT) BAXTER AG.
Scheifflinger F, Kerschbaumer R, Falkner F, Dörner F;
WPI; 2001-290358/30.
New factor IX/factor IXa antibodies and their derivatives useful for
increasing amidolytic activity of factor IXa, and for treating blood
coagulation disorders such as hemophilia A and hemorrhagic diathesis.
Claim 7; Page 74; 138pp; English.

The present sequence is that of complementarity determining region 3

CC (CDR3) of an antibody having anti-Factor IX (FIX) or anti-activated
 CC Factor IX (FIXa) activity. Such antibodies and their derivatives
 CC (including those that comprise the present CDR3 peptide) have Factor
 CC VIIa (FVIIa) cofactor activity or FIXa activating activity.
 CC Administration of the antibodies or their derivatives leads to an
 CC increase in the procoagulant activity of FIXa, even in the presence of
 CC FVIIa inhibitors. This allows for rapid blood coagulation even in the
 CC absence of FVIII or FVIIIa, and in the case of FVIII inhibitor patients.
 CC The antibodies or their derivatives are used in a claimed pharmaceutical
 CC composition for treating patients with blood coagulation disorders,
 CC especially haemophilia A and haemorrhagic diathesis
 CC
 XX Sequence 16 AA;

Query Match 90.0%; Score 72; DB 4; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.5e-05;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAYXXC 16
 |||||
 Db 1 CXXYGNSPKGFAYXXC 16

RESULT 2
 AAB20433
 ID AAB20433 standard; protein; 242 AA.

XX AC AAB20433;

DT 21-JUN-2001 (first entry)

DE Anti-FIX/FIXa antibody 193/AD3 scFv.

XX Factor IX; FIX; Factor IXa; FIXa; scFv; antibody; procoagulant;
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 XW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse.

XX Mus musculus.
 OS Synthetic.
 OS Chimeric.

XX Key Location/Qualifiers
 FT Protein 1..119
 FT /label= VH
 FT Region 98..108
 FT /label= CDR3
 FT Peptide 120..134
 FT /label= Linker
 FT Protein 135..242
 FT /label= VL
 FT Region 223..231
 FT /label= CDR3

XX WO200119992-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-EP008936.

XX 14-SEP-1999; 99AT-00001576.

XX (BAXT) BAXTER AG.

XX Scheiflinger F, Kerschbaumer R, Falkner F, Dörner F;

XX WPI; 2001-290358/30.

XX N-PSDB; AAF30723.

XX New factor IX/factor IXa antibodies and their derivatives useful for
 PT increasing amidolytic activity of factor IXa, and for treating blood
 PT coagulation disorders such as haemophilia A and hemorrhagic diathesis.
 XX
 PS Claim 8; Fig 14; 138pp; English.

XX The present sequence is that of a single chain Fv (scFv) derivative of
 CC antibody 193/AD3, comprising the heavy (VH) and light (VL) chain variable
 CC regions of 193/AD3 joined by an artificial, flexible linker peptide. The
 CC scFv was obtained by PCR amplification of cDNAs for 193/AD3 VH and VL
 CC regions and cloning in vector pDAP2. 193/AD3 is an example of anti-human
 CC Factor IX (FIX)/activated Factor IX (FIXa) antibodies of the invention.
 CC Anti-FIX/FIXa and their derivatives, including scFv and CDR3 fragments,
 CC have Factor VIIa (FVIIa) cofactor activity or FIXa activating activity.
 CC Administration leads to an increase in the procoagulant activity of FIXa,
 CC even in the presence of FVIII inhibitors. This allows for rapid blood
 CC coagulation even in the absence of FVIII or FVIIIa, and in the case of
 CC FVIII inhibitor patients. The antibodies and derivatives are used in a
 CC claimed pharmaceutical composition for treating patients with blood
 CC coagulation disorders, especially haemophilia A and hemorrhagic
 CC diathesis
 XX
 XX Sequence 242 AA;

Query Match 82.5%; Score 66; DB 4; Length 242;
 Best Local Similarity 84.6%; Pred. No. 0.0077;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
 |||||
 Db 96 CALYGNSPKGFAY 108

RESULT 3

AAB20388

ID AAB20388 standard; peptide; 10 AA.

XX AC AAB20388;

DT 21-JUN-2001 (first entry)

DE Anti-FIX/FIXa antibody 193/AD3 CDR3.

XX Factor IX; FIX; Factor IXa; FIXa; antibody; procoagulant;
 KW Factor VIII cofactor; blood coagulation disorder; haemophilia A;
 XW haemorrhagic diathesis; haemostatic; amidolytic; therapy; mouse;
 KW complementarity determining region; CDR.

XX Mus musculus.

XX WO200119992-A2.

XX 22-MAR-2001.

XX 13-SEP-2000; 2000WO-EP008936.

XX 14-SEP-1999; 99AT-00001576.

XX (BAXT) BAXTER AG.

XX Scheiflinger F, Kerschbaumer R, Falkner F, Dörner F;

XX WPI; 2001-290358/30.

XX New factor IX/factor IXa antibodies and their derivatives useful for
 PT increasing amidolytic activity of factor IXa, and for treating blood
 PT coagulation disorders such as haemophilia A and hemorrhagic diathesis.

XX Claim 7; Page 74; 138pp; English.

XX The present sequence is that of complementarity determining region 3
 CC (CDR3) of the heavy chain of an antibody expressed by mouse hybridoma
 CC 193/AD3. This antibody has anti-Factor IX (FIX) or anti-activated Factor
 CC IX (FIXa) activity. It is an example of anti-FIX/FIXa antibodies of the
 CC invention. Such antibodies and their derivatives (including those that
 CC comprise the present CDR3 peptide) have Factor VIIa (FVIIa) cofactor
 CC activity or FIXa activating activity. Administration of the antibodies or
 CC their derivatives leads to an increase in the procoagulant activity of

CC FIXa, even in the presence of FVIIa inhibitors. This allows for rapid
 CC blood coagulation even in the absence of FVII or FVIIa, and in the case
 CC of FVII inhibitor patients. The antibodies or their derivatives are used
 CC in a claimed pharmaceutical composition for treating patients with blood
 CC coagulation disorders, especially haemophilia A and haemorrhagic
 CC diathesis
 XX
 SQ Sequence 10 AA;

Query Match 72.5%; Score 58; DB 4; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0057;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 YGNSPKGFAY 13
 Db 1 YGNSPKGFAY 10
 |||||

RESULT 4

AAW59884
 ID AAW59884 standard; protein; 365 AA.

XX AC AAW59884;

XX DT 20-NOV-1998 (first entry)

XX DE Amino acid sequence of the cDNA clone Bcl-like (HAICH29).

XX KW Bcl-like (HAICH29); chronic inflammatory disease; allergic reaction;
 XX immunological disorder; autoimmune disease; anti-infectious agent.

XX OS Homo sapiens.

XX PN WO9831800-A2.

XX PD 23-JUL-1998.

XX PF 21-JAN-1998; 98WO-US000960.

XX PR 21-JAN-1997; 97US-0034204P.

XX PR 21-JAN-1997; 97US-0034205P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (AUCK-) AUCKLAND UNISERVICES LTD.

XX PI Ni J, Rosen CA, Gentz RL, Feng P, Krissansen GW, Su JY;

XX DR WPI; 1998-414099/35.

XX DR N-PSDB; AAV41925.

XX PT New isolated polynucleotides and encoded polypeptides - used to develop
 XX products for treating e.g. inflammatory diseases, infections,
 XX immunological disorders, autoimmune diseases, allergies or tumours.

XX PS Claim 1; Fig 12A-12D; 120pp; English.

XX CC This is the amino acid sequence of the cDNA clone Bcl-like (HAICH29),
 XX used in the method of the invention. The products of the clone can be
 XX used for treating conditions associated with abnormal expression of the
 XX polypeptides. They can be used for e.g. treating chronic inflammatory
 XX diseases, immunological disorders, autoimmune diseases, inflammatory
 XX diseases, various allergies, and as anti-infectious agents. The products
 XX can also be used for detection and diagnosis

XX SQ Sequence 365 AA;

Query Match 55.0%; Score 44; DB 2; Length 365;

Best Local Similarity 53.8%; Pred. No. 53;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXXYGNPKGFAY 13
 : |||||

Db 264 CDKPSGHPKGFAY 276
 : |||||

RESULT 5

ABG95556

ID ABG95556 standard; protein; 365 AA.

XX AC ABG95556;

XX DT 15-JAN-2003 (first entry)

XX DE Human novel secreted protein gene 120 polypeptide #1.

XX KW Human; secreted protein; autoimmune disease; chemotaxis;
 XX rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;
 XX liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;
 XX cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;
 XX nervous system disorders; Alzheimer's disease; infection;
 XX ocular disorder; corneal infection; wound healing; tissue regeneration;
 XX epithelial cell proliferation; organ transplantation; food additive;
 XX preservative; nutritional.

XX OS Homo sapiens.

XX PN US6420526-B1.

XX PD 16-JUL-2002.

XX PF 08-SEP-1998; 98US-00149476.

XX PR 07-MAR-1997; 97US-0038621P.

XX PR 07-MAR-1997; 97US-0040161P.

XX PR 07-MAR-1997; 97US-0040162P.

XX PR 07-MAR-1997; 97US-0040163P.

XX PR 07-MAR-1997; 97US-0040333P.

XX PR 07-MAR-1997; 97US-0040334P.

XX PR 07-MAR-1997; 97US-0040336P.

XX PR 07-MAR-1997; 97US-0040626P.

XX PR 11-APR-1997; 97US-0043311P.

XX PR 11-APR-1997; 97US-0043312P.

XX PR 11-APR-1997; 97US-0043313P.

XX PR 11-APR-1997; 97US-0043314P.

XX PR 11-APR-1997; 97US-0043315P.

XX PR 11-APR-1997; 97US-0043568P.

XX PR 11-APR-1997; 97US-0043569P.

XX PR 11-APR-1997; 97US-0043576P.

XX PR 11-APR-1997; 97US-0043578P.

XX PR 11-APR-1997; 97US-0043580P.

XX PR 11-APR-1997; 97US-0043669P.

XX PR 11-APR-1997; 97US-0043670P.

XX PR 11-APR-1997; 97US-0043671P.

XX PR 11-APR-1997; 97US-0043672P.

XX PR 11-APR-1997; 97US-0043674P.

XX PR 23-MAY-1997; 97US-0047492P.

XX PR 23-MAY-1997; 97US-0047500P.

XX PR 23-MAY-1997; 97US-0047501P.

XX PR 23-MAY-1997; 97US-0047502P.

XX PR 23-MAY-1997; 97US-0047503P.

XX PR 23-MAY-1997; 97US-0047581P.

XX PR 23-MAY-1997; 97US-0047582P.

XX PR 23-MAY-1997; 97US-0047583P.

XX PR 23-MAY-1997; 97US-0047584P.

XX PR 23-MAY-1997; 97US-0047585P.

XX PR 23-MAY-1997; 97US-0047586P.

XX PR 23-MAY-1997; 97US-0047587P.

XX PR 23-MAY-1997; 97US-0047588P.

XX PR 23-MAY-1997; 97US-0047589P.

XX PR 23-MAY-1997; 97US-0047590P.

XX PR 23-MAY-1997; 97US-0047592P.

XX PR 23-MAY-1997; 97US-0047593P.

XX PR 23-MAY-1997; 97US-0047594P.

XX PR 23-MAY-1997; 97US-0047595P.

XX PR 23-MAY-1997; 97US-0047596P.

XX PR 23-MAY-1997; 97US-0047597P.

PR 23-MAY-1997; 97US-0047598P.
 PR 23-MAY-1997; 97US-0047599P.
 PR 23-MAY-1997; 97US-0047600P.
 PR 23-MAY-1997; 97US-0047601P.
 PR 23-MAY-1997; 97US-0047610P.
 PR 23-MAY-1997; 97US-0047612P.
 PR 23-MAY-1997; 97US-0047613P.
 PR 23-MAY-1997; 97US-0047614P.
 PR 23-MAY-1997; 97US-0047615P.
 PR 23-MAY-1997; 97US-0047617P.
 PR 23-MAY-1997; 97US-0047618P.
 PR 23-MAY-1997; 97US-0047632P.
 PR 23-MAY-1997; 97US-0047633P.
 PR 06-JUN-1997; 97US-0048964P.
 PR 06-JUN-1997; 97US-0048974P.
 PR 13-JUN-1997; 97US-0049610P.
 PR 08-JUL-1997; 97US-0051926P.
 PR 16-JUL-1997; 97US-0052874P.
 PR 18-AUG-1997; 97US-0055724P.
 PR 22-AUG-1997; 97US-0056630P.
 PR 22-AUG-1997; 97US-0056631P.
 PR 22-AUG-1997; 97US-0056632P.
 PR 22-AUG-1997; 97US-0056633P.
 PR 22-AUG-1997; 97US-0056636P.
 PR 22-AUG-1997; 97US-0056637P.
 PR 22-AUG-1997; 97US-0056662P.
 PR 22-AUG-1997; 97US-0056664P.
 PR 22-AUG-1997; 97US-0056845P.
 PR 22-AUG-1997; 97US-0056882P.
 PR 22-AUG-1997; 97US-0056886P.
 PR 22-AUG-1997; 97US-0056887P.
 PR 22-AUG-1997; 97US-0056889P.
 PR 22-AUG-1997; 97US-0056890P.
 PR 22-AUG-1997; 97US-0056892P.
 PR 22-AUG-1997; 97US-0056893P.
 PR 22-AUG-1997; 97US-0056894P.
 PR 22-AUG-1997; 97US-0056903P.
 PR 22-AUG-1997; 97US-0056908P.
 PR 22-AUG-1997; 97US-0056909P.
 PR 22-AUG-1997; 97US-0056910P.
 PR 22-AUG-1997; 97US-0056911P.
 PR 05-SEP-1997; 97US-0057650P.
 PR 05-SEP-1997; 97US-0057669P.
 PR 05-SEP-1997; 97US-0057761P.
 PR 12-SEP-1997; 97US-0058785P.
 PR 02-OCT-1997; 97US-0061060P.
 PR 06-MAR-1998; 98WO-US004493.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX Ruben SM, Rosen CA, Rischer CL, Soppet DP, Carter KC,
 PI Bednarik DR, Endres GA, Yu G, Ni J, Feng P, Young PE, Greene JM;
 PI Ferrie AM, Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;
 PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;
 XX WPI; 2002-634796/68.
 XX New isolated human secreted protein for diagnosing, preventing, treating
 PT or ameliorating medical conditions and used as a food additive or
 PT preservative.
 XX Disclosure; Col 103; 129pp; English.

CC The invention relates to an isolated protein that is one of 186 human
 CC secreted proteins, given in the specification, encoded by one of 309 cDNA
 CC sequences also given in the specification. The protein is used in a
 CC pharmaceutical composition used to prevent, treat or ameliorate a medical
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
 CC chickens or sheep. Disorders which are diagnosed or treated include
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. Alzheimer's disease,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional
 CC components. The present sequence represents one of the novel human
 CC secreted proteins of the invention
 XX Sequence 365 AA;
 SQ
 Query Match 55.0%; Score 44; DB 5; Length 365;
 Best Local Similarity 53.8%; Pred. No. 53;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CXXYGNSPKGRAY 13
 DB 264 CDKFSGHPRGRAY 276
 RESULT 6
 AB034750
 ID AB034750 standard; protein; 365 AA.
 XX AC AB034750;
 XX 22-SEP-2003 (first entry)
 DT Fragment #68 of a human secreted protein.
 DE
 XX Human; secreted protein; hyperproliferative disorder; leukaemia;
 KW breast cancer; wound; reproductive disorder; blood-related disorder;
 KW haemophilia; thrombocytopaenia; immunodeficiency; thymic hypoplasia;
 KW Wiskott-Aldrich syndrome; autoimmune disorder; multiple sclerosis;
 KW graft-versus-host disease; Hashimoto's thyroiditis; allergy; asthma;
 KW viral infection; bacterial infection; fungal infection; AIDS; sepsis;
 KW renal disorder; kidney failure; cardiovascular disorder; cytostatic;
 KW angina pectoris; cerebral ischaemia; congenital heart defect;
 KW respiratory disorder; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; inflammation; Crohn's disease; vulvovaginitis;
 KW immunosuppressive; antibacterial; haemostatic; thrombolytic;
 KW anticoagulant; neuroprotective; thyromimetic; antiallergic;
 KW antiparkinsonian; virucide; fungicide; anti-HIV; nephroprotective; antidiabetic;
 KW antineoplastic; cardiant; nootropic; antiparkinsonian;
 KW antineoplastic; cardiant; nootropic; antiparkinsonian;
 XX Homo sapiens.
 OS
 PN US2003049618-A1.
 XX
 PD 13-MAR-2003.
 XX
 PF 16-MAR-2001; 2001US-00809391.
 XX
 PR 07-MAR-1997; 97US-0038621P.
 PR 07-MAR-1997; 97US-0040162P.
 PR 07-MAR-1997; 97US-0040163P.
 PR 07-MAR-1997; 97US-0040333P.
 PR 07-MAR-1997; 97US-0040334P.
 PR 07-MAR-1997; 97US-0040336P.
 PR 07-MAR-1997; 97US-0040626P.

CC multiple sclerosis or Hashimoto's thyroiditis), allergies (e.g. asthma),
 CC viral or bacterial or fungal infections (e.g. AIDS or sepsis), renal
 CC disorders (e.g. kidney failure), cardiovascular disorders (e.g. angina
 CC pectoris, cerebral ischaemia or congenital heart defects), respiratory
 CC disorders, neurological disorders (e.g. Alzheimer's disease or
 CC Parkinson's disease), and inflammations (e.g. Crohn's disease). The
 CC polynucleotide or polypeptide may also be used as vaccine adjuvants.
 CC AB034374-AB034815 represent human secreted proteins or their fragments.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO web site at seqdata.uspto.gov/psipdsIDEntry.html
 XX
 XX Sequence 365 AA;

Query Match 55.0%; Score 44; DB 6; Length 365;
 Best Local Similarity 53.8%; Pred. No. 53;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
 DB 264 CDKFSGHKPGFAY 276

RESULT 7
 ABP62216
 ID ABP62216 standard; protein; 132 AA.
 XX
 AC ABP62216;
 XX
 DT 10-OCT-2002 (first entry)
 XX
 DE Human immunopeptide to HCV E2 glycoprotein Fab variable region #63.
 XX
 KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
 KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
 KW NS3 protein; viral infection.
 XX
 OS Homo sapiens.
 XX
 FN WO200259340-A1.
 XX
 PD 01-AUG-2002.
 XX
 PF 25-JAN-2002; 2002WO-US002303.
 XX
 PR 26-JAN-2001; 2001US-0264451P.
 XX
 PA (SCRI) SCRIPPS RES INST.

XX Maruyama T, Jones IM, Burton DR, Fox RI;
 XX WPI; 2002-599801/64.
 XX P-PSDB; ABQ92715, ABQ92416.
 XX
 XX New human immunopolypeptide with binding specificity for certain envelope
 PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
 PT diagnosing or treating patients having or suspected of having HCV
 PT infection.
 XX
 PS Claim 10; Fig 12; 308pp; English.

XX The present invention relates to human immunopolypeptides, produced by a
 CC phage transfected cell library. The present sequence is one such
 CC immunopolypeptide. The immunopolypeptides have binding specificity for
 CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
 CC virus (HCV). E2 glycoprotein is believed to be responsible for target
 CC cell binding and contains neutralising epitopes, while NS3 is thought to
 CC be involved in the replication of HCV. The immunopolypeptides are useful
 CC for diagnosing and treating a patient having or suspected to be having
 CC HCV infection

XX Sequence 132 AA;

Query Match 52.5%; Score 42; DB 5; Length 132;
 Best Local Similarity 63.6%; Pred. No. 39;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGF 11
 DB 87 CQYGDSPVGF 97

RESULT 8
 ABR82455
 ID ABR82455 standard; protein; 583 AA.
 XX
 AC ABR82455;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE FACLLABE related M. tuberculosis protein (Q10976).
 XX
 KW Fatty acid CoA ligase-like AMP-binding enzyme; FACLLABE; neuroprotective;
 KW nontropic; antiparkinsonian; gastrointestinal; cardiant; hypotensive;
 KW anticulcer; antiinflammatory; cytostatic; cardiovascular; analgesic;
 KW anorectic; antidiabetic; immunosuppressive; nephrotropic; gene therapy;
 KW chromosome 10; enzyme.
 XX
 OS Mycobacterium tuberculosis.

XX
 XX WO2003060129-A1.
 XX
 PD 24-JUL-2003.
 XX
 PF 15-JAN-2003; 2003WO-EP000314.
 XX
 PR 16-JAN-2002; 2002US-0348386P.
 PR 27-AUG-2002; 2002US-0406042P.
 XX
 PA (FARB) BAYER AG.

XX Zhu Z;
 XX WPI; 2003-598535/56.
 XX
 XX

XX New genes and encoded fatty acid CoA ligase-like AMP-binding enzyme
 PT (FACLLABE), useful for identifying modulators of FACLLABE activity, and
 PT in gene therapy for treating e.g. Alzheimer's disease, obesity, diabetes
 PT or ischemia.
 XX

PS Disclosure; Page 156-158; 173pp; English.

XX The invention relates to an isolated polynucleotide, which encodes a
 CC fatty acid CoA ligase-like AMP-binding enzyme (FACLLABE) polypeptide. The
 CC FACLLABE polynucleotide and polypeptide are useful for identifying test
 CC compounds, which may act as agonists or antagonists at the receptor site
 CC and which can be regulated to provide therapeutic effects. The vectors
 CC comprising the polynucleotide and the reagents are useful for modulating
 CC the activity of FACLLABE in a disease, e.g. obesity, diabetes, a central
 CC nervous system disorder, a gastrointestinal disorder, cancer, a
 CC cardiovascular disorder, or a genitourinary disorder. These diseases
 CC include Alzheimer's disease, Parkinson's disease, pain, colon tumor, pre-
 CC esophageal dysphagia, gastritis, ulcers, lymphoma, Kaposi's sarcoma,
 CC urinary incontinence, pelvic pain, lupus nephritis, erectile dysfunction,
 CC ovary tumor, lung tumor, thyroid tumor, carcinoma, congestive heart
 CC failure, myocardial infarction, ischaemia, and hypertensive vascular
 CC diseases. These are also useful for preventing or ameliorating the above
 CC mentioned diseases. Sequences ABR82455-47 represent FACLLABE related
 CC protein sequences

XX Sequence 583 AA;

Query Match 52.5%; Score 42; DB 6; Length 583;
 Best Local Similarity 77.8%; Pred. No. 1.8e+02;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

Qy      4 YGNSPKGFA 12
Db      30 YGSDPKGFA 38

RESULT 9
ABR83540
ID ABR83540 standard; protein; 583 AA.
XX AC ABR83540;
XX DT 14-OCT-2003 (first entry)
XX DE M. tuberculosis putative fatty acid-CoA ligase fadD26 SEQ ID NO:4.
XX KW Human; fatty acid CoA ligase-like AMP-binding enzyme; enzyme; nootropic;
XX KW neuroprotective; analgesic; antiparkinsonian; haemostatic; antianaemic;
XX KW immunostimulant; anorectic; antidiabetic; gene therapy; obesity; anaemia;
XX KW diabetes; haematological disorder; central nervous system disorder;
XX KW neutropaenia; thrombocytopaenia; Alzheimer's disease; pain;
XX KW Parkinson's disease.
XX OS Mycobacterium tuberculosis.
XX PN WO2003057867-A2.
XX PR 17-JUL-2003.
XX PF 09-JAN-2003; 2003WO-EP000140.
XX PR 10-JAN-2002; 2002US-0346602P.
XX PR 23-AUG-2002; 2002US-0405289P.
XX PA (FARB ) BAYER AG.
XX PI Xiao Y;
XX WPI; 2003-587123/55.
XX PT New genes and its encoded fatty acid CoA ligase-like AMP-binding enzyme
XX PT (FACIAMP-BE), useful for identifying modulators of FACIAMP-BE activity,
XX PT and in gene therapy for treating e.g. obesity, diabetes, anemia,
XX PT Alzheimer's or pain.
XX PS Disclosure; Page 112-114; 127pp; English.
XX CC The present invention describes a human fatty acid CoA ligase-like AMP-
XX CC binding enzyme (I). (I) has nootropic, neuroprotective, analgesic,
XX CC antiparkinsonian, haemostatic, antianaemic, immunostimulant, anorectic
XX CC and antidiabetic, and can be used in gene therapy. (I) polynucleotides
XX CC and polypeptides can be used for identifying test compounds, that may act
XX CC as agonists or antagonists at the receptor site and which can be
XX CC regulated to provide therapeutic effects. Vectors comprising the
XX CC polynucleotide can be used in the preparation of a medicament for
XX CC modulating the activity of (I) in a disease, particularly obesity,
XX CC diabetes, a haematological disorder or a central nervous system (CNS)
XX CC disorder. In particular, these are useful for treating anaemia,
XX CC neutropaenia, thrombocytopaenia, Alzheimer's disease, Parkinson's disease
XX CC and pain. The present sequence represents a Mycobacterium tuberculosis
XX CC putative fatty acid-CoA ligase fadD26 (acyl-CoA synthetase), which is
XX CC given in comparison with (I) in the present invention
XX SQ Sequence 583 AA;

Query Match 52.5%; Score 42; DB 7; Length 583;
Best Local Similarity 77.8%; Pred. No. 1.8e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 YGNSPKGFA 12
Db      30 YGSDPKGFA 38

RESULT 10
AAB66460
ID AAB66460 standard; protein; 626 AA.
XX AC AAB66460;
XX DT 09-APR-2001 (first entry)
XX DE Protein encoded by Mycobacterium tuberculosis fad26 (RV2930) gene.
XX KW Mycobacterium tuberculosis; attenuated microorganism; fad26; RV2930;
XX KW signature tagged transposon mutant; mutant library;
XX KW mycobacterial infection; actinomycetales; antibacterial; immunostimulant;
XX KW vaccine.
XX OS Mycobacterium tuberculosis.
XX PN WO200102555-A1.
XX PR 11-JAN-2001.
XX PF 06-JUL-2000; 2000WO-IB000950.
XX PR 06-JUL-1999; 99US-0142982P.
XX PR 08-JUL-1999; 99US-0142833P.
XX PA (INSP ) INST PASTEUR.
XX PI Gicquel B, Guilhot C, Camacho L;
XX WPI; 2001-091804/10.
XX PR N-PSDB; AAF31827.
XX PT Screening a mutant library for mutants unable to grow under specific
XX PT conditions and for identifying loci involved in pathogenicity, comprises
XX PT using signature tagged transposon mutagenesis.
XX PS Example 8; Fig 5A; 159pp; English.
XX CC The present sequence is given in a specification relating to a method for
XX CC screening a library of mutants. The method comprises constructing a
XX CC library with insertions in genes and/or regulatory regions of the
XX CC organisms of interest, where the insertion contains a tag and/or a
XX CC transposon associated with a tag. The mutants are identified by
XX CC hybridisation of the tags to known sequences. The method is useful for
XX CC treating an individual suffering from a mycobacterial infection,
XX CC suspected of being infected with a Mycobacterium, or having been exposed
XX CC to an infectious Mycobacterium. It is also useful for identifying and
XX CC isolating mutants of actinomycetales and for identifying compounds that
XX CC have antibiotic activity. The method is used to identify mutants of
XX CC microorganisms, preferably an actinomycetales, such as M. tuberculosis,
XX CC M. bovis, M. leprae, M. avium, M. intracellulare and M.
XX CC paratuberculosis, that is unable to grow under specific conditions. It is
XX CC especially useful for identifying loci involved in pathogenicity. It is
XX CC useful in constructing vaccines. The method can be used to screen
XX CC multiple libraries concurrently. It can screen libraries of different
XX CC organisms or different strains of the same organism. The present protein
XX CC is encoded by a gene which is disrupted by the insertion of the IS 1095
XX CC transposon to produce an attenuated mutant of Mycobacterium tuberculosis
XX SQ Sequence 626 AA;

Query Match 52.5%; Score 42; DB 4; Length 626;
Best Local Similarity 77.8%; Pred. No. 2e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      4 YGNSPKGFA 12
Db      73 YGSDPKGFA 81

RESULT 11
AEM15850

```

ID ABM15850 standard; protein; 429 AA.
 XX AC ABM15850;
 XX DT 26-SEP-2003 (first entry)
 XX DE Mycobacterium tuberculosis mycobacterial antigen protein SEQ ID NO:65.
 XX KW Mycobacterium tuberculosis; mycobacterial; antigen; infection; vaccine;
 XX KW tuberculostatic; mycobacterial peptide; mycobacterial infection.
 XX OS Mycobacterium tuberculosis.
 XX PN WO2003033530-A2.
 XX PD 24-APR-2003.
 XX PF 14-OCT-2002; 2002WO-GB004647.
 XX PR 12-OCT-2001; 2001GB-00024593.
 XX PA (MTCR-) MICROBIOLOGICAL RES AUTHORITY.
 XX PI James B, Bacon J, March P;
 XX DR WPI; 2003-393501/37.
 XX DR N-PSDB; ACF39344.
 XX PT New isolated mycobacterial peptide encoded by a gene that is induced or
 PT up-regulated under high oxygen tension, useful for diagnosing, treating
 PT or preventing a mycobacterial infection.
 XX PS Claim 1; Page 160-162; 392pp; English.
 XX CC The present invention describes an isolated mycobacterial peptide (I), or
 CC its fragment, variant or derivative encoded by a gene whose expression is
 CC induced or up-regulated during culture of a mycobacterium under
 CC continuous culture conditions of a dissolved oxygen tension of at least
 CC 30% air saturation measured at 37 plus degrees Celsius when compared with
 CC a dissolved oxygen tension of up to 10% air saturation measured at 37
 CC plus degrees Celsius. (I) has tuberculostatic activity and can be used in
 CC vaccines. The mycobacterial peptide (I) or its fragment, variant or
 CC derivative, inhibitor, antibody, attenuated mycobacterium, attenuated
 CC microbial carrier, DNA sequence, DNA plasmid, RNA sequence, or RNA vector
 CC from the present invention can be used for manufacturing a medicament for
 CC treating or preventing a mycobacterial infection. The peptide or its
 CC fragment, variant or derivative, the antibody, or a polynucleotide probe
 CC comprising at least 8 nucleotides, where the probe binds to at least a
 CC part of the gene, is useful for manufacturing a diagnostic reagent for
 CC identifying a mycobacterial infection. The present sequence represents a
 CC Mycobacterium tuberculosis mycobacterial antigen, which is used in the
 CC exemplification of the present invention
 XX SQ Sequence 429 AA;
 Query Match 51.2%; Score 41; DB 6; Length 429;
 Best Local Similarity 53.8%; Pred. No. 2e+02;
 Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CXXYGNSPKGFAY 13
 DB 88 CSSAGNHAQGFAY 100
 RESULT 12
 ID ABB64427
 XX ABB64427 standard; protein; 2515 AA.
 XX AC ABB64427;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 20073.

XX KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200171042-A2.
 XX PD 27-SEP-2001.
 XX PF 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 XX PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-656860/75.
 XX DR N-PSDB; ABL08530.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.
 XX PS Disclosure; SEQ ID NO 20073; 21pp + Sequence Listing; English.
 XX CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABBS57737-
 CC ABB2702). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX SQ Sequence 2515 AA;
 Query Match 51.2%; Score 41; DB 4; Length 2515;
 Best Local Similarity 87.5%; Pred. No. 1.3e+03;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 YGNSPKGF 11
 DB 2171 YGNSPKSF 2178
 RESULT 13
 ID ABG76564
 XX ABG76564 standard; protein; 107 AA.
 XX AC ABG76564;
 XX DT 05-NOV-2002 (first entry)
 XX DE HCV E1 antigen monoclonal antibody #52.
 XX KW Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
 KW hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
 XX OS Homo sapiens.
 XX PN WO200260954-A1.
 XX PD 08-AUG-2002.
 XX PF 14-JAN-2002; 2002WO-SE000044.
 XX PR 12-JAN-2001; 2001US-0260889P.
 XX

PA (KARO-) KAROLINSKA INNOVATIONS AB.
PI Drakenberg K, Persson MAA;
XX
DR WPI; 2002-608502/65.
XX
PT Vaccine comprising a human monoclonal antibody against hepatitis C virus
PT (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
XX
PS Disclosure; Page 56; 64pp; English.
XX
CC The invention relates to a human monoclonal antibody or its antigen
CC binding fragments, which exhibit immunological binding affinity for a
CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
CC homologous to the binding portion of a human antibody Fab molecule from a
CC combinatorial antibody library. The vaccine composition comprising the
CC antibodies or antigen binding fragments against HCV E1 or E2 antigen or
CC its hypervariable region is useful in treating or preventing HCV
CC infection in a subject. Sequences ABG76513-ABG76568 represent human
CC monoclonal antibodies against HCV E1 antigen
XX
SQ Sequence 107 AA;

Query Match 50.0%; Score 40; DB 5; Length 107;
Best Local Similarity 63.6%; Pred. No. 66;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGF 11
DB 88 CQRYGTSPKTF 98

RESULT 14
ABP62206
ID ABP62206 standard; protein; 136 AA.
XX
AC ABP62206;
XX
DT 10-OCT-2002 (first entry)
XX
DE Human immunopeptide to HCV E2 glycoprotein Fab variable region #53.
XX
KW Virucide; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KW nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KW NS3 protein; viral infection.
XX
OS Homo sapiens.
XX
PN WO200259340-A1.
XX
FD 01-AUG-2002.
XX
XX 25-JAN-2002; 2002WO-US002303.
XX
XX 26-JAN-2001; 2001US-0264451P.
XX
PA (SRI) SRIIPS RES INST.
XX
PI Maruyama T, Jones IM, Burton DR, Fox RI;
XX
XX WPI; 2002-599801/64.
XX
XX N-PSDB; ABQ92705.
XX
XX New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
XX Claim 10; Fig 12; 308pp; English.
XX
XX The present invention relates to human immunopolypeptides, produced by a
CC phage transfected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for

CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralising epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection
XX
SQ Sequence 136 AA;

Query Match 50.0%; Score 40; DB 5; Length 136;
Best Local Similarity 46.2%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
DB 89 CQCYGSPPGYTF 101

RESULT 15
ABP43671
ID ABP43671 standard; protein; 261 AA.
XX
AC ABP43671;
XX
DT 26-FEB-2003 (first entry)
XX
DE Methionine adenosyltransferase II alpha clone MGC:2907.
XX
KW Neuroprotective; immunomodulator; cancer; chromosome 2p11.2; cytostatic;
KW anti-inflammatory; gene therapy; nutritional supplement; wound; burn;
KW ulcer; Alzheimer's disease; Huntington's disease;
KW amyotrophic lateral sclerosis; autoimmune disorder; inflammation;
KW vulnary.
XX
XX Homo sapiens.
XX
XX WO200231111-A2.
XX
XX 18-APR-2002.
XX
XX 11-OCT-2001; 2001WO-US027760.
XX
XX 12-OCT-2000; 2000US-00687527.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX
XX Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX
XX WPI; 2002-426278/45.
XX
XX N-PSDB; ABQ60915.
XX
XX New polypeptides and their encoded proteins, useful as nutritional
PT sources or supplements, or in gene therapy, particularly for treating
PT wounds, Alzheimer's disease, amyotrophic lateral sclerosis, cancer or
PT inflammation.
XX
XX Claim 20; SEQ ID # 574; 357pp + Sequence Listing; English.
XX
XX The invention relates to 446 newly isolated polynucleotide sequences. The
CC activity of polynucleotides of the invention may be described as,
CC vulnary, neuroprotective, immunomodulator, cytostatic and anti-
CC inflammatory. Compositions comprising nucleic acids of the invention are
CC useful for treating a mammalian subject, or as nutritional sources or
CC supplements. These are useful in gene therapy, particularly for treating
CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC inflammation. The nucleic acids and polypeptides are also useful in
CC diagnostic and research methods. The sequences given in records ABP43544-
CC ABP43989 represent polypeptides encoded by polynucleotides of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX
SQ Sequence 261 AA;
Query Match 50.0%; Score 40; DB 5; Length 261;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 4 YGNSPKGFAYXXC 16
| : |||||
Db 92 YDSSKGFYKTC 104

Search completed: July 29, 2004, 08:46:40
Job time : 6.9295 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 29, 2004, 08:50:28 ; Search time 3.92689 Seconds
(without alignments)
1278.091 Million cell updates/sec

Title: US-09-661-992B-105

Perfect score: 80

Sequence: 1 CXYGNSPKGFAYXXC 16

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	44	55.0	249	14	US-10-153-668-118
2	44	55.0	306	14	Sequence 118, App
3	44	55.0	365	10	US-10-153-668-120
4	44	55.0	365	10	Sequence 120, App
5	44	55.0	365	10	US-09-809-391-696
6	44	55.0	365	12	Sequence 696, App
7	42	52.5	503	16	US-09-882-171-696
8	42	52.5	503	16	Sequence 696, App
9	40	50.0	289	15	US-10-424-599-160543
10	40	50.0	382	15	Sequence 160543, App
11	40	50.0	382	15	Sequence 160543, App
12	40	50.0	382	15	Sequence 160543, App
13	40	50.0	404	15	Sequence 160543, App
14	40	50.0	404	15	Sequence 160543, App
15	40	50.0	439	15	Sequence 160543, App

Query Match 55.0%; Score 44; DB 14; Length 249;
Best Local Similarity 53.8%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXYGNSPKGFAY 13

16	39	48.8	86	16	US-10-437-963-115600	Sequence 115600,
17	39	48.8	117	12	US-10-424-599-250560	Sequence 250560,
18	39	48.8	239	12	US-10-425-114-51772	Sequence 51772, A
19	39	48.8	343	12	US-10-424-599-250558	Sequence 250558,
20	39	48.8	401	12	US-10-282-122A-77312	Sequence 77312, A
21	38	47.5	75	16	US-10-437-963-138231	Sequence 138231,
22	38	47.5	84	12	US-10-424-599-267874	Sequence 267874,
23	38	47.5	91	16	US-10-038-591-22	Sequence 22, Appl
24	38	47.5	105	9	US-09-828-708-3	Sequence 3, Appli
25	38	47.5	105	9	US-09-828-708-7	Sequence 7, Appli
26	38	47.5	107	8	US-08-844-215-10	Sequence 10, Appl
27	38	47.5	108	12	US-10-180-648-14	Sequence 14, Appl
28	38	47.5	108	14	US-10-269-805-32	Sequence 32, Appl
29	38	47.5	108	14	US-10-269-805-36	Sequence 36, Appl
30	38	47.5	108	16	US-10-663-244-9	Sequence 9, Appli
31	38	47.5	109	12	US-10-371-942-24	Sequence 24, Appl
32	38	47.5	109	12	US-10-371-942-64	Sequence 64, Appl
33	38	47.5	211	9	US-09-764-903-39	Sequence 39, Appl
34	38	47.5	235	12	US-10-180-648-4	Sequence 4, Appli
35	38	47.5	351	9	US-09-978-295A-226	Sequence 226, App
36	38	47.5	351	9	US-09-978-697-226	Sequence 226, App
37	38	47.5	351	9	US-09-978-192A-226	Sequence 226, App
38	38	47.5	351	9	US-09-999-832A-226	Sequence 226, App
39	38	47.5	351	10	US-09-978-189-226	Sequence 226, App
40	38	47.5	351	10	US-09-978-608A-226	Sequence 226, App
41	38	47.5	351	10	US-09-978-585A-226	Sequence 226, App
42	38	47.5	351	10	US-09-978-191A-226	Sequence 226, App
43	38	47.5	351	10	US-09-978-403A-226	Sequence 226, App
44	38	47.5	351	10	US-09-978-564A-226	Sequence 226, App
45	38	47.5	351	10	US-09-999-833A-226	Sequence 226, App

ALIGNMENTS

RESULT 1
US-10-153-668-118
; Sequence 118, Application US/10153668
; Publication No. US20030092616A1
; GENERAL INFORMATION:
; APPLICANT: HONDA, Goichi
; APPLICANT: MATSUDA, Akio
; APPLICANT: MURAMATSU, Shuji
; APPLICANT: ISHIZAWA, Kenya
; TITLE OF INVENTION: STAT6 Activating Gene
; FILE REFERENCE: 1254-0207P
; CURRENT APPLICATION NUMBER: US/10/153,668
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/293,172
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/316,031
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/328,403
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: JP 2001-157043
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: JP 2001-260681
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: JP 2001-313175
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 488
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 118
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-668-118

Db 148 CDKFSGHKPGFAY 160

RESULT 2

US-10-153-668-120

; Sequence 120, Application US/10153668

; Publication No. US2003092616A1

; GENERAL INFORMATION:

; APPLICANT: HONDA, Goichi

; APPLICANT: MATSUDA, Akiio

; APPLICANT: MURAMATSU, Shuji

; APPLICANT: ISHIZAWA, Kenji

; TITLE OF INVENTION: STAT6 Activating Gene

; FILE REFERENCE: 1254-0207P

; CURRENT APPLICATION NUMBER: US/10/153,668

; CURRENT FILING DATE: 2002-05-24

; PRIOR APPLICATION NUMBER: US 60/293,172

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: US 60/316,031

; PRIOR FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: US 60/328,403

; PRIOR FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: JP 2001-157043

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: JP 2001-260681

; PRIOR FILING DATE: 2001-08-30

; PRIOR APPLICATION NUMBER: JP 2001-313175

; PRIOR FILING DATE: 2001-10-10

; NUMBER OF SEQ ID NOS: 488

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 120

; LENGTH: 306

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-153-668-120

Query Match 55.0%; Score 44; DB 14; Length 306;

Best Local Similarity 53.8%; Pred. No. 24;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13

Db 205 CDKFSGHKPGFAY 217

RESULT 3

US-09-809-391-696

; Sequence 696, Application US/09809391

; Publication No. US20030049618A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P2

; CURRENT APPLICATION NUMBER: US/09/809,391

; CURRENT FILING DATE: 2001-03-16

; Prior application data removed - consult PALM or file wrapper

; NUMBER OF SEQ ID NOS: 761

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 696

; LENGTH: 365

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-809-391-696

Query Match 55.0%; Score 44; DB 10; Length 365;

Best Local Similarity 53.8%; Pred. No. 28;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13

Db 264 CDKFSGHKPGFAY 276

RESULT 4

US-09-882-171-696

; Sequence 696, Application US/09882171

; Publication No. US20030175858A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: 186 Human Secreted proteins

; FILE REFERENCE: PZ002P2

; CURRENT APPLICATION NUMBER: US/09/882,171

; CURRENT FILING DATE: 2001-06-18

; PRIOR APPLICATION NUMBER: 09/809,391

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 09/149,476

; PRIOR FILING DATE: 1998-09-08

; PRIOR APPLICATION NUMBER: PCT/US98/04493

; PRIOR FILING DATE: 1998-03-06

; PRIOR APPLICATION NUMBER: 60/040,162

; PRIOR FILING DATE: 1997-03-07

; PRIOR APPLICATION NUMBER: 60/040,333

; PRIOR FILING DATE: 1997-03-07

; PRIOR APPLICATION NUMBER: 60/038,621

; PRIOR FILING DATE: 1997-03-07

; PRIOR APPLICATION NUMBER: 60/040,626

; PRIOR FILING DATE: 1997-03-07

; PRIOR APPLICATION NUMBER: 60/040,334

; PRIOR FILING DATE: 1997-03-07

; PRIOR APPLICATION NUMBER: 60/040,336

; PRIOR FILING DATE: 1997-03-07

; PRIOR APPLICATION NUMBER: 60/040,163

; PRIOR FILING DATE: 1997-03-07

; PRIOR APPLICATION NUMBER: 60/047,600

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,615

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,597

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,502

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,633

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,583

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,617

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,618

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,503

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,592

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,581

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,584

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,500

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,587

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,492

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,598

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,613

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,582

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,596

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,612

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,632

; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,601
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,580
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,568
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,314
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,569
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,311
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,671
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,674
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,669
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,312
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,313
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,672
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,315
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/048,974
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/055,886
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/055,877
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/055,889
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/055,893
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,630
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,878
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; PRIOR FILING DATE: 1997-08-22
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; PRIOR APPLICATION NUMBER: 60/055,882
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,637
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/055,903
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,888
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; PRIOR APPLICATION NUMBER: 60/056,879
; PRIOR FILING DATE: 1997-08-22
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; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,894
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/055,911
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/055,636
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,874
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,910
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,864
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/055,631
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,845
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,892

; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,761
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/047,595
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,599
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,588
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,585
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,586
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,590
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,594
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,589
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,593
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,614
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,578
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/043,576
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/047,501
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/043,670
; PRIOR FILING DATE: 1997-04-11
; PRIOR APPLICATION NUMBER: 60/056,632
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,664
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,876
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,881
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,909
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,875
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,862
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,887
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/056,908
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/048,964
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/057,650
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/056,884
; PRIOR FILING DATE: 1997-08-22
; PRIOR APPLICATION NUMBER: 60/057,669
; PRIOR FILING DATE: 1997-09-05

Query Match 55.0%; Score 44; DB 10; Length 365;
Best Local Similarity 53.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CXXYGNSPKGFAY 13
| : |||||
Db 264 CDKFGHPRKGFAY 276

RESULT 5

US-10-164-861-696
; Sequence 696, Application US/10164861
; Publication No. US20030225248A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002PI
; CURRENT APPLICATION NUMBER: US/10/164,861
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US/09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; NUMBER OF SEQ ID NOS: 757
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-164-861-696

Query Match 55.0%; Score 44; DB 12; Length 365;
Best Local Similarity 53.8%; Pred. No. 28;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
Db 264 CDKFSCHPKGFAY 276

RESULT 6

US-10-424-599-160543
; Sequence 160543, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 160543
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_WRT3847_11598C.1.pep
US-10-424-599-160543

Query Match 53.8%; Score 43; DB 12; Length 63;
Best Local Similarity 53.8%; Pred. No. 6.9;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
Db 43 CIOFGNHVKGIFY 55

RESULT 7

US-10-349-852-4
; Sequence 4, Application US/10349852
; Publication No. US20040076970A1
; GENERAL INFORMATION:
; APPLICANT: MacNicol, Angus, M.
; TITLE OF INVENTION: Human Cytoplasmic Polyadenylation Element Binding
; FILE REFERENCE: D6443
; CURRENT APPLICATION NUMBER: US/10/349,852
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 60/351,121
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 4
; LENGTH: 503

; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARSPLIC
; OTHER INFORMATION: sequence of the short form of cytoplasmic
; OTHER INFORMATION: polyadenylation element binding protein
US-10-349-852-4

Query Match 52.5%; Score 42; DB 16; Length 503;
Best Local Similarity 53.8%; Pred. No. 87;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
Db 288 CPPKGNMPKGYVY 300

RESULT 8

US-10-349-852-3
; Sequence 3, Application US/10349852
; Publication No. US20040076970A1
; GENERAL INFORMATION:
; APPLICANT: MacNicol, Angus, M.
; TITLE OF INVENTION: Human Cytoplasmic Polyadenylation Element Binding
; FILE REFERENCE: D6443
; CURRENT APPLICATION NUMBER: US/10/349,852
; CURRENT FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US 60/351,121
; PRIOR FILING DATE: 2002-01-23
; NUMBER OF SEQ ID NOS: 16
; SEQ ID NO 3
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARSPLIC
; OTHER INFORMATION: sequence of the long form of cytoplasmic
; OTHER INFORMATION: polyadenylation element binding protein
US-10-349-852-3

Query Match 52.5%; Score 42; DB 16; Length 566;
Best Local Similarity 53.8%; Pred. No. 98;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 CXXYGNSPKGFAY 13
Db 351 CPPKGNMPKGYVY 363

RESULT 9

US-10-369-493-12486
; Sequence 12486, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 12486
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Aspergillus nidulans
; FEATURE:

; NAME/KEY: unsure
; LOCATION: (1)..(289)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-12486

Query Match 50.0%; Score 40; DB 15; Length 289;
Best Local Similarity 53.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
| : | | | | | | | |
Db 114 YDSEKGFYKTC 126

RESULT 10

; US-10-369-493-22332
; Sequence 22332, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22332
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-22332

Query Match 50.0%; Score 40; DB 15; Length 382;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
| : | | | | | | | |
Db 79 YDSAKGFYKTC 91

RESULT 11

; US-10-369-493-22594
; Sequence 22594, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 22594
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-22594

Query Match 50.0%; Score 40; DB 15; Length 382;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;

Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 4 YGNSPKGFAYXXC 16
| : | | | | | | | |
Db 79 YDSEKGFYKTC 91

RESULT 12

; US-10-369-493-1699
; Sequence 1699, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1699
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1699

Query Match 50.0%; Score 40; DB 15; Length 384;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
| : | | | | | | | |
Db 81 YDSAKGFYKTC 93

RESULT 13

; US-10-369-493-6000
; Sequence 6000, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6000
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6000

Query Match 50.0%; Score 40; DB 15; Length 404;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
| : | | | | | | | |
Db 80 YDSKGFYKTC 92

RESULT 14
US-10-369-493-6001
; Sequence 6001, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6001
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6001

Query Match 50.0%; Score 40; DB 15; Length 404;
Best Local Similarity 53.8%; Pred. No. 1.5e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
DB 80 YDDSSKGFYKTC 92

RESULT 15
US-10-369-493-3733
; Sequence 3733, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 3733
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Neurospora crassa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(439)
; OTHER INFORMATION: unsure at all Xaa locations
US-10-369-493-3733

Query Match 50.0%; Score 40; DB 15; Length 439;
Best Local Similarity 53.8%; Pred. No. 1.7e+02;
Matches 7; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 4 YGNSPKGFAYXXC 16
DB 113 YDDSSKGFYKTC 125

Search completed: July 29, 2004, 09:12:27
Job time : 3.92689 secs